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TASK BOOK ON THE COURSE OF BASIC AND MEDICAL GENETICS

EDUCATIONAL AND METHODOLOGICAL MANUAL

TOMSK
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The collection presents problems that consider the molecular basis of heredity and variability (DNA replication, transcription, properties of the genetic code, protein biosynthesis), the interaction of allelic genes (complete and incomplete dominance, co-dominance), the interaction of non-allelic genes (complementation, epistasis, polymery), multiple allelism, pleiotropy and modifier genes, penetrance and expressiveness, linked inheritance of traits (including coupling with gender), crossing and genetic mapping, genealogical, twin and population-statistical methods of genetics.

The educational and methodological manual is intended for students at medical universities who master the core academic programs of the specialty "General medicine" of the English-medium academic program.

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СБОРНИК ЗАДАЧ ПО ОБЩЕЙ И МЕДИЦИНСКОЙ ГЕНЕТИКЕ

УЧЕБНО-МЕТОДИЧЕСКОЕ ПОСОБИЕ

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В сборнике представлены задачи, рассматривающие молекулярные основы наследственности и изменчивости (репликация ДНК, транскрипция, свойства генетического кода, биосинтез белка), взаимодействие аллельных генов (полное и неполное доминирование, кодоминирование), взаимодействие неаллельных генов (комплементарность, эпистаз, полимерия), множественный аллелизм, плейотропию и гены-модификаторы, пенетрантность и экспрессивность, сцепленное наследование признаков (в том числе сцепление с полом), кроссинговер и генетическое картирование, генеалогический, близнецовый и популяционно-статистический методы генетики.

Учебно-методическое пособие предназначено для студентов медицинских вузов, осваивающих основную образовательную программу специалитета «Лечебное дело» на английском и русском языках.

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CONTENTS

INTRODUCTION

In less than 120 years after the second discovery of Mendel's laws, genetics developed from a natural philosophical understanding of the principles of heredity and variability through an experimental accumulation of facts of formal genetics to a molecular biological understanding of the essence of the gene, its structure and function. Previously, the gene was first discussed as an abstract unit of heredity.

Understanding the material nature of a gene as a fragment of the DNA molecule that encodes the amino acid structure of a protein served as the basis for the development of cellular and molecular biology. Modern achievements in this field have made it possible to clone individual genes and create detailed genetic maps of human chromosomes.

Molecular genetic research methods, based on the polymerase chain reaction, allow us to identify genes whose mutations are associated with severe hereditary diseases. Methods of biotechnology and genetic engineering allow us to produce organisms with specified hereditary characteristics. At present, it has become possible to talk about the so-called gene therapy of inherited and acquired diseases with the aim of targeted correction of mutant human genes.

The foundations of general and medical genetics are an essential element of medical education since heredity and variability are universal properties of living organisms. The basic laws of genetics, which are of universal significance and are fully applicable to humans, are presented in this manual.

The solution of situational genetic problems allows us to consolidate knowledge about the patterns of inheritance of traits, about the main genetic laws and rules; allows us to confirm the statistical nature of the segregation of traits; demonstrates the possibility of mathematical calculation of variants by genotype and phenotype, which is carried out also to predict the onset of hereditary diseases in humans and their early diagnosis.

This collection presents problems that consider the molecular basis of heredity and variability (DNA replication, transcription, properties of the genetic code, protein biosynthesis), the interaction of allelic genes (complete and incomplete dominance, co-dominance), the interaction of non-allelic genes (complementation, epistasis, polymery), multiple allelism, pleiotropy and modifier genes, penetrance and expressiveness, linked inheritance of traits (including coupling with gender), crossing and

genetic mapping, genealogical, twin and population-statistical methods of genetics. The publication provides examples of solving problems for different variants of the interaction of genes, provides an interpretation of terms and concepts, interpretation of symbols used in basic and medical genetics.

The educational and methodological manual is for students of medical universities who master the core academic programs of the specialty "General Medicine" of the English-medium academic program.

1. MOLECULAR BASES OF HEREDITY AND VARIABILITY

The genetic code is common to most pro- and eukaryotes. Table 1 shows all 64 codons and the corresponding amino acids. The order of bases is from the 5' to 3' end of the mRNA. Table 2 shows deviations from the standard genetic code.

Table 1

Genetic code

		2nd base				**3rd base**
		U (Uracil)	**C (Cytosine)**	**A (Adenine)**	**G (Guanine)**	
1st base	**U**	UUU Phenylalanine UUC Phenylalanine UUA Leucine UUG Leucine	UCU Serine UCC Serine UCA Serine UCG Serine	UAU Tyrosine UAC Tyrosine UAA Ochre ***(Stop)*** UAG Amber ***(Stop)***	UGU Cysteine UGC Cysteine UGA Opal ***(Stop)*** UGG Tryptophan	**U** **C** **A** **G**
	C	CUU Leucine CUC Leucine CUA Leucine CUG Leucine	CCU Proline CCC Proline CCA Proline CCG Proline	CAU Histidine CAC Histidine CAA Glutamine CAG Glutamine	CGU Arginine CGC Arginine CGA Arginine CGG Arginine	**U** **C** **A** **G**
	A	AUU Isoleucine AUC Isoleucine AUA Isoleucine AUG Methionine, ***Start***	ACU Threonine ACC Threonine ACA Threonine ACG Threonine	AAU Asparagine AAC Asparagine AAA Lysine AAG Lysine	AGU Serine AGC Serine AGA Arginine AGG Arginine	**U** **C** **A** **G**
	G	GUU Valine GUC Valine GUA Valine GUG Valine	GCU Alanine GCC Alanine GCA Alanine GCG Alanine	GAU Aspartic acid GAC Aspartic acid GAA Glutamic acid кислота GAG Glutamic acid	GGU Glycine GGC Glycine GGA Glycine GGG Glycine	**U** **C** **A** **G**

Table 2

Deviations from the standard genetic code

Sample	Codon	Ordinary meaning	Deviation
Some types of yeast of the genus *Candida*	CUG	Leucine	Serine
Mitochondria, in *Saccharomyces cerevisiae*	CU (U,C,A,G)	Leucine	Serine
Mitochondria of higher plants	CGG	Arginine	Tryptophan
Mitochondria (in all studied organisms without exception)	UGA	Stop	Tryptophan
Mitochondria of mammals, Drosophila, S. cerevisiae and many protozoa	AUA	Isoleucine	Methionine = Start
Prokaryotes	GUG	Valine	Start
Eukaryotes (rare)	CUG	Leucine	Start
Eukaryotes (rare)	GUG	Valine	Start
Prokaryotes (rare)	UUG	Leucine	Start
Eukaryotes (rare)	ACG	Threonine	Start
The mitochondria of mammals	AGC, AGU	Serine	Stop
The mitochondria of Drosophila	AGA	Arginine	Stop
The mitochondria of mammals	AG (A,G)	Arginine	Stop

Task 1. A section of one of the strands of the deoxyribonucleic acid (DNA) molecule was studied in the research laboratory. It turned out that it consists of 24 monomers-nucleotides: GTG TAA CGA CCG ATA CTG TAC ACC...

Determine the structure of the corresponding section of the second strand of the same DNA molecule.

Task 2. The polypeptide chain of one animal protein has the following beginning: lysine – glutamine – threonine – alanine – alanine – alanine – lysine.

Determine the beginning of the nucleotide sequence for the gene corresponding to this protein.

Task 3. One of the chains of ribonuclease (a pancreatic enzyme) consists of 16 amino acids: Glu – Gly – Asp – Pro – Tyr – Val – Pro – Val – Pro – Val – His – Phe – Asn – Ala – Ser – Val.

Determine the structure of the section of DNA encoding this part of the ribonuclease.

Task 4. The small chain of monomers in the insulin molecule (chain A) ends with the following amino acids: leucine – tyrosine – asparagine – tyrosine – cysteine – asparagine.

Determine the sequence of DNA nucleotides that encode this chain of the molecule.

Task 5. It is known that the protein is encoded by the following sequence of DNA nucleotides: …TGA TGC GTT TAT GCG CCC...

Determine the order of amino acids in the section of the protein molecule.

Determine the changes in the protein if the ninth and thirteenth nucleotides are removed by chemical means.

Task 6. A section of a protein molecule is synthesized based on information encoded in the DNA molecule by the following order of nucleotides: …TCT CCC AAA AAG ATA GGG CAT...

Name the successive monomers of the protein molecule site.

Explain the consequence in the structure of the protein if there is a loss of the first nucleotide from the DNA molecule.

Task 7. In the mRNA, the last codon AAA is changed to UAA.

Specify the nucleotide that is replaced in the antisense strand of DNA and explain the result of such a replacement.

Task 8. In a person with cystinuria, amino acids are released in the urine, these amino acids correspond to the mRNA codons: CUU, GUU, CUG, GUG, UCG, GUC, AUA.

Alanine, serine, glutamic acid, and glycine are found in the urine of a healthy person.

Determine the allocation of which amino acids in the urine is characteristic of patients with cystinuria.

Task 9. It is known that the fourth peptide of hemoglobin **A** contains 8 amino acids in the following sequence: Val – His – Leu – Thr – Pro – Glu – Glu – Lys. In hemoglobin **S**, the sixth amino acid (glutamine) is replaced by valine, in hemoglobin **C** by lysine, and in hemoglobin **G**, the seventh amino acid (glutamine) is replaced by glycine.

Explain the result of a mutation in the section of DNA that controls the sequence of amino acids in the fourth peptide of hemoglobins, on the percentage of nitrogenous bases.

Task 10. The hemoglobin **A** molecule consists of two **α**- and two **β**-chains of polypeptides connected to the heme group (the iron-containing part of hemoglobin). Each chain contains about 140 amino acids.

Determine how many nucleotide pairs each section of the DNA molecule that controls the synthesis of these polypeptide chains contains.

Task 11. One nucleotide occupies 3.4 A (Angstrom) of the DNA strand. 1 A = 0.1 nm (nanometer) = 0.0001 microns (micrometer) = 0.0000001 mm = 0.00000000001 m.

Identify the length (in meters) of the section of DNA encoding the synthesis of insulin containing 51 amino acids in two chains.

Task 12. The initial section of the B-chain of insulin is represented by the following amino acids: Phe – Val – Asp – Gly – His – Leu – Cys – Leu – Cys – Gly – Ser – Lys.

Determine the quantitative ratios of A+T / G+C in the DNA strand encoding this section of DNA.

Task 13. The percentage of nucleotides in the mRNA strand is as follows: adenylic – 27%, guanylic – 35%, cytidylic – 18%, uracil – 20%.

Determine the percentage of nucleotides of the section of the DNA molecule (gene) that is the matrix for this mRNA.

Task 14. The distance between two neighboring nucleotides is equal to 3.4 A.

Determine the length of the section of the DNA molecule encoding myoglobin (muscle protein) in modern animals if myoglobin contains a single chain of 155 amino acids.

Task 15. It is known that the average molecular weight of a nucleotide is 340 Da.

Determine the molecular weight of the gene that controls the formation of the pancreatic ribonuclease protein consisting of 124 amino acids.

Task 16. The protein molecule is encoded by the following nucleotides of the DNA molecule: ... CAT AAG TTA CAT CGA ...

Write down the sequence of amino acids.

Name the sequence of amino acids in the protein molecule if between the second and third nucleotides there is an insertion of cytosine and thymine.

Task 17. The protein molecule contains 157 amino acids.

Determine the length of the controlling gene if it is known that the distance between two nucleotides in the DNA molecule is 3.4 Å.

Task 18. The protein molecule contains 491 amino acids.

Determine the length of the controlling gene if it is known that the distance between two nucleotides in the DNA molecule is 3.4 Å.

Task 19. The protein contains 658 amino acids.

Determine the length of the gene that controls its synthesis if the distance between the nucleotides in the DNA molecule is equal to 3.4 Å.

Task 20. The gene section has the following nucleotide composition: …TGG TCG CAG GAG GGG TTT....

Determine how the encoded composition of the amino acids will change if under the influence of ionizing radiation:

a) the 10th nucleotide on the left is knocked out;

b) the 10th, 11th and 12th nucleotides are knocked out.

Task 21. Due to the degeneracy of the genetic code, any amino acid in a protein molecule can be encoded not by one, but by two or four different triplets.

Encode the following sequence of amino acids: lysine – histidine – serine – glycine – tyrosine, using two different sets of triplets of the genetic code.

Task 22. In one of the strands of DNA molecules the nucleotides are arranged in the following sequence: …TAG AGT CCC GAC ACG...

Determine the sequence of nucleotides in another strand of the same molecule.

Task 23. The protein contains 400 amino acids.

Determine the length of the controlling gene if the distance between two nucleotides in the DNA molecule is $3.4 \cdot 10^{-4}$ μM.

Task 24. A section of the DNA strand is formed by self-replication from the template strand … CACCGTACAGAATCGCTGAT…

Specify the order of nucleotides.

Task 25. The following sequence is presented …AGGCCTAGGCTAATAGCCGT…

Write the sequence of DNA nucleotides that is complementary to the sequence specified in the task.

Task 26. A part of the DNA molecule was divided into short single-stranded fragments:

…TAGACTGGTACACGTGGTGA…,
…TAAATGCGGGCCCCTTT…,
…ATCTGGCCATGTGCACCAT…,
…ATCTGACCATGTGCACCACT…,
…TAGACTGGTACGGGTGA…,
…TAGACCGGTACACGTGGTA…

Specify which fragments can, under certain conditions, complementarily pair completely one more time, and which of them can do that partially.

Task 27. The larger of the two chains of the insulin protein (B-chain) begins with the residues of the following amino acids: phenylalanine, valine, asparagine, glutamic acid, histidine, and leucine.

Determine the nucleotide sequence of the section of the DNA molecule that stores information about the primary structure of the polypeptide.

Task 28. A section of the glucagon molecule has the following sequence of amino acid residues: Thr-Ser-Asp-Tyr-Ser-Lys-Tyr.

Specify the monomer sequence of the DNA molecule containing information about the sequence of amino acid residues in this section.

Task 29. The initial section of the polypeptide chain of ribonuclease has the following sequence of amino acid residues: Lys-Gln-Thr-Ala-Ala-Ala-Lys.

Specify the sequence of nucleotides that encode information about the primary structure of the initial ribonuclease site.

Task 30. A section of the polypeptide chain of a protein consists of the following sequence of amino acid residues: Pro-Val-Arg-Pro-Leu-Val-Arg.

Specify the sequence of DNA nucleotides that encode information about the primary structure of the section of the protein polypeptide chain.

Task 31. The gene site has the following structure: …CGGCGCTCAAAATCG...

Determine the primary structure of the polypeptide chain section, information about which this sequence of nucleotides contains.

Describe the changes in the primary structure of the protein when the fourth nucleotide on the left is removed from the section of the DNA strand.

Task 32. Information about a polypeptide chain section is encoded by the following sequence of DNA nucleotides: …TGATGCGTTTATGCGC...

Determine the order of amino acids in the specified part of the polypeptide chain.

Describe what changes will take place when the ninth and twelfth nucleotides from the DNA molecule on the left are removed.

Task 33. The sequence of amino acids is encoded by the following sequence of DNA nucleotides: …CCTAGTGTGAACCAG...

Specify the sequence of amino acids if thymidine monophosphate is inserted between the sixth and seventh nucleotides of the DNA sequence.

Task 34. It was found that uridine monophosphate accounts for 20% of the total number of nucleotides of informational RNA, with cytidine monophosphate – 26% and adenosine monophosphate – 24%.

Describe the nucleotide composition of the section of double-stranded DNA, the RNA was transcribed with one of the mentioned strands.

Task 35. Ionizing radiation can knock out individual nucleotides from the nucleic acid molecule without violating its integrity. Let us assume that in the first case only one nucleotide is removed from the molecule, in the second – three nucleotides in a row, and in the third – also three nucleotides, but located in different places.

Describe the changes in DNA that will affect the primary structure of the protein.

Specify the cases (out of these three) when the resulting polypeptide will differ as much as possible and as little as possible from the normal one.

Task 36. It is known that under the influence of nitrogenous acid, cytosine turns into guanine.

Identify the amino acid sequences for the section of the synthesized polypeptide after exposure to nitrogenous acid on the tobacco mosaic virus, if normally the protein molecule in this section consists of the residues of the following amino acids: serine, glycine, serine, isoleucine, threonine, proline, serine.

Task 37. The protein consists of 158 amino acid residues.

Determine the length of the gene (without introns) that stores information about the primary structure of this protein if the distance between two neighboring nucleotides in a helical DNA molecule, measured along the axis of the helix, is 0.34 nm.

Task 38. The nucleic acid of the phage has a molecular weight of about 10^7.

Calculate the approximate number of protein molecules the specified acid contains if it is known that a typical protein consists of an average of 400 monomers, and the molecular weight of a nucleotide is about 300 Da.

Task 39. Assuming that the average molecular weight of an amino acid is about 110 Da, and that of a nucleotide is about 300 Da.

Determine if the protein or gene that contains information about this protein is heavier.

Task 40. A sequence of five amino acid residues is presented: Pro-Lys-His-Val-Tyr.

Determine the number of variants that can encode the specified sequence using the genetic code.

Task 41. A polypeptide consists of the following amino acid residues: valine, alanine, glycine, lysine, tryptophan, valine, serine, and glutamic acid.

Determine the primary structure of the section of DNA containing information about this polypeptide.

Task 42. In the pancreatic ribonuclease molecule, a section of one of the polypeptides consists of the residues of the following amino acids: lysine, aspartic acid, glycine, threonine, aspartic acid, glutamic acid, and cysteine.

Determine the sequence of nucleotides of the mRNA site that served as a matrix for the synthesis of this polypeptide.

Task 43. Characteristic feature of the biochemical urinalysis of a patient with cystinuria is the determination of amino acids, which correspond to the following mRNA triplets: UCU, UGU, GCU, GGU, CAG, CGU, AAA.

In the urine of a healthy person, alanine, serine, glutamic acid and glycine are found.

Identify the DNA triplets that encode the amino acids present in the urine of a healthy person and a patient with cystinuria.

Task 44. The DNA section containing information about the primary structure of the protein is represented by the following sequence of nucleotides: …AATACATTTAAAGTC...

Describe changes in the primary structure of the protein if the fifth and twelfth nucleotides on the left are removed.

Task 45. The initial section of the B chain of the insulin molecule is represented by a sequence of ten amino acids: phenylalanine, valine, aspartic acid, glutamine, histidine, leucine, cysteine, glycine, serine, histidine.

Determine the structure of the DNA section encoding this part of the insulin chain.

Determine the ratio of A+T / G+C in the DNA strand containing information about this section of the insulin molecule.

Task 46. It is known that the distance between two neighboring nucleotides in a helical DNA molecule measured along the helix axis is 0.34 nm.

Determine the length of structural genes (without introns) containing information about the primary structure of one of the chains of the normal hemoglobin molecule, which includes 287 amino acid residues.

Task 47. It is known that the bovine insulin molecule consists of 51 monomers, and the distance between two neighboring nucleotides in DNA is 0.34 nm.

Identify the length for the gene (without introns) containing information about the sequence of amino acid residues in the bovine insulin molecule.

Task 48. In the aminoacyl section of the ribosome, tRNAs with the following anticodons were sequentially bound to mRNA codons: AAU, AUU, GUA, CCU.

Specify the amino acids from which the short oligopeptide was synthesized.

Task 49. A section of one of the DNA molecule strands has the following nucleotide composition: …AATTTCAGTACGTATTGCGCG.

Identify transcription and translation products.

Task 50. It was found that the initial section of the DNA molecule stores information about the sequence of residues of the following amino acids: valine, serine, proline, cysteine.

Determine the primary structure that has the initial section of the DNA molecule.

2. INTERACTION OF ALLELIC GENES

Algorithm for solving the task for monohybrid crossing

Task (case study). Positive Rh factor (Rh+) is determined by a dominant allele, and negative (Rh-) is recessive. A Rh-negative father and a Rh-positive mother had a Rh-negative child.

Determine the genotypes of the parents and child.

Explain the results.

The algorithm for solving the task is in table 3.

Table 3

Algorithm for solving the task for monohybrid cross

P	♀ **Rr**	×	♂ **rr**
G	**R, r**		**r**
F_1	**Rr, rr**		

Answer. R dominates r. The mother's genotype – Rr, the father's genotype – rr, and the child's genotype – rr.

Note: hereinafter, P – parents, F – generation (children), G – gametes, capital (R) – dominant trait; lowercase (r) – recessive trait.

Task 51. In yellow daisies, the center of the flower is usually purple. Plant breeders produced a mutant with a yellow center. First-generation hybrids from cross of a mutant plant with ordinary daisies had a purple center of the flower. Among 60 plants of the second generation, 14 had a mutant phenotype.

Explain the results of crossbreeding and determine the genotypes of plants of all generations.

Task 52. In oats, early maturing is determined by a dominant allele, and late maturing is determined by a recessive allele. At the experimental site, a large amount of seed material was obtained from crossing late-maturing oats with heterozygous early-maturing oats. Early maturing plants grew from 69,134 seeds.

Determine the theoretically expected number of late-maturing plants.

Task 53. The tomato fruits are round and pear-shaped. This pair of allelomorphs is determined by alleles of a single autosomal gene, and the development of round-shaped fruits is due to the presence of a fully dominant allele in the plant genotype. Seedlings obtained from seeds of hybrid plants are planted in greenhouses. 31,750 bushes had pear-shaped fruits, and 92,250 – round.

Identify the theoretically expected number of heterozygotes among plants in greenhouses.

Task 54. Albinism in plants is lethal, but in many species, it is quite often manifested in the offspring of normal plants.

Determine the type of inheritance for this trait.

Explain why albinos are not completely eliminated from the population if they die.

Task 55. The absence of stripes in watermelon fruits is a recessive trait, and the presence of stripes is dominant.

Specify the type of fruit maturing on heterozygous plants.

Specify what will be the fruit of descendants from crossing two heterozygous plants.

Task 56. Datura, which has purple flowers, after self-pollination gave 30 plants with purple and 9 plants with white flowers.

Draw conclusions about the genetic determination of the trait.

Specify which part of the resulting plants after self-pollination will only produce descendants with homogeneous phenotypes.

Task 57. After crossing the gray blowflies with each other, a new generation was produced, consisting of 1,392 gray blowflies and 467 black blowflies.

Specify the dominant trait. Determine the genotypes of the parents.

Task 58. After crossing common fruit flies (Drosophila), a new generation was produced with 25% of flies with smaller eyes. The latter were crossed with their parents and in this generation there were 37 flies with smaller eyes and 39 with normal eyes.

Determine the genotypes of common fruit flies crossed in both experiments.

Task 59. DDT[1]-resistant male cockroaches were crossed with insecticide-sensitive females. In the first generation, all individuals were resistant to DDT, and in the second generation there was a split – 5,768 DDT-resistant and 1,919 DDT-sensitive cockroaches.

Specify which part of the resistant individuals from F2 (when crossing with each other) will produce DDT-sensitive offspring.

Task 60. In four different crosses of carps with an abdominal fin and carps without a fin, the following results were obtained:

a) 96 individuals with a fin and 101 individuals without a fin;

b) 118 individuals with fin;

c) 20 individuals with fin;

d) 45 individuals with a fin and 39 individuals without a fin.

Specify the dominant trait.

Determine the genotypes of all the fish used for crossbreeding.

Task 61. From the crossing of red and gray varieties of char (Latin Salvelinus, a genus of salmonid fish) in the first generation, all the individuals were gray, and in the second – 214 gray and 81 red individuals.

Determine the genotypes of the parents and hybrids of the first generation.

Specify the theoretically expected number of red fish among 350 individuals of the second generation.

Task 62. In chickens, a rose comb dominates a simple one. The poultry breeder suspects that several of his Wyandotte chickens, which have a rose comb, may be heterozygous.

How can we establish heterozygosity and test this assumption?

Task 63. Two breeds of chickens were taken to obtain a new breed. The initial breeds have some desirable and some undesirable traits. The two breeds were taken in equal proportions. The undesirable trait of the first breed was feathered legs (dominant allele), the undesirable trait of the second breed was a leaf-like comb (recessive allele).

Specify which of the traits will be easier to get rid of when selecting a new breed – from the recessive allele of the leaf-like comb or the dominant allele of feathered legs.

[1] 1,1,1-Trichloro-2,2-di(p-chlorophenyl)ethane is an insecticide according to the IUPAC nomenclature, according to the rational nomenclature-Dichlorodiphenyltrichloroethane.

Task 64. After crossing white hens with a gray rooster, all the offspring turned out to be gray. From crossing these offspring again with white chickens, there were 172 individuals, of which 85 were gray.

Specify the dominant trait.

Determine the genotypes of parents and offspring.

Task 65. Two black female mice were crossed with a brown male. One female produced 20 black and 17 brown offspring, while the other produced 33 black offspring.

Based on the results of crossing, determine the dominant and recessive traits of color.

Establish the genotypes of parents and offspring.

Task 66. In Guinea pigs the allele for hairy fur is dominant over the allele for smooth fur. A rough-coated Guinea pig from several crosses with a smooth-coated male gave birth to 18 rough-coated and 20 smooth-coated offspring.

Establish the genotypes of parents and offspring.

Indicate whether it is possible for these Guinea pigs to produce only smooth-coated individuals.

Task 67. Horses have a hereditary disease of the larynx. When running, these horses have a characteristic wheeze. Healthy foals are often born from sick parents.

Determine if a dominant or recessive allele provides a manifestation of this disease.

Task 68. On the farm, 16 daughters of stallion 1 were bred with stallion 2. Five of 42 foals born had curly hair, which was never seen in related animals. The father of stallion 1 was the maternal grandfather, and the mother was the paternal grandmother of stallion 2.

Explain the appearance of curly hair.

Specify how many foals with normal hair should have been expected among the 42 offspring of stallion 1.

Specify how many foals with normal hair will have the allele of curly hair.

The breeder may like the offspring of stallion 2, but he will prefer those foals who do not have the allele of curly hair. Determine the probability of offspring of this stallion with normal hair not having the allele of curly hair.

Task 69. Mr. Smith purchased a bull from Mr. Brown for his herd of black-and-white Holstein Friesian cows and got 32 calves, of which 6 were red-and-white. Before that, there were no red-and-white animals in his herd. When he demanded that Mr. Brown return the money paid for the bull, Mr. Brown admitted partial responsibility, but said that it happened not only because of the bull.

Explain Mr. Smith's mistake. Give evidence to prove that the bull purchased from Mr. Brown is not the only factor.

If Mr. Brown's explanation is correct, and half the cows in Mr. Smith's herd were heterozygous.

Determine the number of heterozygous calves among the black-and-white calves.

Let us assume that Mr. Smith and Mr. Brown continue to do business, and both of them agree to solve a common problem.

Determine how you can use the resulting 6 red-and-white calves in the herd, three of which are female.

Find out if the cows that brought the red-and-white calves can be useful. Explain your answer.

Task 70. Black lear allele in cattle is dominant over the red lear allele.

Describe the offspring that will result from crossing a black purebred bull with red cows.

Describe the offspring that will result from crossing the first-generation hybrids.

Task 71. Polled cattle is dominant over hornedness. Polled bull Vaska crossed with three cows: Zorka, Burenka and Zvezdochka. The horned Zorka and polled Zvezdochka gave birth to horned calves. And horned Burenka gave birth to a polled calf.

Determine the genotypes of all animals.

Task 72. From crossing of a polled bull with horned cows, polled and horned calves were born. The cows had no polled animals in their pedigree.

Determine the genotypes of parents and offspring.

Task 73. Two consecutive years of the Siberian long-hair cat Murzik was interbred with a neighbor's cat Murka. In the first year, Murka had 5 kittens, among which there were three short-hair and two long-hair kittens,

in the second year Murka bore two long-hair and two short-hair kittens. It is known that cats are short-hair provided by the dominant allele.

Determine if Murka is long-hair or short-hair.

Explain the deviation of the practical segregation from the theoretical one.

Describe the offspring to be expected from interbreeding Murzik with a long-hair daughter.

Task 74. In one of the Indian zoos, an albino tiger cub was born to tigers of normal color. Albino tigers are extremely rare, and many zoos would happily purchase them.

Describe the options for interbreeding tigers from this family that should be used to quickly get the maximum number of albino cubs.

Task 75. In dogs, the dominant allele determines wire coat, while the recessive allele determines the silky one. Parents with wire coats have a puppy with wire coat.

Describe the interbreeding that needs to be done to find out whether the puppy has an allele in the genotype that provides the formation of silky coat.

Task 76. Irish setters may be blind as a result of a recessive allele of a single autosomal gene. A pair of animals with normal vision gave a litter of several puppies, one of which was blind.

Set the parents' genotypes.

Determine the probability of one of the sighted puppies has a recessive allele, if it is known that such a puppy from this litter is decided to leave for breeding.

Task 77. At the Royal Veterinary College in Stockholm, in Bjerke and elsewhere, cerebellar ataxia was studied in Fox Terriers, which was manifested in puppies at the age of 5-6 months. The disease was not deadly but caused a progressive mobility disorder of the affected dogs. Among 92 puppies born in 23 litters, the disease was found in 25 puppies of both sexes.

Conclude based on the presented data about the genetic condition of cerebellar ataxia.

Task 78. The recessive allele of an autosomal gene determines red hair color in humans.

Determine the probability that a dark-haired heterozygous mother and a red-haired father will have a red-haired son.

Task 79. The ability of a person to taste phenylthiocarbamide is a dominant trait. In a family, mother and daughter taste phenylthiocarbamide, but father and son do not.

Determine the genotypes of all family members.

Task 80. In humans, the allele that controls one of the forms of inherited deaf-muteness is recessive in relation to the allele of normal hearing. From the marriage of a deaf-mute woman with a normal man, a deaf-mute child was born.

Determine the genotypes of all family members.

Task 81. A white streak of hair in a person is a dominant trait.

Determine the genotypes of parents and children, if it is known that the mother has a white streak of hair, the father does not, and only one of the two children has a white streak.

Task 82. One form of schizophrenia is determined by a recessive allele of an autosomal gene.

Determine the probability of having a child with schizophrenia in healthy parents if it is known that the paternal grandmother and maternal grandfather suffered from this disease.

Task 83. Phenylketonuria[2] is a recessive trait that controls the allele of an autosomal gene. The wife is heterozygous, and the husband is homozygous for the normal allele of this gene.

Determine the probability of their having a sick child.

Task 84. Two parents with normal skin pigmentation had an albino child. The second child had normal pigmentation.

Determine the genotypes of parents and children.

Task 85. Petya and Sasha have brown eyes, while their sister Masha has blue eyes. The mother of these children is blue-eyed, although her

[2] A rare hereditary disease of the group of enzymes defects, associated with a violation of the metabolism of amino acids, mainly phenylalanine, is accompanied by the accumulation of phenylalanine and its toxic products, which leads to severe damage to the central nervous system, manifested, in particular, in the form of impaired mental development.

parents had brown eyes.

Determine the dominant trait.

Determine the father's eye color.

Determine the genotypes of all the listed individuals.

Task 86. Rh factor is determined by two alleles of the autosomal gene: positive – dominant (Rh+), negative – recessive (Rh-).

A) Husband and wife are Rh-positive.

Identify the child's Rh-negative inheritance.

Specify the genotypes of the parents.

B) The child is Rh-positive.

Specify the Rh factor of the child's parents.

Specify all possible genotypes of the parents.

Task 87. Polydactyly in humans is determined as an autosomal dominant. In a family where one parent has a normal structure of the hand, and another parent has got six fingers, a child with normal hands was born.

Determine the probability of the next child being born without disorders.

Task 88. In humans, the allele for brown eyes are completely dominant over the allele for blue eyes.

Determine the location of the blue eye allele if a woman, who is heterozygous for the eye color gene, the brown eye allele got into the ovum.

Identify the number of ovum types that are formed in this woman.

Determine the types of spermatozoa that are formed in a blue-eyed man.

Task 89. In humans, the dominant allele of a single gene determines a birth defect of the development of the skeleton – cleidocranial dysostosis (changes in the bones of the skull and poorly developed or absent collarbones).

A) A woman with a normal bone structure married a man with cleidocranial dysostosis. The child from this marriage has a normal skeleton structure.

Determine the father's genotype by analyzing the child's phenotype.

B) A woman with cleidocranial dysostosis married a man with a normal skeleton structure. The child inherited a skeletal defect from its mother.

Determine the mother's genotype by analyzing the child's phenotype.

C) Both parents suffer from cleidocranial dysostosis. The child from this marriage has a normal skeleton structure.

Determine the genotypes of both parents and the child.

Task 90. An infantile form of family idiocy[3] is a recessive autosomal trait. The disease is usually fatal by the age of four or five. The first child in the family died of this disease at the time when the second was due to be born.

Determine the probability that the second child will also have this disorder.

Task 91. Fusion of incisors in the lower jaw is a dominant trait. In the family, the firstborn was found to have fused incisors. Parents do not remember if they had this anomaly.

Determine all possible genotypes of parents.

Task 92. Myoplegia paroxysmalis (periodic paralysis) is a genetically inherited disease determined by the autosomal dominant.

Determine the probability of having children with this disease in a family where the father is heterozygous, and the mother does not suffer from myoplegia.

Task 93. In humans, the allele that determines the development of polydactyly dominates the allele responsible for the normal hand anatomy. In a family where one parent has a normal hand anatomy, and another parent has got six fingers, a child with a normal hand anatomy was born.

Determine the probability of having a second child without this disorder.

Task 94. Parahemophilia[4] (or Owren's disease) is a recessive autosomal trait.

Determine the probability of having children with this disease in a family where both spouses suffer from it.

Task 95. Late corneal degeneration (develops after the age of 50) is a dominant autosomal trait.

Determine the probability of occurrence of the disease in family

[3] The maximum degree of mental retardation, characterized by almost complete absence of speech and thinking.

[4] Genetic disease from the group of hemorrhagic diatheses caused by insufficient factor V of the blood clotting system; like hemophilia in clinical manifestations – severe bleeding with minor injuries).

members (parents and son), if it is known that the maternal grandparents and all their relatives who lived to 70 years old, suffered from this disease, and on the father's side, all the ancestors were healthy.

Task 96. Afibrinogenemia [5] is autosomal recessive. In a family of healthy parents, a child was born with signs of afibrinogenemia.

Determine the probability of having a second child with the same disease.

Task 97. Syndactyly (a condition wherein two or more digits are fused) is autosomal dominant.

Determine the probability of having children with fused digits in a family where one of the parents is heterozygous, and the other has a normal hand anatomy.

Task 98. In Mirabilis jalapa (or four o'clock flower), the red color of the corolla petals does not determine the fully dominant allele, and the white color is not completely recessive. Heterozygotes have pink flowers.

Specify the flowers from crossing two plants with pink flowers.

Specify the flowers from crossing two plants with pink and white flowers.

Explain why plants with pink flowers can only have descendants with pink flowers.

Task 99. After crossing plants of red and white varieties of fragaria (strawberries) received hybrid seeds. On hybrid plants, pink fruits are ripe. After crossing the plants with pink fruits among themselves, 1,600 seeds were collected.

Specify among them the theoretically expected number of seeds of plants with pink fruits.

Task 100. In one Japanese bean variety, self-pollination of a plant grown from a light-spotted seed produced 685 dark-spotted, 1,320 light-spotted, and 630 seeds without spots.

Describe the offspring that will result from crossing plants with dark-spotted seeds with a plant that has seeds without spots.

[5] The absence of plasma fibrinogen, which causes a complication of bleeding, which often ends in death, is associated with mutations in the genes of the fourth chromosome.

Task 101. Blue Andalusian hens[6] are heterozygous for the gene that determines the color of their plumage. Homozygous hens are white or black.

Specify the plumage color of chicks if a blue hen and a black rooster were interbred.

Specify the plumage color of chicks if a blue hen and a white rooster were interbred.

Task 102. A group of hens and an unknown rooster interbred, 1,250 chicks were born. 616 chicks have blue plumage, 314 chicks – white and 320 chicks – black.

Describe the trait determination if the individuals of the parent generation were genotypically homogeneous.

Task 103. In cattle of the Shorthorn breed, the allele of red color and the allele of white color jointly determine roan color in heterozygotes.

Specify the part of the individuals that will be roan from interbreeding two roan animals.

Task 104. In sheep, long-eared trait does not completely dominate earless one.

Describe the offspring that should be expected from interbreeding an earless ram with a long-eared bright sheep.

Task 105. Minks with light hair with a black cross on the back are obtained by interbreeding white minks with dark ones. When white minks interbreed the offspring have got white hair, dark minks interbreed the offspring have got dark hair.

Describe the hair of the offspring born from a mink with light hair and a black cross on the back with a white mink.

At the animal farm, the interbreeding of minks with light hair with a black cross on the back produced the following individuals: 74 white minks, 77 black minks and 152 minks with light hair with a black cross on the back.

Determine the number of homozygotes and what color they are.

Task 106. Innately tailless cat Murka from interbreeding with a normal cat gave birth to 5 kittens, all with short tails.

[6] Andalusian Blue – the breed of hens in Andalusia is also known as the "Andalusian blue" due to its color.

Determine the splitting along the length of the tails, which theoretically should be expected in kittens (F2), obtained from interbreeding between her descendants.

Task 107. The development of sickle cell disease (normal hemoglobin A is replaced with hemoglobin S) depends on the presence of an autosomal allele that is not completely dominant in the genotype. In people who are homozygous for this allele, the disease usually leads to death before puberty, heterozygotes are usually viable, and anemia in them is most often subclinical. Interestingly, the Plasmodium falciparum cannot use hemoglobin S for its nutrition, so people who have this form of hemoglobin do not get malaria.

Determine the probability of having children resistant to malaria in a family where one parent is heterozygous, and the other is homozygous for a recessive allele and has normal red blood cells.

Determine the probability of having children resistant to malaria in a family where both parents are resistant to the disease.

Task 108. A rare recessive allele *a* causes inherited anophthalmia (absence/underdevelopment of the eyeball) in a person. The dominant allele of the same *A* gene causes the development of normal eyes. In heterozygotes, the eyeballs are reduced.

Determine the proportion of heterozygotes among children in families where the mother and father have reduced eyes.

A man with reduced eyeballs married a woman with normal eyes.

Determine the probability of having a normal child.

Task 109. Familial hypercholesterolemia is an autosomal dominant. In heterozygotes, high cholesterol levels are detected in the blood, and tumors develop in homozygotes.

Determine the possible degree of development of the disease in children in a family where one parent is healthy, and another parent has high cholesterol and tumors.

Task 110. People with curly and fluffy hair are often called "woolly". Such hair grows quickly but is split and never long. This trait is dominant. So far, no marriages between people with such characteristics have been registered, so the phenotype of the homozygote for the dominant allele is unknown.

Determine the probability of having a child with normal hair in a family where the mother has "woolly" and the father has normal hair.

Task 111. One form of cystinuria (disorder of amino acid metabolism) is inherited as an autosomal recessive. In heterozygotes, there is an increased content of cystine in the urine, the formation of cystine stones in the kidneys occurs in homozygotes.

Identify possible forms of cystinuria in children in a family where one of the spouses had kidney stones and the other has never had cystinuria.

Task 112. The offspring of interbreeding flies with spread wings are phenotypically heterogeneous: 2/3 has spread wings, and 1/3 has normal, non-spread wings. Descendants from interbreeding flies with spread and normal wings make up the same two phenotypic classes, but in a ratio of 1/2:1/2.

Explain the results of interbreeding.

Task 113. In bees, the gene that determines that the wing ends are lower than the stinger appears only in heterozygous; in homozygous it causes the death. It is known that in bees, males develop from unfertilized eggs and are homozygous.

Determine the phenotypes and genotypes of offspring from interbreeding a bee with wing ends lower than the stinger with a normal drone.

Task 114. A phenotypically heterogeneous offspring was obtained from interbreeding mirror carps[7] with each other: 152 offspring were with mirror scales and 78 with normal scales.

Explain the results and specify the offspring that will result from interbreeding the mirror carp with common carp.

Task 115. Because of very short legs, one of the breeds of chickens is called crawling hens. During the incubation of 15,000 eggs obtained from interbreeding crawling chickens with each other, 11,247 chicks hatched, of which 3,723 chicks were with normal legs, the rest had short legs.

Determine the genotypes of newly hatched chicks.

Describe the type of inheritance.

[7] A breed of fish characterized by underdevelopment of scales, which is preserved only on the midline of the body.

Task 116. In chickens, the dominant allele of the autosomal gene determines both the development of shorter legs and beak. In homozygous allele chicks, the beak is so small that they are unable to break through the shell and die without hatching. In the incubator of the farm that breeds chickens with short legs, 3,000 chickens hatched.

Determine the theoretically expected number of individuals with short legs.

Task 117. Mice of the yy genotype are gray, mice with the Yy genotype are yellow, and mice with the YY genotype die at the embryonal stage.

Describe the offspring from interbreeding a gray female with a yellow male.

Describe the offspring from interbreeding a yellow female with a yellow male.

Specify the interbreeding that can be expected to produce a larger litter.

Task 118. In mice, the dominant short-tailed allele causes the death of the embryo, which is homozygous for this allele, in the early stages of development. Heterozygotes have shorter tails than normal individuals.

Determine the phenotypes and genotypes of offspring obtained from interbreeding mice with long and short tails.

Task 119. In the Karakul sheep[8] the dominant allele with a pleiotropic effect determines beautiful silver-gray coat, as well as the underdevelopment of stomach and parasympathetic nervous system disorders. Lambs that are homozygous for this allele die after they stop feeding on their mother's milk. The recessive allele of this gene determines black coat.

Determine what phenotype segregation will be among the descendants of interbreeding two gray sheep.

Specify the phenotype of the ram with which you need to interbreed the gray Karakul sheep, so that you can raise all the lambs to adulthood.

Task 120. Norwegian bull Viking and its daughters had a normally developed spine. As a result of mating a bull with its daughters, 60 calves

[8] Fat-tailed rough-haired breed of sheep ftir-milk direction, the name of the breed comes from the name of the area Karakul (from the Uzbek "black lake").

were produced, of which 12 individuals had a severely shortened spine. All calves with the described spinal defect died.

Determine the type of inheritance for this defect.

Task 121. In the Mexicana Great Dane, the allele that determines the absence of hair causes the death of homozygotes. In a litter from two dogs, several puppies appeared hairless and died. There were no hairless puppies from interbreeding the same male with another female. However, from interbreeding dogs from these two litters, some offspring again died due to absence of hair.

Determine the genotypes of all interbred individuals.

Task 122. Foxes with the Pp genotype have platinum fur, and foxes with the pp genotype are silver-black. Usually, 1/3 of the descendants from interbreeding platinum foxes among themselves possess a silvery-black fur and 2/3 of platinum. Sometimes white puppies are born, which soon die (most often these puppies die in the early embryonal stages).

Specify the genotype of white puppies.

Algorithm for solving the task for multiple alleles

Task (case study). The blood group (according to the ABO blood group system) is controlled by three alleles of the same gene – O, A, and B. Alleles A and B are dominant in relation to the O allele. The first group (O) determines the recessive allele O, the second group (A) determines a dominant allele A, the third group (B) defines a dominant allele B, and the fourth (AB) or two dominant alleles AB (codominance). The father has blood group O, the mother has blood group A.

Determine the genotypes of the parents, the possible blood groups and genotypes of their children. Explain the results.

The algorithm for solving the task is shown in the table 4.

Table 4

Algorithm for solving the task for multiple alleles

P	♀ **OO**	×	♂ **AB**
G	**O**		**A, B**
F_1	**AO**, **BO**		

Answer. Alleles A and b are dominant over allele O. These parents may have children with the second (AO) or third (BO) blood groups in equal proportions (1:1).

Task 123. The child has blood group A, the husband of the child's mother has got blood group A, a potential father has got blood group O.

Find out which of the men is the biological father of the child.

Explain whether knowing that mother has blood group A will be useful in this case.

Task 124. It is known that mother is blood group B, and father has blood group O.

Determine the blood groups their children may have.

Task 125. Both parents have: a) blood group A; b) blood group B; c) blood group AB; d) blood group O.

Identify and explain the inheritance of blood groups children might have.

Task 126. Mother and father have blood group A. Their daughters got married. The first daughter had children with blood groups B and AB; the second daughter gave birth to children with blood group AB; the third daughter had children with blood groups A and B.

Determine what blood groups of the daughters' husbands.

Task 127. Father and mother had blood group O, daughter had blood group B, son had blood group AB. All grandchildren (15 people) had blood group O.

Determine the genotypes of daughter, her husband, son, and his wife.

Task 128. Two boys were mixed up in hospital. The parents of one of them have blood groups A and O, the parents of the second child have blood groups A and AB. Laboratory blood tests showed that the first boy had blood group A, and the second boy had blood group B.

Decide on the sons and parents.

Task 129. Mother has blood type B, the child has blood group AB. Father's blood type is unknown.

Identify which blood (father's or mother's) can be transfused to the child.

Explain if it is possible to transfuse father's blood to the child, without defining his blood group.

Task 130. A wealthy Canadian banker, Jean Mazepa, who died at an incredibly old age, bequeathed all his capital to his second wife, Marie, and two young sons from this marriage, Pierre and Charles. Mazepa's children from his first marriage, Anna and Lizzie, went to court, demanding to recognize the will as illegal and deprive Maria and her children of the right to inheritance. In a statement presented to the court by the lawyer of Anna and Lizzie, it was said that Pierre and Charles are not Mazepa's sons.

The grounds for accusing Mary of adultery and denying her and her children the right to inheritance were data on the discrepancy between the blood groups of Mazepa and the boys, whom he considered his sons. Maria and the first wife of Mazepa have blood group A; Anna Lizzie have the same group. Mazepa had blood group O. Pierre's blood group is AB, and Charles has blood group B.

Explain what the court will resolve based on the available data.

Task 131. Father has blood group B, mother has blood group AB.

Set the genotype of parents if they have many children with the following blood groups: a) all O; b) half of their children with group O and the other half with group AB; c) 25% of children have blood group A, 25% of children have blood group B, 25% of children – blood group AB, and 25% of children – blood group O.

Task 132. The boy has blood group A, and his sister has blood group O.

Determine which blood groups their parents may have.

Task 133. Father has blood group O, mother has blood group A.

Find out what is the possibility of children having blood of the same groups as their parents.

Task 134. Spouses are blood groups B and AB individuals.

Specify the blood group that their future children may have.

Task 135. Two boys were mixed up in hospital. Parents of one of them are blood group A and B individuals, while parents of the other are blood group B and O individuals. Boys are blood group A and B individuals.

Identify the parents of both children.

Task 136. A woman with blood group AB initiated a case to recover alimony from a man who has blood group A, claiming that he is the father of the child. The child has blood group A.

What would the court resolve?

Specify the cases when the forensic examination can give an unambiguous answer about the child's paternity after a blood test to determine whether it belongs to a particular group.

Task 137. A woman with blood group A married a man homozygous for an allele that determines blood group B. They had one child.

Specify the child's blood type and genotype.

Task 138. Mother has blood group B, and father has blood group AB.

Set the genotype of the parents if their first child has blood group O.

Task 139. The child has blood group A, his mother has blood group AB, father has blood group B.

Determine the genotypes of the parents.

Determine the probability of these parents having children with blood groups B, AB and O.

Task 140. When reviewing the court case on paternity, it was established that the child has blood group O, mother is blood group B individual, and the reputed father is blood group A individual.

What would be medical examiner's conclusion about paternity?

Specify the blood group that the man must have that would completely exclude his paternity.

Task 141. Blood transfusion is only possible if brother and sister have the same blood group.

Specify the possible genotypes of parents and their children in the case when you can transfuse sister's blood to her brother.

Task 142. Mother with blood group B has a child with blood group A.

Determine the blood group that the father may have.

Task 143. In maternity hospital, four babies were born the same night with blood groups A, B, AB and O. Parents had the following blood groups: a) A and A; b) O and A; c) B and AB; d) AB and AB.

Identify the parents of these babies.

Task 144. A woman went to court to establish paternity. The child had blood group A, mother had blood group AB, and the reputed fathers had blood groups B and AB.

Indicate whether the court resolve who the child's father is.

Task 145. A man with blood group O and a woman with blood group B had three children with blood groups B, O and A.

Determine the genotypes of parents and children.

Specify what may seem doubtful in the description of this family.

Task 146. Two couples think they are the parents of a child with blood group B. One couple has blood groups A and O, the other couple has blood groups A and AB.

Identify the spouses who are more likely to be the parents of the child.

Task 147. Father has blood group AB, mother has blood group B.

Determine the genotypes of parents if all their 12 children have blood group O.

Task 148. The boy's maternal grandfather has blood group O, and the other grandfather and two grandmothers have blood group A.

Determine the probability that the boy has blood group A, B, AB and O.

Task 149. In rabbits, alleles of the same gene determine different variants of coat color. The allele of the wild rabbit's coat color (C) is dominant over all other alleles. The allele of chinchilla (c^{ch}) and Himalayan (c^{h}) coat colors dominates the albinism (c) gene. Heterozygotes from chinchilla and Himalayan coat color give a light gray color.

Determine the genotypes and phenotypes of descendants F1 and F2 when crossbreeding rabbits with chinchilla and Himalayan coat colors.

Prove whether it is possible to create a group of rabbits of light gray color when crossbreeding such rabbits among themselves.

Task 150. In cats, the gene that determines coat coloration is represented by the following alleles: C-wild type (gray), c^{8} – Siamese cats (ivory with black ears and black paws), c – white cats with red eyes (albinos). Each of the alleles fully dominates the next in the following sequence: $C>c^{8}>c$. From crossbreeding a gray cat with a Siamese cat, two kittens were born: Siamese and an albino.

Specify the phenotypes of kittens that could still appear during this crossing.

Describe the segregation that should be expected in offspring from crossbreeding a Siamese cat with a white, red-eyed cat.

Algorithm for solving the task for dihybrid and polyhybrid crossing

Task (case study). When crossing a pea plant with smooth yellow seeds with a plant with wrinkled green seeds, the entire generation was uniform and had smooth yellow seeds. When crossing plants obtained in the first crossing with a plant with wrinkled green seeds in the offspring, plants with smooth yellow, wrinkled yellow, smooth green and wrinkled green seeds were obtained, all in equal proportions.

Make a diagram of each crossing.

Determine the genotypes of parents and offspring. Explain the results.

The algorithm for solving the task is shown in table 5.

Table 5

Algorithm for solving the task of dihybrid and polyhybrid crossing

P	**AABB** smooth yellow	×	**aabb** wrinkled green
G	**AB**		**ab**
F_1	**AaBb** smooth yellow		
P	**AaBb** smooth yellow	×	**aabb** wrinkled green
G	**AB, Ab, aB, ab**		**ab**
F_2	**AaBb** – smooth yellow **aaBb** – wrinkled yellow		**Aabb** – smooth green **aabb** – wrinkled green

Answer. The allele that determines the development of smooth seeds (A) completely dominates the allele of wrinkled (a), the allele of yellow (B) over the allele of green (b) seeds. Dihybrid crossing, independent inheritance of traits. Splitting in F2 offspring 1/4:1/4:1/4:1/4.

Task 151. In the offspring there was a split in the phenotype:

a) 1/4:1/4:1/4:1/4; b) 3/8: 3/8:1/8:1/8.

Determine the genotypes of the parents under the condition of complete dominance and absence of linkage of genes.

Task 152. The genotype of the organism is presented AaBbCc. Genes are inherited independently.

Specify types and number of gametes formed in the organism with the original genotype.

Task 153. The organism has a genotype AaBbCCddEE. The genes are in different pairs of chromosomes.

Specify the types of gametes formed in it.

Task 154. Crossed two trihybrid AaBbCc between them. Alleles A, B and C dominate completely.

Identify the types of gametes that produce these trihybrids.

Determine the segregation in the offspring by phenotype.

Specify which part of the offspring will have all dominant traits.

Specify which part of the offspring will have all recessive traits.

Specify which part of the offspring will have two dominant and one recessive trait.

Task 155. Crossed hybrids $AAbbDD^1$ and $aaBbDD^1$. Alleles A and B are completely dominant, and alleles D is not completely dominant over D^1.

Determine types and number of gametes these hybrids produce.

Specify the segregation that will be observed by the phenotype.

Task 156. Tetrahybrid MmNnPpRr crossed with a recessive in all four genes.

Determine the segregation that will be in the offspring by phenotype.

Specify which part of the offspring will have all dominant traits.

Specify which part of the offspring will have all recessive traits.

Specify which part of the offspring will have only one dominant trait.

Task 157. It is known that the plant has a genotype AaBb, moreover, the genes are inherited independently, and for each pair of alleles there is complete dominance.

Specify the number and ratio of phenotypes, which can be obtained in the offspring from crossing this plant with the plant AaBB.

Specify the number and ratio of genotypes, which will be the descendants after self-pollination of this plant.

Task 158. Crossed homozygous plants that differ from each other in five independently inherited traits. Three traits of these traits (of the parent plant) are dominant and two traits are recessive.

Specify what the segregation of hybrids in the second generation will be, which will be obtained during the self-pollination of hybrids of the first generation.

Specify the percentage of second generation hybrids that are phenotypically like "grandma" and which are similar to "grandpa".

Task 159. A plant has a genotype AaBbCc. Genes are inherited independently.

Specify the types of gametes that this plant can have.

Determine the number and ratio of phenotypes in the offspring of this plant after self-pollination, assuming complete dominance over all three pairs of alleles.

Determine the number of genotypes in the offspring of this plant after self-pollination.

Determine the number of phenotypes in the offspring of this plant after self-pollination, assuming complete dominance for two pairs of alleles and incomplete for the third.

Task 160. It is known that the plant has a genotype AaBbcc. Genes are inherited independently.

Specify the types and number of gametes, which this plant forms.

Specify the number of genotypes and phenotypes, as well as the ratio in the offspring of this plant after self-pollination, assuming complete dominance over all pairs of alleles.

Specify the number and ratio of genotypes in the offspring of this plant after self-pollination under conditions of incomplete dominance for the first pair of alleles.

Task 161. In sweet peas, the full height (T) dominates the dwarf (t), the green color of the beans (G) over the yellow (g), and the smooth seeds (R) over the wrinkled (r).

Determine the phenotype and genotype of descendants from crossing plants with genotypes TTGgRr and ttGgrr.

Calculate the percentage of triheterozygotes among descendants.

Determine which part of the descendants will be individuals homozygous for all three pairs of alleles.

Task 162. After self-pollination of pea plants that grew from smooth yellow seeds, the offspring was subsequently obtained, consisting of 99 plants with yellow smooth, 36 plants with yellow wrinkled, 29 plants with green smooth, 12 plants with green wrinkled seeds.

Determine the genotype of the original plants.

Determine whether the empirical segregation corresponds to the theoretical one.

Task 163. From two pea plants with red flowers and tall stems after self-pollination, plants were obtained, of which 64 tall plants with red flowers and 21 short plants with red flowers are descendants of one initial plant, and 64 tall plants with red flowers and 20 tall plants with white flowers are descendants of another initial plant.

Determine the genetic determination of traits.

Determine the genotypes of all plants.

Task 164. In peas, yellow seed (A) is dominant over green, smooth seed (B) – over wrinkled, pod of a simple form (C) – over the pod with dissepiment between the seeds.

A) Crossed a pea plant heterozygous for three genes with a plant homozygous for recessive alleles of these genes.

Determine the segregation in the offspring by phenotype.

B) Crossed the AaBbcc plant with aabbCc plant.

Determine the segregation in the offspring by phenotype.

Task 165. After cross-pollination of two pea plants, yellow smooth seeds were collected. Two-thirds of the plants that grew from these seeds had yellow smooth seeds and one-third of the plants had yellow wrinkled seeds. Plants that grew from yellow wrinkled seeds were crossed with a plant that grew from yellow smooth seeds. Among their offspring appeared plants with yellow smooth and yellow wrinkled seeds in a ratio of 1:1. Plants that grew from different shaped seeds were re-crossed. In the next offspring, there was a segregation: 37.5% of pea plants had yellow smooth, 37.5% – yellow wrinkled, 12.5% – green smooth and 12.5% – green wrinkled seeds.

Determine the genotypes of parents and offspring in all crosses.

Task 166. In the Snapdragon, tall plants are dominant, and short plants are recessive, this trait being controlled by alleles of a single gene.

Two alleles of another gene determine the red and white color of corolla lobes in homozygotes. Heterozygotes have pink flowers. From crossing a tall plant with red flowers with a short plant with pink flowers, seeds are obtained. From these seeds, the following year, the plants grew tall with red, tall with pink, low with red, and short with pink flowers.

Determine the required crossing of descendants to obtain short plants with white flowers.

Task 167. In strawberries, red berries and a normal calyx not determined fully dominant allele, and white berries and a leaf-like calyx– not completely recessive alleles of two genes. Heterozygotes for both genes have pink fruits and an intermediate calyx. Both pairs of alleles are inherited independently of each other.

Determine the number of classes by phenotype and genotype and the ratio between them in the offspring obtained by crossing diheterozygous plants.

Determine the possible genotypes and phenotypes of offspring obtained from crossing plants with normal and leaf-shaped calyx heterozygous for the gene that determines the color of the berry.

Task 168. Two watermelon plants (No. 1 and No. 2) belonging to the long green fruit variety were crossed with plants (No. 3 and No. 4) belonging to the round striped fruit variety. The following results were obtained:

a) No. 1 x No. 3 – all plants with round green fruits;

b) No. 2 x No. 4 – 20 plants with round green, 18 with round striped, 22 with long green and 25 with long striped fruits.

Determine the genetic determination of traits.

Determine the genotypes of the original plants.

Explain what the result will be if you cross plant No. 1 with plant No. 4 and plant No. 2 with plant No. 3.

Task 169. In wheat, the awnlessness dominates the spinosity, and the red color of the spike dominates the white. The following offspring were obtained from crossing a plant of an awnless variety with a red spike with wheat of a awned variety with a white spike: 1/4 – awnless with red spikelet, 1/4 – awnless with white spikelet, 1/4 – awned with red spikelet, 1/4 – awned with white spikelet.

Determine the genotypes of crossed plants.

Task 170. In tomatoes, the purple stem color is dominant, and the green color is recessive. The formation of a divided leaf blade is controlled by a dominant allele and an integrate one is controlled by a recessive allele of the same gene. By crossing plants of two tomato varieties, one of which had purple stems and divided leaves, and green stem and divided leaves was obtained the following: 350 plants with purple stems and divided leaves, 112 plants with purple stems and integrate leaves, 340 plants with green stems and divided leaves, 115 plants– with a green stem and integrate leaf pallet.

Determine the most likely genotypes of parent plants.

Task 171. In tomatoes red fruit color and the normal height of the stem is determined by the dominant alleles of two non-linked autosomal genes, and yellow fruits and dwarfism – recessive alleles of the same genes. Plants of one variety have yellow fruits and normal stem, the other – red fruits and short stems.

Explain the appropriate use of the source material to get homozygous forms: red fruit with normal stem and short stem with yellow fruits.

Specify the form that is easier to get.

Task 172. Tomato fruits are red and yellow, smooth and pubescent. The allele of red fruit color is dominant, and the allele of fruit pubescence is recessive. Different pairs of traits are inherited independently.

A) Hybrid seeds (F1) were obtained from crossing plants of two varieties: with red smooth fruits (type 1) and with yellow pubescent ones (type 2).

Specify what the fruits of plants grown from F1 seeds will be if they are pollinated with pollen from plants of type 2.

Specify the fruits of tomatoes grown from seeds formed as a result of this pollination.

B) From three hundred and sixty tomato bushes they gathered smooth red fruit, from one hundred and twenty – red pubescent ones.

Specify the theoretically expected number of tomato bushes with yellow pubescent fruits, if the seeds for planting all bushes were obtained from crossing diheterozygous plants with each other.

Task 173. In tomatoes, purple stem color and dissected leaves are dominant traits, while green stem color and whole leaf blade are recessive traits. Both pairs of traits are inherited independently.

Determine what are the most likely genotypes of the original plants in each of the following crosses:

The phenotype of the parents	The phenotype of the descendants			
	Purple split	Purple one-piece	Green split	Green one-piece
	Number of individuals			
Purple one-piece, Green split	70	91	86	77
Purple split, Green one-piece	404	-	387	-
Purple split, Green split	228	231	-	-
Purple split, Purple one-piece	219	207	64	41
Purple split, Green split	321	101	310	107

Task 174. Two pumpkin plants are crossed and seeds are received. The following year, these seeds grew into 11 plants with yellow globular fruits and 36 plants with white globular fruits. The white color dominates the yellow; the discoid fruit shape dominates the globular one.

Determine the genotype and phenotype of the initial plants.

Task 175. Two pumpkin plants were crossed, the ripened seeds were sown the following year and 18 plants with white discoid grew from them: 5 plants with white globular fruits and 4 plants with yellow discoid fruits were obtained.

Determine the genotypes of the initial plants.

Specify the color and shape of the fruit that the initial plants had.

Specify the plants and describe fruits that may still appear in this generation.

Task 176. In pumpkin, white color and discoid fruit shape are dominant traits, while yellow color and globular shape are recessive. The result of crossing two plants is offspring, including 3/8 with white discoid fruits, 3/8 with white globular fruits, 1/8 with yellow discoid fruits and 1/8 with yellow globular fruits.

Determine the genotypes of parents and offspring.

Task 177. Two breeds of silk moth interbred. Single-colored silkworms of the first breed weave yellow cocoons, and striped silkworms of the second breed weave white cocoons. In the first generation, all the silkworms were striped and wove yellow cocoons. In the second generation, the following segregation occurred: 6,385 striped silkworms wove yellow cocoons, 2,147 striped ones – white cocoons, 2,099 single-colored ones – yellow cocoons, and 692 single-colored ones – white cocoons.

Identify the determination of breed traits.

Set the color inheritance pattern for silkworms and cocoons.

Determine the genotypes of the initial forms and hybrids of the first and second generations.

Task 178. Two fruit flies with upturned wings and shortened bristles were interbred. When analyzing the offspring obtained from this crossbreeding, flies were found to have upturned wings and shortened bristles, upturned wings and normal bristles, normal wings and shortened bristles, normal wings and normal bristles in a ratio of 4:2:2:1.

Determine the genotypes of the initial flies and first-generation hybrids.

Task 179. In Drosophila, the gray body color and the presence of bristles are autosomal dominant traits that are inherited independently.

Indicate which offspring is to be expected from a cross of a black female without bristles with a diheterozygous male.

Task 180. In Drosophila, gray body color and straight wings are dominant traits, while black body color and upturned wings are recessive. From crossing gray flies with straight and upturned wings, one quarter of the offspring had a black body. Half of the offspring had straight wings, and another half had upturned wings.

Determine the genotypes of the parent generation of flies.

Task 181. In chickens, the simple comb and bare legs are recessive, while the rose comb and feathered legs are dominant traits. A hen with bare legs and homozygous for the allele of the rose comb was crossbred with a rooster with recessive traits.

Identify the part of the offspring that will inherit both traits of the mother.

Task 182. Three blue Andalusian hens with a rose comb and a rooster with similar traits were interbred. From two hens in the F1 generation were obtained: 69 blue chicks with a rose comb; 32 black chicks with a rose comb; 10 black chicks with a common comb; 24 blue chicks with a common comb; 36 white chicks with a rose comb; 11 white chicks with a common comb. In the F1 offspring obtained from the third hen, all the chicks had a rose comb, while 1/4 of them had black plumage, 1/4 had white plumage, and 1/2 had blue plumage.

Explain the results.

Determine the genotypes of the initial hens and rooster.

Task 183. In chickens, feathered legs dominate bare legs, rose comb dominates common comb, and white plumage dominates colored one. A hen with feathered legs, a rose comb and white plumage was interbred with a similar rooster. Among their offspring was a chicken with bare legs, common comb, and colored plumage.

Determine the genotypes of the parents.

Task 184. In chickens, pea comb and common comb are determined by fully dominant and fully recessive alleles of the same gene. Black and white plumages are not fully dominant and not fully recessive. Heterozygotes have blue plumage.

Determine which part of the descendants after crossbreeding birds that are heterozygous for both pairs of alleles will have: a) a common comb; b) blue plumage; c) a common comb and blue plumage; d) white plumage and a pea comb.

Task 185. In chickens, pea comb and feathered legs are dominant traits. From a group of genetically uniform chickens with leaf combs and bare legs, after crossbreeding with a rooster with a pea comb and feathered legs, the following offspring were obtained: 69 chicks with a pea comb and bare legs, 72 chicks with a pea comb and feathered legs, 63 chicks with a leaf comb and feathered legs, and 66 chicks with a leaf comb and bare legs.

Determine the genotypes of parents and offspring.

Task 186. Rooster 1 and rooster 2 were crossbred with hen 3 and hen 4. All four birds have feathered legs and pea combs. After crossbreeding rooster 1 with both hens, the chicks had feathered legs and pea combs.

After crossbreeding rooster 2 with hen 3, chicks were bare-legged and feathered legs, all with a pea comb. After crossbreeding rooster 2 with hen 4, all chicks had feathered legs, some of them had a pea comb, and some had a common comb. In chickens, feathered legs and a pea comb are dominant traits.

Determine the genotypes of the initial birds.

Identify the crossbreeding options that should be performed to test the assumption about the genotypes of birds.

Task 187. In Guinea pigs, curly coat dominates silky one, and black coat coloration dominates white.

Determine the first and second generation after crossbreeding a homozygous curly black pig with a silky white one.

Specify the offspring from both back crossing.

Task 188. In cattle, hornless trait dominates horned one, and roan color is possessed by descendants from crossbreeding animals with white and red coat coloration. After crossbreeding a hornless roan bull with a horned roan cow, a horned roan calf was born. Subsequently, the same bull was crossed with red-horned, white-horned, roan, white and red hornless cows. All calves were horned roans.

Determine the genotypes of the bull and all six cows crossed with it.

Task 189. In horses, the black color dominates the chestnut color, and trot dominates amble gait.

Specify the phenotype of F1 offspring from crossbreeding a homozygous black Pacer with a homozygous chestnut Trotter.

Determine the offspring that will result from crossing animals from the first generation.

Task 190. In pigs, white color dominates black color, and the presence of wattles dominates their absence.

Determine the genotype of the white boar with wattles: a) if after interbreeding it with any sows white offspring with wattles are born; b) if after interbreeding another boar with the same phenotype black sow without wattles is born 50% white pigs with wattles and 50% black pigs with wattles.

Task 191. In pigs, white color dominates black color, one-toed over two-toed. Two boars No. 1 and No. 2 have one-toed feet and white color. Boar No. 1 when crossed with any pigs gives one-toed white descendants. Boar No. 2 when crossed with black pigs gives half black, half white descendants, when crossed with two-toed pigs – half one-toed, half two-toed descendants.

Determine the genotypes of boars.

Task 192. From crossing a black-and-white Cocker Spaniel dog and a brown Cocker Spaniel dog five puppies were born: 1 black, 1 brown, 1 black-and-white and 2 brown-and-white. Black coat coloration dominates brown color, one-color coat coloration dominates spotting.

Determine the genotypes of parents and descendants.

Specify what will happen if a brown-and-white offspring are recrossed with a black-and-white female.

Task 193. In dogs, short-hair dominates long-hair, black coat coloration over brown coat coloration, lop ear dominates erect ear.

Determine which gametes are formed: a) in a black short-hair male with lop ears, heterozygous for the genes of color and length of hair and homozygous for the gene of lop ears; b) in a heterozygous female for all genes.

Task 194. When crossing two dogs with genotypes AaBB and Aabb the offspring should be: 4 dogs with genotype AABb, 8 dogs with genotype AaBb and 4 dogs with aaBb.

Find an error.

Task 195. In dogs, short hair and black color are dominant, and long hair and coffee color are recessive traits determined by independently inherited genes.

Determine the percentage of black short-hair puppies by crossing two diheterozygous individuals.

Check the genotype of the purchased dog; if the hunter bought a black dog with short hair and wants to be sure that it does not have coffee-colored alleles and long hair.

Task 196. A blue-eyed right-handed man married a brown-eyed right-handed woman. They had two children, a brown-eyed left-hander and a

blue-eyed right-hander. From the second marriage of this man with another brown-eyed right-handed woman, 9 brown-eyed children were born, all right-handed.

Determine the genotypes of all three parents.

Set the attributes to be dominant and recessive.

Task 197. A fair-haired Rh-positive woman with blood group O married a dark-haired Rh-positive man with blood group A, whose mother had fair hair. It is known that a man and a woman are heterozygous for the Rh factor gene. Rh factor and dark hair are inherited as autosomal dominant traits.

Determine the probability of fair-haired Rh negative children and their possible blood groups.

Task 198. A round-faced woman with blood group B married a round-faced man with blood group AB. It is known that the woman's mother had an oval face and blood group A, the man's father had an oval face and blood group O, and the man's mother had a round face and blood group A.

Determine the offspring of this marriage, if the round shape of the face dominates the oval.

Task 199. A boy has blood group O, he is also Rh positive, and his brother has blood group A and he is Rh negative.

Determine the parents' blood groups.

Task 200. Red blood cell membranes contain many antigens, including those of the ABO, MN, and Rh systems. It is assumed that the presence or absence of ABO antigens is determined by three alleles of the same gene I°, I^A, I^B, the MN system antigens are alleles L^M and L^N and the Rh system D (Rh+), d (Rh -). Alleles I^A, I^B and L^M, L^N are codominant, and alleles I° and d are recessive with respect to alleles I^A, I^B and D, respectively.

Determine which phenotypes of the three blood group systems exist in humans, if you consider all possible combinations of ABO, Rh and MN antigens?

Determine the number and combination of antigens that are possible in children, if the genotype of the mother is $I^AI^0L^ML^MDd$, the father is $I^BI^BL^ML^NDd$.

Determine the number of different genotypes and phenotypes in

children; if the genotype of the mother is $I^0I^0L^NL^NDd$, the father is $I^AI^BL^ML^Mdd$.

Determine the probability that the child will have the same combination of antigens as the father, if a woman with the phenotype A (Rh -) MN, whose father had blood group A, married a man whose blood contains antigens A, B, D and N. the man's mother was Rh negative.

Determine the number and combination of blood antigens that are possible in children if the mother's phenotype is ABMRh–, the father's is ONRh+. One of the father's parents was Rh negative.

Task 201. The blood test of all three family members gave the following results: the woman has Rh positive blood group O with M antigen; her husband has Rh negative blood group A with N antigen. The child's blood is Rh positive blood group A with M antigen.

Analyze the information.

Task 202. In humans, brown eyes dominate blue eyes, and myopia dominates good eyesight. A blue-eyed woman with myopia married a brown-eyed man with good eyesight and gave birth to a brown-eyed child with myopia.

Identify the parents' genotypes, if it is possible.

Task 203. In humans, right-handedness dominates left-handedness, and achondroplasia dominates the normal anatomy of the skeleton. A man and a woman who are both right-handed and suffer from achondroplasia got married. They had three children: a right-handed person with achondroplasia, a left-handed person with achondroplasia, and a right-handed person with normal skeletal anatomy.

Determine the probability of them having a child who is left-handed and has achondroplasia.

Task 204. In humans, brown eyes and curly hair are dominant, while blue eyes and smooth hair are recessive.

A) a curly-haired, blue-eyed man and a brown-eyed, smooth-haired woman have four children, each of whom differs in one trait from the other.

Determine the genotypes of the parents in this family.

B) A blue-eyed, curly-haired man whose father had smooth hair married a brown-eyed, smooth-haired woman from a family whose

members all had brown eyes.

Determine the offspring that can be born in this family.

Task 205. A short-sighted man (dominant trait) left-handed (recessive trait) married a right-handed woman with good eyesight. It is known that both spouses had brothers and sisters who suffered from phenylketonuria, but the spouses are healthy. In their family, the first child is normal in terms of all three traits, the second child is short-sighted and left-handed, and the third child has phenylketonuria.

Determine the genotypes of parents and all children.

Determine the probability that their fourth child will be a healthy right-handed person with good eyesight.

Task 206. In humans, two forms of deaf-muteness are known, determined by recessive alleles of different autosomal genes.

Determine the probability of children being born deaf-mute in a family where the father and mother suffer from the same form of deaf-muteness, and both are heterozygous for the gene of another form of deaf-muteness.

Determine the probability of children being born deaf-mute in a family where both parents suffer from different forms of deaf-muteness, and both of them are heterozygous for the gene of another form of deaf-muteness.

Task 207. Polydactyly, myopia, and the absence of small molars are dominant autosomal traits. The following is known about the family: the woman's mother was six-fingered, her father had myopia, and the woman inherited both anomalies, the man's mother did not have molars, was five-fingered and had good eyesight, his father had no anomalies, and the man inherited his mother's anomaly.

Determine the probability of them having children without anomalies.

Task 208. There are two forms of fructosuria. Patients with one form of fructosuria have no clinically expressed symptoms (essential fructosuria), while the second (severe) form leads to inhibition of mental and physical development. Both forms of fructosuria are determined by recessive alleles of unconnected autosomal genes. One of the spouses has an increased content of fructose in the urine and, therefore, is homozygous for the allele of fructosuria, which does not manifest itself clinically, but

heterozygous for the gene of the second form of the disease. The second spouse was once treated for the second form of fructosuria but is heterozygous for the gene of the asymptomatic form.

Determine the probability of their children suffering from the second form of fructosuria.

Task 209. There are several inherited forms of cataract (an ophthalmic disease associated with clouding of the lens of the eye and causing various degrees of vision disorders). Most of them are dominant autosomal traits, some are recessive non-sex-linked traits.

Determine the probability of having children with an anomaly if both parents' cataracts are caused by the presence of dominant alleles of the same autosomal gene in their genotype, and they are triheterozygotes, carriers of recessive alleles of two more forms of cataract.

Task 210. In one family, brown-eyed parents have four children. Two blue-eyed children have blood groups A and O, and two brown-eyed children have blood groups B and AB.

Determine the genotypes of parents and the probability of birth in this family of a brown-eyed child with blood group A.

Task 211. Recessive alleles of two different autosomal genes in humans determine the development of two types of blindness. Genes are not linked.

Determine the probability that a child will be blind if father and mother suffer from the same type of inherited blindness and are homozygous for the dominant alleles of another gene.

Determine the probability of a child born blind if father and mother suffer from different types of inherited blindness and are homozygous for both pairs of alleles.

Determine the probability of a child born blind if his parents are sighted, grandmothers suffer from different types of hereditary blindness and are homozygous for both pairs of alleles, and there was no hereditary blindness in the pedigree of grandfathers.

Determine the probability of a child born blind if his parents are sighted, grandmothers suffer from the same type of hereditary blindness and are homozygous for the dominant alleles of another blindness gene, and grandfathers are healthy and homozygous for both pairs of alleles.

Task 212. The farmer had two sons. The first son was born when the farmer was young and grew up to be a handsome, strong young man, of whom his father was immensely proud. The second son, born much later, was a sickly child, and neighbors urged the farmer to file a lawsuit to establish paternity.

The reason for the claim was that being the father of such a fit young man as his first son was, the farmer could not be the biological father of the second son. Members of the farmer's family had the following blood groups: the farmer – O, M; his wife – AB, N; the first son – A, N; the second son – B, MN.

Prove right or wrong the fact that the farmer is the biological father of both sons based on these data.

Determine the genotypes of all family members.

Task 213. Is it possible to exclude paternity if the mother has blood groups O and MN, the reputed father – AB and N, and children: a) O and M; b) A and M; C) O and MN?

Provide your answer with an explanation.

Task 214. In humans, albinism, and the ability to predominantly use the left hand are recessive traits that are inherited independently.

Determine the genotypes of parents with normal pigmentation who are right-handed, if they have an albino child who is left-handed.

Task 215. Deafness and Wilson disease (impaired copper metabolism) are recessive traits. A deaf man and a woman with Wilson disease had a child with both anomalies.

Determine the probability of a healthy child born in this family.

Task 216. In humans, brachydactyly (short finger) is a dominant trait, and albinism is recessive.

Determine the probability of diheterozygous parents to have a child with two anomalies.

Task 217. Glaucoma[9] has two forms: the first is determined by the dominant allele of one gene, and the second – by the recessive allele of another gene. The genes are located on different chromosomes.

[9] Eye disease characterized by a constant or periodic increase in intraocular pressure followed by the development of typical visual field defects, reduced vision and atrophy of the optic nerve.

Determine the probability of having a sick child in a family where the spouses suffer from different forms of glaucoma and are homozygous for both pairs of alleles.

Determine if it is possible to have healthy children in a family where the spouses are heterozygous for both pairs of alleles.

Task 218. A dark-haired (dominant trait), non-freckled man married a fair-haired woman with freckles (dominant trait). They had a fair-haired son without freckles.

Determine the probability of their having a dark-haired child with freckles.

Task 219. Brachydactyly, myopia, and albinism are determined by the recessive alleles of three genes located in different pairs of chromosomes. A man with normal pigmentation, brachydactyly and myopia married a healthy woman with albinism. Their first child had brachydactyly, the second child had myopia, and the third child had albinism.

Determine the genotypes of parents and children.

Task 220. Brown eyes, dark hair, and right-handedness are dominant traits that are inherited independently. Father is brown-eyed, dark-haired, and left-handed and mother is blue-eyed, fair-haired and right-handed. Their children: son is a blue-eyed, fair-haired left-hander and daughter is a brown-eyed, dark-haired right-hander.

Determine the genotypes of all family members.

Task 221. Sickle cell disease and thalassemias (microcytic hemolytic anemia) are not completely determined by the dominant alleles of autosomal uncoupled genes. Heterozygotes are resistant to malaria. Individuals who are homozygous for mutant not fully dominant alleles in most cases die in childhood.

Determine the probability of having healthy children in a family where father is heterozygous for one gene, and mother is hetreozygous for another.

3. INTERACTION OF NON-ALLELIC GENES

The expression "interaction of genes" should be understood as the interaction of their products, i.e., proteins that are a substrate or catalyst for biochemical reactions.

In the process of inheritance, many genes simultaneously function in the body, both linked and located in different pairs of chromosomes, and their products can take part in the formation of the same trait, that is, interact. The criteria for gene interaction are the appearance in descendants of a new variant of the trait that the parent forms did not have, and the splitting by phenotype among second-generation hybrids, which differs from the splitting in independent inheritance.

There are three types of gene interaction: **epistasis, complementation,** and **polymery.**

Epistasis (Greek: epístasis – stop, obstacle) is an interaction of genes in which one gene (epistatic) suppresses the phenotypic effect of another gene **(hypostatic)**. If an epistatic gene does not have its own phenotypic manifestation, then it is called an **inhibitor** and is designated by the letter **I (i)**. Epistasis can be **dominant** and **recessive**. In the first case, the dominant allele of one of the interacting genes is epistatic; in the second, it is a recessive allele.

With dominant epistasis, when two genes interact, the following variants of splitting by phenotype are possible among the descendants of diheterozygotes: **13:3** и **12:3:1** (Fig. 1A, 1B). In all zygotes that have a dominant suppressor allele in the genotype, the suppressed allele (hypostatic) does not produce a phenotypic effect. In the case of recessive epistasis, segregation among the descendants of diheterozygotes occurs in the following proportions **9:3:4** (Fig. 1C), **9:7** (Fig. 3B – double recessive epistasis or complementation). Epistasis would occur only in homozygotes for recessive alleles of the suppressor.

Complementation (complement, supplement) – the interaction of genes, in which genes together, complementing the action of each other, participate in the formation of a new variant of the trait, usually a normal one.

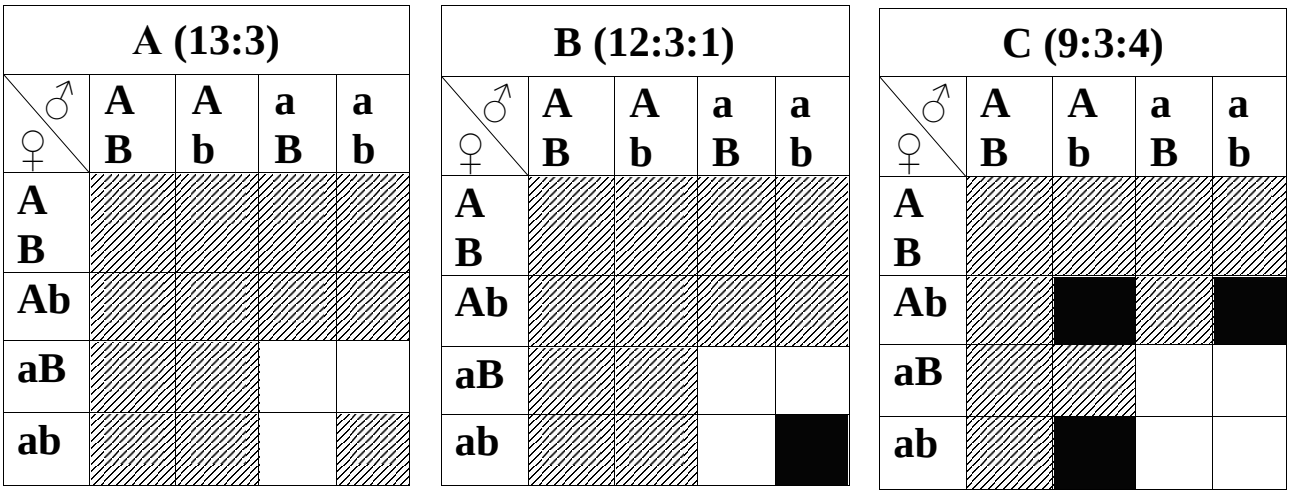
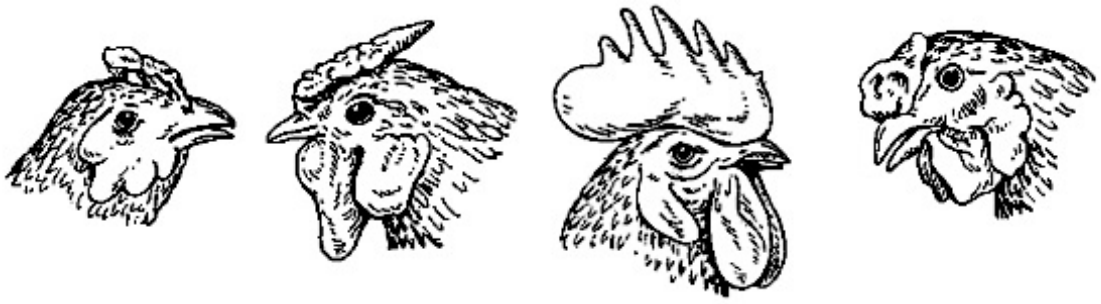


Figure 1. Scheme of splitting traits in the dominant (A, B) and recessive (C) epistasis

For example, in chickens, the pea comb is determined by the dominant allele of one gene, and the rose comb is determined by the dominant allele of another gene. Birds that have dominant alleles of two genes in their genotype develop a walnut comb. In homozygotes, recessive alleles of both genes develop a simple leaf-like comb (a trait of wild species). Descendants from crossing birds born from dihybrid cross with a walnut comb form four phenotypic classes in the ratio of **9:3:3:1** (Fig. 2, 3A).



A B C D

Figure. 2. Variants of combs in chickens. A – pea comb; B – rose comb; C – leaf-like comb; D – walnut comb

Alleles that determine rose and pea combs are inherited independently, but according to the phenotype of second-generation descendants. It is impossible to establish the independence of inheritance (splitting for each pair of features in relation to 3:1). In all zygotes that have dominant alleles of both genes in the genotype, each allele independently does not have the phenotypic effect, but the trait develops

when they interact, and it should be noted that this trait will be a new one. When two genes interact in a complementary way, other splitting options are possible: **9:7**, **9:6:1** (Figures 3B and 3C) and **9:3:4** (Fig. 1C).

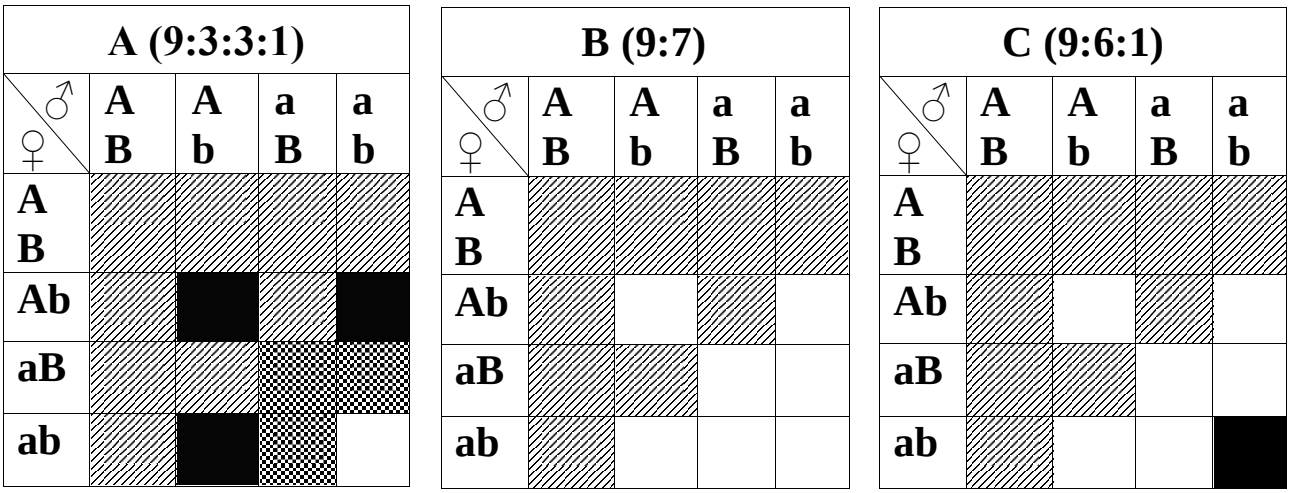


Figure 3. Scheme of splitting traits in the second generation in the complementary interaction of two genes

Polymery is a type of interaction of genes whose dominant alleles **uniquely** affect the development of the same trait. Genes with an unambiguous action are called polymeric**.** Polymery can be **cumulative** or **non-cumulative**. In **cumulative** polymery, the intensity of the trait value depends on the summing effect of genes: the more dominant alleles of interacting genes in the genotype of an individual, the greater the degree of trait manifestation. In **non-cumulative** polymery, there is no summing effect of genes and individuals with any number of dominant alleles of interacting genes in the genotype have the same phenotype. If there are no dominant alleles in the genotype, the phenotype will be different.

Polymer genes are designated by a single letter symbol; alleles of one gene have the same numeric index ($\mathbf{A_1a_1\ A_2a_2\ A_3a_3}$ – the genotype of the triheterozygote). Cleavage during cumulative polymerization – **1:4:6:4:1** (Fig. 4A), which can be reduced to **15:1** by combining the first four classes into one.

Cumulative polymery occurs when forming the color of wheat grains, oat seed flakes, human growth and skin color, and so on. For example, the red color of wheat caryopses is determined by two genes. Each of the dominant alleles of these genes determines the presence of pigment, a recessive allele determines the absence of pigment. If there is one dominant allele in the genotype, the grains are slightly colored, if there

are two dominant alleles in the genotype, and then the grain color is brighter, and so on. Only in homozygotes, the recessive alleles of all the genes are not pigmented.

Thus, in the offspring of grain obtained from dihybrid cross, there is a split in the ratio of 15 colored caryopses to one white. Of the 15/16 colored caryopses, 1/15 will be red, since it contains four dominant alleles in the genotype, 4/15 will be slightly lighter, since their genotype will have three dominant alleles and one recessive, 6/15 – even lighter with two dominant and two recessive alleles, and 4/15 – the lightest, having only one dominant and three recessive alleles.

Non-cumulative polymery is characterized by a 15:1 splitting (Fig. 4B). **Non-cumulative polymery** occurs when inheriting the fruit shape of Capsella. Among plants of the second generation, 15/16 have fruits of a triangular shape (in the genotype one two, three or four dominant alleles), 1/16 – oval (in the genotype there are no dominant alleles).

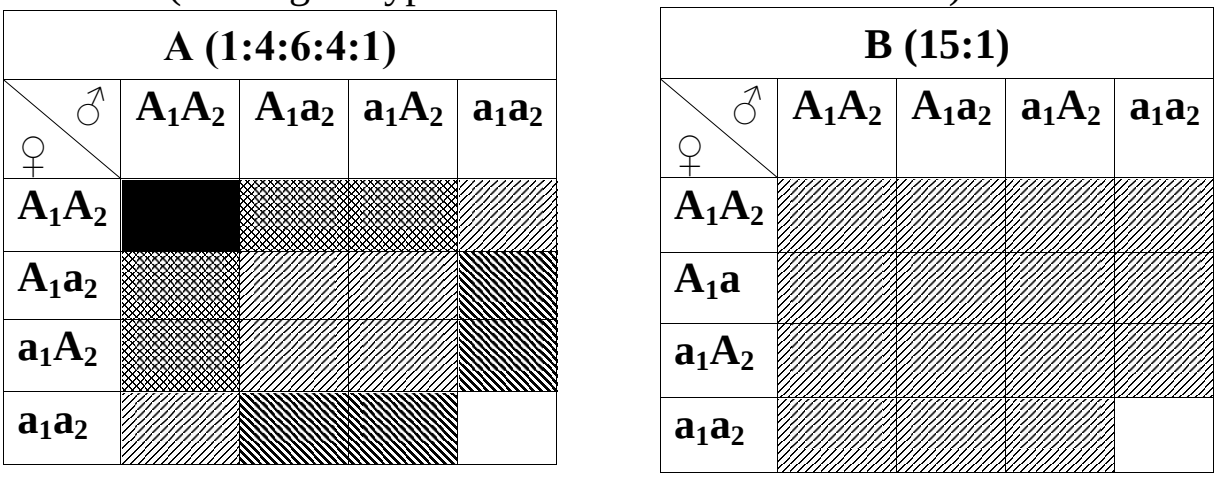


Figure. 4. Splitting scheme for cumulative polymery (A) and non-cumulative polymery (B)

Algorithm for solving the task of gene interaction

Task (case study). The plumage color of parrots is determined by two genes. The dominant allele of the first (A) determines the development of the blue plumage, the dominant allele of the second (B) yellow plumage. The presence of two dominant alleles leads to the development of green color. Recessive alleles determine the development of white plumage.

What segregation will be from crossing homozygous birds with yellow and blue plumage? What will be the splitting in F_2?

The algorithm for solving the task is shown in table 6.

Table 6

Algorithm for solving the task of gene interaction

<table>
<tr><td>P</td><td colspan="2">AAbb
Blue color</td><td>x</td><td>aaBB
Yellow color</td></tr>
<tr><td>G</td><td colspan="2">Ab</td><td></td><td>aB</td></tr>
<tr><td>F₁</td><td colspan="4">AaBb
Green color</td></tr>
<tr><td>P</td><td colspan="2">AaBb
Green color</td><td>x</td><td>AaBb
Green color</td></tr>
<tr><td>G</td><td colspan="2">AB, Ab, aB, ab</td><td></td><td>AB, Ab, aB, ab</td></tr>
<tr><td>F₂</td><td colspan="4">
<table>
<tr><td>♀ \ ♂</td><td>AB</td><td>Ab</td><td>aB</td><td>ab</td></tr>
<tr><td>AB</td><td>AABB
green</td><td>AABb
green</td><td>AaBB
green</td><td>AaBa
green</td></tr>
<tr><td>Ab</td><td>AABb
green</td><td>AAbb
blue</td><td>AaBb
green</td><td>Aabb
blue</td></tr>
<tr><td>aB</td><td>AaBB
green</td><td>AaBb
green</td><td>aaBB
yellow</td><td>aaBb
yellow</td></tr>
<tr><td>ab</td><td>AaBa
green</td><td>Aabb
blue</td><td>aaBb
yellow</td><td>aabb
white</td></tr>
</table>
</td></tr>
<tr><td colspan="5">Answer. In the F_1 generation, all birds will have the AaBb genotype (green plumage). In the F_2 generation, the phenotype cleavage will be in the ratio of 9:3:3:1.</td></tr>
</table>

Task 222. A plant homozygous for recessive alleles of three genes, has a height of 32 cm, and homozygous for the dominant alleles of these genes is 50 cm. We assume that the phenotypic effect of each dominant allele is the same and is summed up. In F_2, 192 descendants were obtained from crossing these plants.

Determine the number of plants that theoretically will have a genetically determined growth of 44 cm.

Task 223. The height of Sorghum, homozygous for recessive alleles of four polymer genes, is 40 cm. The height of a plant that is homozygous for the dominant alleles of these four genes is 240 cm. Plants with genotypes $A_1A_1a_2a_2A_3A_3a_4a_4$ and $a_1a_1a_2a_2a_3a_3A_4A_4$ were crossed.

Calculate the height of the stem of these plants.

Calculate the expected height of first-generation plants.

Indicate the possible phenotypes of the plants of the second generation.

Specify the frequency of occurrence of each phenotype.

Task 224. The red color of an onion bulb is determined by the dominant allele, and the yellow color is determined by the recessive allele of an autosomal gene. Phenotypic expression of this gene is possible only if the dominant allele of another gene in the genotype is not linked to the first one. Homozygotes for the recessive allele of the second gene have white bulbs. The red-bulb plant was crossed with the yellow-bulb one. Plants of the new generation had red, yellow and white bulbs.

Determine the genotypes of the parents and offspring.

Task 225. Crossing rye with green grains resulted in 886 plants with green grains, 302 plants with yellow and 391 plants with white grains in the next generation.

Write a crossbreeding scheme and explain the results of the crossbreeding.

Task 226. When crossed with white-grain rye, green-grain rye results in plants with green grains in the first generation. Splitting by color in the second generation: 89 plants with green grains, 28 plants with yellow grains, 39 plants with white grains.

Explain the results and write a crossbreeding scheme.

Explain the result of crossing first-generation hybrids with a homozygous yellow-grain plant.

Explain the result of crossing first-generation hybrids with a homozygous white-grain plant.

Task 227. Crossing rye plants with anthocyanin resulted in the following splitting in the next generation: 132 plants with anthocyanin and 104 plants without anthocyanin.

Write a crossbreeding scheme and explain the results of the crossbreeding.

Task 228. Green-grain and white-grain rye plants were crossed. The first-generation hybrids had green seeds. 178 plants of the second generation had seeds of green color, 56 – yellow, 78 – white.

Explain the genetic determination of the trait.

Determine the seed color of the first-generation hybrids if they are crossed with homozygous yellow-grain and white-grain plants.

Task 229. From crossing rye plants of different varieties (the first variety has red auricles on the leaves and yellow grains, the second variety has white auricles and white grains), hybrids of the first generation with red auricles and green grains were obtained. There was the following splitting in the second generation: 360 plants with red auricles and green grains, 117 plants with red auricles and yellow grains, 164 plants with red auricles and white grains, 122 plants with white ears and green grain, 42 plants with white auricles and yellow grains, 54 plants with white auricles and white grains.

Determine the genetic determination of traits.

Determine the genotypes of the parents and offspring.

Task 230. Color of wheat grains is controlled by two genes that are not linked. Their dominant alleles determine the red color, while the recessive ones – white. From red grains, there were obtained 75% of red-grain plants and 25% of white-grain plants. Red-grain plants had seeds with different degree of color.

Determine the genotypes of the original plants and their offspring.

Task 231. From crossing wheat plants with red grains, 397 plants with red grains and 23 plants with white grains were obtained in the next generation.

Write a crossbreeding scheme and explain the results of the crossbreeding.

Task 232. In wheat, white and red grain color is controlled by three pairs of alleles. Plants that are recessive in all three pairs of alleles have white grains. The presence of one or more dominant alleles determines the red color of the grain (which increases with the number of dominant alleles).

A) From crossing a homozygous red plant with a white one, there was the following splitting in the second generation: 15 red to 1 white.

Determine the possible genotypes of the parent plants.

B) From crossing homozygous wheat with red seeds and a plant having white seeds, the following splitting was obtained in the second generation: 1 plant with white seeds and 63 with red seeds.

Write a crossbreeding scheme and determine the number of dominant alleles that the parent red plant had.

Task 233. Having two forms of wheat – an awnless one with black spikes and an awned one with red spikes, the breeder crossed them to get an awnless variety with red spikes. In the first generation from this crossing, all the plants were awnless and had black spikes.

In the second generation, there was the following splitting: 714 awnless plants with black spikes, 181 awnless plants with red spikes, 58 awnless with white spikes, 231 awned plants with black spikes, 61 awned with red spikes and 20 awned with white spikes.

Explain the splitting.

Calculate the number of genes that control the traits being studied.

Determine the nature of gene inheritance and determine the genotypes of the original forms.

Determine the part of the awnless plants with red spikes homozygous for all genes.

Task 234. When crossing homozygous awned wheat plants with red spikes and homozygous awnless plants with white spikes, all plants in the first generation had red spikes and were awnless. In the second generation, 564 plants had awnless red spikes, 184 plants had awned red spikes, 38 plants had awnless white spikes and 10 plants were awned and had white spikes. The offspring from the test cross were 103 red awnless, 90 red awned, 30 white awnless and 27 white awned plants.

Determine the genotypes of the original plants and first-generation hybrids.

Determine the plant that was homozygous for recessive alleles.

Explain the obtained results.

Task 235. From crossing wheat plants with a red dense spike with plants that have a white loose spike, there were obtained red spikes of medium density in the first generation. In the second generation there was the splitting: 186 red with a dense spike, 358 red with a medium-density spike, 184 red with a loose spike, 12 white with a dense spike, 25 white with a medium-density spike and 10 white with a loose spike.

Determine the inheritance of traits.

Establish the genotypes of the original plants.

Check whether your assumption is correct.

Task 236. Crossing oat plants with black grains resulted in obtaining 317 plants with black grains, 76 – with gray and 24 – with white grains in the next generation.

Write a crossbreeding scheme and explain the results of the crossbreeding.

Task 237. In oat, the color of the grains is determined by two unlinked genes. The dominant allele of one gene determines the black color of the grains, the dominant allele of the other – the gray color of the grains. The black color allele suppresses the gray color allele. Recessive alleles of both pairs determine the white color of the grains. From crossing white-grain oats with black-grain ones, there were obtained the offspring, 1/2 of which had black grains and 1/2 – gray grains.

Write a crossbreeding scheme and explain the results of the crossbreeding.

Task 238. From crossing oat plants with paniculate inflorescences 188 plants with paniculate inflorescences and 10 plants with simple inflorescences were obtained in the next generation.

Write a crossbreeding scheme and explain the results of the crossbreeding.

Task 239. Nilsson-Ehle in 1907 made experiments with oat. The color of oat bracts is determined by two polymer genes: $A_1A_1A_2A_2$-black color, $a_1a_1a_2a_2$ – white color. Color depends on the number of dominant alleles. When crossing plants with black and white bracts, all plants in the first generation had gray scales, and there were obtained 12 black, 56 dark gray, 98 gray, 63 light gray and 15 white plants in the second generation.

Write a crossbreeding scheme and explain the results of the crossbreeding.

Task 240. In oat, the color of the grain is controlled by two unlinked genes. The dominant allele of one of them determines the black color of the grain; the dominant allele of the second gene manifests as the gray color. The black gene suppresses the expression of the gray gene. If the genotypes of plants have only recessive alleles of both genes, the grain is white. We crossed the plants that grew from white seeds with the plants that grew from black seeds. Their seeds ripened and were sown. Half of the resulting plants had black grains, and the other half – gray grains.

Determine the genotypes of the parents and offspring.

Task 241. Let us assume that in two high-inbred oat lines, the yield was 4 g and 10 g per plant, respectively. Plants of these lines were crossed,

approximately 1/64 individuals of the second generation had a yield of 10 g per plant.

Calculate the number of genes that control differences between inbred lines.

Task 242. In corn of one variety, the cob consists of 20 rows of grains, and in another one – of 8 rows. The offspring from crossing plants of these varieties had cobs with 14 rows of grains on average. Plants of the second generation are phenotypically heterogeneous, the number of grain rows in their cobs varies from 8 to 20. Moreover, about one in every 32 cobs has the same number of grain rows as one of the plants of the parent generation.

Calculate the number of genes that control this trait.

Task 243. From crossing two dwarf maize plants, hybrid plants of normal height are obtained. Among the second-generation plants, 452 were of normal height and 352 were dwarf.

Determine the genotypes of plants of all generations.

Task 244. From crossing 2 green maize plants, the offspring of 191 green plants and 146 uncolored plants was obtained.

Write a crossbreeding scheme and explain the results of the crossbreeding.

Task 245. In corn, the interaction of dominant alleles of the C and R genes is necessary for the development of the red color of seeds. In the absence of the C allele, the seeds have purple color, in the absence of the R allele – pink, in the absence of both dominant genes – white color.

Write a crossbreeding scheme and explain the results of the crossbreeding: a) of heterozygous red plants with each other; b) of purple plants with white ones; c) of heterozygous red plants with white ones.

Task 246. From crossing corn with white wrinkled grains with a plant that has purple smooth grains, in F1 all the grains turned out to be white smooth, and in F2 there was the following splitting: 808 white smooth, 249 white wrinkled, 202 purple smooth, 50 purple wrinkled. In the test cross we obtained: 135 white smooth, 150 white wrinkled, 40 purple smooth, 52 purple wrinkled.

Determine the type of inheritance for these traits.

Determine the genotypes of the original plants, F1 plants and the phenotype of the plant homozygous for recessive allele.

Task 247. From crossing maize plants with red wrinkled grains with plants having white smooth grains, all plants in the first generation had purple smooth grains. In the second generation, the following splitting occurred: 840 purple smooth, 280 purple wrinkled, 378 white smooth, 123 white wrinkled, 273 red smooth, 89 red wrinkled.

Determine the type of inheritance for these traits.

Determine the genotypes of the original plants.

Determine the splitting in the test cross and identify the plant that is homozygous for recessive allele.

Task 248. Crossbreeding of two white-grain maize plants resulted in white-grain hybrids of the first generation. In the second generation 138 white-grain plants and 39 plants with purple grains were obtained.

Write a crossbreeding scheme and explain the results of the crossbreeding.

Determine what offspring will be obtained in the test cross and back cross.

Task 249. From crossing two lilac plants with lilac flowers, 72 plants with lilac, 56 with white and 6 plants with pink flowers were obtained in the next generation.

Write a crossbreeding scheme and explain the results of the crossbreeding.

Task 250. There were crossed flax plants of two varieties: one of them had pink flowers and simple petals, and the other one – white flowers and simple petals. The first-generation plants had pink flowers with simple petals. Among plants of the second generation, there was the splitting in the phenotype: 40 plants with pink simple petals, 8 plants with pink corrugated petals, 4 with white corrugated petals and 14 with white simple petals.

Find out the determination of the color and type of petals.

Task 251. There were crossed gillyflowers of two varieties: one had double red flowers, and the other one – double white flowers. The first-generation hybrids had simple red flowers, and the second-generation

hybrids had parental traits in different combinations: 68 plants with double white flowers, 275 with simple red, 86 with simple white and 213 with double red flowers.

Find out the genetic determination of the flower color and shape.

Determine the genotypes of the parents and offspring.

Task 252. From crossing beans with purple fruits the following splitting was obtained in the next generation: 58 plants with purple fruits and 37 plants with green fruits.

Write a crossbreeding scheme and explain the results of the crossbreeding.

Task 253. There were crossed alfalfa plants (a forage plant of the legume family) with purple and yellow flowers. All the first-generation plants turned out to have green flowers. In the second generation, 890 plants with green flowers, 311 with purple flowers, 306 with yellow flowers and 105 with white flowers were obtained.

Determine, theoretically, the number of homozygotes among plants with purple flowers.

Task 254. In sweet peas, a purple color of flowers is obtained when two dominant alleles of two genes are combined in the genotype. In the absence of two dominant alleles of two genes, plants develop a white color.

A) The sweet pea plant with white flowers was crossed with the same white-flowered plant. The offspring produced 23 plants with purple flowers and 77 plants with white flowers.

Determine the genotypes of the parents and offspring.

Determine the color of flowers in the offspring from crossing plants with purple flowers.

B) A sweet pea plant with white flowers was crossed with a purple-flowered plant. The offspring turned out to be: 3/8 plants with purple flowers are 5/8 plants with white flowers.

Write a crossbreeding scheme and explain the results of the crossbreeding.

Task 255. Sweet pea plants of the parent generation had white axillary and white terminal flowers. In the F1 generation, all the plants turned out to have purple axillary flowers. In the F2 generation, 415 plants with

purple axillary flowers, 140 plants with purple terminal flowers, 350 with white axillary flowers, and 95 with white terminal flowers were obtained.

Determine the type of inheritance for these traits.

Determine the plants that should be taken for a test cross, write a crossbreeding scheme and explain the results of the test cross.

Task 256. After self-pollination of the green pea plant, seeds were obtained, and then 670 green and 43 light green plants were obtained from these seeds.

Explain the reason for splitting by phenotype among plants of the new generation.

Determine the genotype of the original green plant.

After crossing a pea plant with the same genotype and phenotype as the original plant with light green offspring, 480 plants were obtained. Determine the theoretically expected number of light green plants.

Task 257. Bean plants of one variety had seeds of white color, and of the other variety – brown color. In the first-generation hybrids, the seeds were purple when these varieties were crossed. 636 plants of the second generation had purple seeds, 215 – brown and 285 – white.

Explain the results of the crossbreeding.

Determine the genotypes of the parents and offspring.

Task 258. From crossing plants of the gorse (a wild plant of the legume family) with yellow flowers, 226 with yellow flowers and 159 with white flowers were obtained in the next generation.

Write a crossbreeding scheme and explain the results of the crossbreeding.

Task 259. From crossing pepper varieties with yellow and brown fruits, plants with red fruits were obtained in the first generation. From crossing the first-generation hybrids among themselves, 182 plants with red fruits, 61 plants with yellow fruits, 59 plants with brown fruits and 20 plants with green fruits were obtained.

Write a crossbreeding scheme and explain its results.

Task 260. In capsella, the shape of the fruit depends on two polymer genes. Plants that have at least one dominant allele produce fruits that are triangular and do not differ in fruit shape from plants that have 2, 3, and 4

dominant alleles. Plants that do not have any dominant alleles produce egg-shaped fruits. A plant with triangular fruits is crossed with a plant with egg-shaped fruits. In the first generation, the ratio in the offspring was 3 triangular to 1 egg-shaped fruit.

Determine the genotypes of the parent plants. Explain the results that may be obtained under the condition of crossing diheterozygous plants.

Task 261. There were crossed a geranium plant with red flowers and a plant of the same phenotype. In the next generation, 131 plants with red flowers, 46 with pink flowers, and 55 with white flowers were obtained.

Write a crossbreeding scheme and explain the results of the crossbreeding.

Task 262. There were crossed plants of two flax varieties, one of which has a pink color of flowers and normal petals, and the other – a white color of flowers and normal petals. All first-generation plants have pink flowers and normal petals. In the second generation, the following splitting occurred: 40 plants with pink flowers and normal petals, 8 plants with pink flowers and corrugated petals, 4 plants with white flowers and corrugated petals, 14 plants with white flowers and normal petals.

Determine the type of inheritance for the flower color and corolla type.

Write a crossbreeding scheme.

Task 263. The shape of the fruit in a pumpkin can be spherical, disc-shaped or elongated and it is determined by 2 pairs of alleles of unlinked genes.

A) From crossing pumpkin plants with spherical fruits, all the plants in the first generation turned out to be disc-shaped. From crossing pumpkin plants with disc-shaped fruits, 121 plants with disc-shaped fruits, 77 plants with spherical fruits and 12 plants with elongated fruits were obtained in the offspring.

Write a crossbreeding scheme and explain the results of the crossbreeding.

Determine the expected splitting in the test cross.

Determine the phenotype of the plant that was homozygous for recessive allele.

B) When crossing a pumpkin with disc-shaped fruits and a pumpkin with elongated fruits, the offspring had the following splitting: 1 plant with

disc-shaped fruits, 2 plants with spherical fruits, 1 plant with elongated fruits.

Determine the genotypes of the crossed plants and their offspring.

C) When crossing a pumpkin with disc-shaped fruits and a pumpkin with spherical fruits, half the offspring obtained consisted of plants with disc-shaped fruits and the other half – of plants with spherical fruits.

Determine the genotypes of the crossed plants and their offspring.

Task 264. From crossing pumpkins with white fruits, 67 plants with white fruits, 19 plants with yellow fruits and 6 plants with green fruits were obtained in the next generation.

Write a crossbreeding scheme and explain its results.

Task 265. From crossing the yellow-fruit pumpkin with the white-fruit one, all the offspring were white-fruit. From crossing the obtained individuals, 204 plants with white fruit, 53 with yellow fruit, and 17 with green fruit were obtained.

Write a crossbreeding scheme and explain its results.

Task 266. Pumpkin fruits are white, yellow and green. Two varieties of pumpkin with white and green fruits were crossed, all the offspring in the first generation had white fruits. In the second generation the following splitting took place: 159 white, 38 yellow and 13 green.

Write a crossbreeding scheme and explain its results.

Task 267. In pumpkin, the allele of white color suppresses the allele of yellow and green colors. In this case, the white color allele of one gene suppresses the manifestations of the yellow and green color alleles of the other gene.

Determine the genotypes of the parents and offspring in the following crosses:

a) white-fruit pumpkins were crossed with yellow-fruit ones, 78 white-fruit, 61 yellow-fruit and 19 green-fruit plants were obtained in the offspring;

b) white-fruit pumpkins were crossed with green-fruit ones, 145 white-fruit, 72 yellow-fruit and 66 green-fruit plants were obtained in the offspring;

c) white-fruit pumpkins were crossed with white-fruited ones, 851 white-fruit, 218 yellow-fruit and 68 green-fruit plants were obtained in the offspring.

Task 268. The shape of pumpkin fruit is determined by two pairs of alleles of unlinked non-allelic genes.

A) Plants of two varieties with a spherical shape of the fruit were crossed. The obtained offspring were crossed among themselves, after which they produced disc-shaped fruits. The seeds taken from disc-shaped fruits produced phenotypically heterogeneous offspring: 916 plants had disc-shaped fruits, 616 – spherical and 116 – elongated.

Determine the genotypes of the original plants and all offspring of the first and second generation.

B) From crossing two varieties of pumpkins with disc-shaped and elongated fruits, the following offspring were obtained: 1/4 with disc-shaped fruits, 2/4 with spherical ones and 1/4 with elongated fruits.

Determine the genotypes of the parents and offspring.

Task 269. When crossing a strawberry plant of the white-fruit variety without runners and a strawberry plant of the red-fruit variety with runners, all the plants in the first generation turned out to be red-fruit and with runners. In the second generation, there was the splitting: 331 with red fruits and runners, 235 with red fruits without runners, 88 with white fruits and runners, and 98 with white fruits without runners.

Find out the genetic determination of traits.

Determine the genotypes of the original plants.

Specify the method for obtaining homozygous plants with runners and red fruits.

Task 270. Cockroaches with ruby and white eyes were crossed, all first-generation offspring had scarlet eyes. In the second generation, 22 cockroaches had red eyes, 17 – pink, 4 – ruby, 32 – scarlet, 6 – white. Dominant alleles determine the dark color while recessive alleles – light.

Write a crossbreeding scheme and explain its results.

Task 271. Green and scarlet swordtails (viviparous fish of the family Poeciliidae, order Cyprinodontiformes) were crossed. In the first generation, all the fish were brick-red in color, in the second generation there were 46 brick-red, 5 lemon, 16 scarlet and 14 green fish.

Find out the genetic determination of the trait.

Determine the genotypes of the original fish.

Explain the result of the cross of scarlet fish and lemon fish.

Task 272. From crossing swordtails that had two black spots on the tail with fish without spots, hybrids with a black stripe on the tail were obtained. Among the second-generation fish, 54 had a black stripe on the tail, 16 had two black spots and 28 had neither spots nor a black stripe on the tail.

Find out the genetic determination of the trait.

Determine the genotypes of the original fish and hybrids of the first generation.

Task 273. In lovebirds, the plumage color is determined by two unlinked genes. The dominant allele of one gene determines the yellow color of feathers, and the dominant allele of the other gene determines the blue color. The presence of dominant alleles of both genes in the genotype (in any doses) determines the green color, but the presence of only recessive ones – the white color of the plumage.

A) Green lovebirds were crossed among themselves, the offspring of 55 green, 18 yellow, 17 blue and 6 white birds were obtained.

Determine the theoretical number of homozygotes for both pairs of alleles in the offspring.

B) The zoo has received an order for white lovebirds. However, it was not possible to breed white birds from crossing the existing green and blue ones.

Determine the genotypes of birds in the zoo.

Task 274. From crossing white chickens without a comb and white ones with a comb, white chickens with a comb were obtained. In the second generation, in addition to 39 white birds with a comb and 12 white ones without a comb, there were 4 red birds without a comb and 9 red birds with a comb.

Determine the genotypes of the second-generation birds.

Determine the ratio of heterozygotes among 39 white chickens with a comb of the second generation.

Task 275. From crossing white hens with black roosters, all offspring in the first generation were white, and in the next generation there was the following splitting: 163 white and 34 black birds.

Write a crossbreeding scheme and explain its results.

Task 276. Two breeds of chickens were crossed. One of them had white plumage and a comb, and the other one – white plumage without a comb. All chickens in the first generation were white and had a comb. In the second generation, the following splitting was obtained: 78 white birds with a comb, 8 red birds without a comb, 24 white birds without a comb, 18 red birds with a comb.

Determine the type of inheritance of color and a comb.

Write a crossbreeding scheme.

Task 277. In some breeds of chickens, the plumage color depends on the interaction of two genes. The dominant allele of one gene determines the presence of the colored plumage, and its recessive allele – white. The dominant allele of the other gene suppresses the formation of pigment. Chickens that have this allele in their genotype, as well as chickens that are homozygous for the recessive allele of the first gene, have white plumage.

A white rooster was crossed with two hens. After the cross with a white chicken, the following offspring were obtained: 7/8 had white plumage and 1/8 – colored. After the cross with a colored chicken 5/8 of the offspring had white plumage and 3/8 – colored.

Determine the genotypes of the rooster and hens of the parent generation and offspring from two crosses.

Task 278. In chickens, the dominant alleles of two genes separately determine the development of a rose and pea comb. Together they determine the development of a walnut comb. If only recessive alleles of both genes are present in the genotype, a simple leaf-like comb is formed. From crossing a rooster with a rose comb and a hen with a walnut one, the following offspring are obtained: 3/8 birds have a walnut comb, 3/8 – rose comb, 1/8 – pea comb and 1/8 – simple leaf-like comb.

Determine the genotypes of the parents and offspring.

Task 279. The plumage color of chickens is determined by two unlinked genes. The dominant allele of one gene determines the colored plumage, while the recessive allele determines the white plumage. The dominant allele of another gene suppresses the phenotypic effect of the dominant allele of the first gene, and the recessive one does not have its own phenotypic expression.

A) The cross of white chickens resulted in the offspring of 1,680 chickens. 315 of them had colored plumage while the rest were white.

Determine the genotypes of the parents and colored chickens.

B) On a poultry farm, white chickens were crossed with colored ones, which resulted in 5,050 white chickens and 3,033 colored ones.

Determine the genotypes of the parents and offspring.

C) White and colored chickens were crossed. 915 colored and 916 white chickens were obtained as a result of the cross.

Determine the genotypes of the parents and offspring.

Task 280. In hens, C and O – dominant alleles of the plumage color (black and mottled color), I – dominant allele – color inhibitor. The genotypes of the breeds: white Leghorn – CCOOII, white Wyandot – ccOOII, white Silkie – CCooII.

Determine the offspring of the first and second generation from crosses between these breeds.

Task 281. Horses with the genotypes AAbb and Aabb have the black coat color, with the genotype aabb – red coat color, with the genotype AABB, AABb, AaBb, aaBb – gray coat color.

Determine the types of interaction between alleles A and a, A and B, B and a.

Determine the coat color of the offspring from the cross of horses with the genotypes AaBb.

Task 282. In horses, the dominant allele (B) of one gene determines the black color of the coat, and the recessive allele of the same gene (b) – red color. The dominant allele (A) of the other gene suppresses the phenotypic effect of the alleles B and b. Horses whose genotype contains the A allele have a gray coat color. The recessive allele of the epistatic gene does not have its own phenotypic manifestation.

Determine the splitting of color among the offspring from the cross of two gray diheterozygous horses.

Determine the genotype of the stallion from the cross of the gray stallion with several heterozygous black mares. The following offspring were obtained: 1/2 – gray, 3/8 – black and 1/8 – red horses.

Task 283. The color of horses is controlled by three unlinked non-allelic genes. Different coat colors correspond to the following genotypes: A_B_E_ – dun horse; A_bbee – palomino; A_B_ee – grullo; aaB_ee – brown; aaB_E_ – bay; aabbE_ – buckskin; A_bbE_ – buckskin dun; aabbee – red.

Determine the splitting of the phenotype among the offspring from the cross of red and triheterozygous dun horses.

Determine the coat color of horses among the numerous offspring from the cross of brown and buckskin dun horses, if the offspring has a red horse.

Task 284. Sheep of one breed have an average coat length of 40 cm, and sheep of the other one – 10 cm. Let us assume that the differences between species depend on the combination of alleles of three polymer genes.

Determine the phenotype of the hybrid sheep of the first and second generations.

Determine the ratio of each phenotypic class.

Task 285. Coat color in mice is determined by two unrelinked genes. The dominant allele of the first gene determines the gray color, the recessive allele – black. The recessive allele of the second gene suppresses the phenotypic expression of alleles of the first gene, and the dominant allele is not epistatic.

Determine the genotype of the parents and offspring if the cross of gray mice resulted in 82 gray, 35 white, 27 black mice.

Determine the genotypes of the parents and offspring if the cross of gray mice resulted in 58 gray and 19 black offspring.

Task 286. White and black Guinea pigs were crossed. The offspring turned out to be gray. There was the following splitting in the next generation: 44 gray, 16 black and 19 white pigs.

Write a crossbreeding scheme and explain the results of the crossbreeding.

Task 287. In 1933, Parkhurst and Wilson bred a new breed of rabbit, the Lilac Rex. In their work, they took into account four genes (8 alleles): A – agouti (uneven distribution of pigment along the length of the hair and body), a – non-agouti (even distribution of pigment along the length of the hair and body); B – black coat color, b – chocolate coat color; D – intense pigmentation, d – weakened pigmentation (in homozygotes dd black coat color is weakened to blue, chocolate – to lilac); P – normal hair length, p – short hair without hard long guard hair, only with a soft down (Rex).

Breeders crossed homozygous castor-Rexes (black agouti rabbits with

short hair) with homozygous lilac non-agouti rabbits with normal length hair. 38 animals of the first generation had all dominant traits. The second generation consisted of five hundred and twenty-four rabbits.

Determine the genotypes of the original, parent individuals.

Define classes according to the phenotype in the second generation.

Determine the chance of getting the breeders in this generation of the desired lilac Rex is not agouti.

Task 288. In rabbits, the development of black color requires the interaction of dominant alleles of the A and B genes. In the absence of the A allele, rabbits have a brown color, in the absence of the B allele – yellow, in the absence of dominant alleles of both genes – orange color. Yellow rabbits were crossed with brown ones, all the offspring turned out to be black. When crossing black rabbits in the second generation, 60 black, 19 brown, 16 yellow and 8 orange color rabbits were obtained.

Write a crossbreeding scheme and explain its results.

Task 289. The ears of ram rabbits have a length of 40 cm, which depends on the presence only of dominant alleles of two unlinked non-allelic genes in the genotype. Mongrel rabbits' ears are 20 centimeters long, which is due to the combination of only recessive alleles of these genes in their genotype.

Determine the splitting in the length of ears among the second-generation hybrids from the cross of ram and mongrel rabbits.

Task 290. White and blue rabbits were crossed. There were 28 black rabbits in the first generation and 67 black, 27 blue and 34 white rabbits in the second generation.

Calculate the number of genes that determine the coat color in rabbits.

Determine the genotypes of the parents and offspring.

Task 291. A female rabbit with black fur of normal length was crossed with a white short-haired male. All the rabbits in the first generation had traits of their mother. Among the second-generation rabbits, there was the following splitting: 31 with black fur of normal length, 9 with blue fur of normal length, 13 with white fur of normal length, 8 with short black fur, 3 with short blue fur, 4 with short white fur.

Determine the genotypes of the parents and offspring of the first and second generations.

Find out the genetic determination of traits.

Task 292. Black rats were crossed with white ones. All offspring in the first generation were white. There were 76 white, 29 black and 8 gray rats in the second generation.

Write a crossbreeding scheme and explain the results of the crossbreeding.

Task 293. Black Cocker Spaniels were crossed. The offspring of 4 coat colors were obtained: 34 black dogs, 13 red dogs, 11 brown dogs and 4 light-yellow dogs.

Write a crossbreeding scheme and explain the results of the crossbreeding.

A black Cocker Spaniel was crossed with a light-yellow one. From this cross there appeared a light-yellow puppy in the offspring.

Determine the ratio of coat colors in the offspring from the cross of the same black Cocker Spaniel with a dog of the same genotype.

Task 294. After crossing dogs with brown and white coat color, many white puppies were obtained. There were 60 white, 16 black and 5 brown individuals in the offspring from numerous crosses of the first-generation hybrids.

Determine the genotypes of the parents and offspring.

Explain the result of the cross of white and black homozygous dogs.

Task 295. From crossing dogs with agouti color (each hair is divided into several color zones: the main zone and the zone of the tips, thus getting the so-called color zoning), the following split was obtained: 86 agouti dogs, 34 black dogs and 42 coffee dogs. Determine the type of inheritance and write a crossbreeding scheme. Crossing the obtained agouti dogs with the obtained black dogs resulted in the following offspring: 3/8 agouti dogs, 3/8 black dogs and 2/8 coffee dogs.

Determine the genotypes of the crossed animals and their offspring.

Task 296. The coat color of minks bred on fur farms (the Mustelidae family) is controlled by two unlinked non-allelic genes. Dominant alleles of both genes determine the brown coat color, recessive ones – platinum.

Determine crosses in which all offspring from minks of different colors will be brown.

Task 297. Minks of two lines with beige and gray coat color were crossed. The first-generation hybrids had brown fur. In the second generation, there was the following splitting: 14 gray, 46 brown, 5 cream, 16 beige minks.

Explain the appearance of mink with brown fur in the first generation, and the appearance of mink with the cream coat color in the second one.

Determine the offspring from the cross of the first-generation brown minks with cream minks.

Task 298. Synthesis of interferon (a protein secreted by the body's cells in response to an invading virus) in humans is determined by the combination of 2 dominant alleles, one of which is located on chromosome 2, and the other one – on chromosome 5. The presence of only one gene in the dominant allele genotype or their absence determines the inability to synthesize interferon.

Determine the probability of having a child who is not able to synthesize interferon in a family where both parents are heterozygous for these genes.

Task 299. In humans, ABO antigens are found not only in red blood cells (RBCs), but also in other cells of the body. In some people (secretors), water-soluble forms of these antigens are secreted with saliva and other fluids. In other people (non-secretors), saliva and other bodily fluids do not contain these antigens.

ABO blood groups determined by alleles I°, I^A, I^B, and the presence of antigens A and B in saliva – by the dominant allele Se. *Secretor* – in this case a symbol consisting of two letters Se is used to denote the gene. The recessive gene (non-secretor) is denoted by the symbol – se.

A) Parents do not secrete antigens A and B in saliva, their genotypes are I^AI^Bsese and I°I°Sese.

Determine the probability of the birth of a child that secretes antigen A in saliva.

B) When examining the blood and saliva of four family members, the following was discovered: the mother has B antigen in RBCs but does not have it in saliva; the father has A antigen in RBCs and saliva; the first child has A and B antigens in RBCs but does not have them in saliva; the second child has blood group A.

Determine the genotypes of the parents and children.

Task 300. The Bombay phenomenon is described in scientific literature. In a family where the father had blood group A and the mother had blood group AB, there was born a girl with blood group A. She married a man with blood group B and they gave birth to two girls: the first girl had blood group O, the second one – blood group A. The appearance of a girl with blood group O in the third generation caused confusion. Some geneticists tend to explain this phenomenon by the presence of a recessive allele in the genotype of the rare epistatic gene that can suppress alleles that determine blood groups A and AB. Accepting this hypothesis:

Determine the probable genotypes of the individuals of all three generations.

Determine the probability of having children with blood group A in the family of the first daughter from the third generation if she marries a man with the same genotype as hers.

Task 301. A person has several forms of inherited myopia. Moderate form (from –2.0 to –4.0) and high form (above –5.0) are inherited as dominant unlinked traits. In a family where the mother was nearsighted and the father had normal vision, a daughter and a son were born. The daughter had a moderate form of myopia, and the son had a high one. It should be borne in mind that people who have genes for both forms of myopia show only one – high.

Determine the probability of having the next child without abnormalities if it is known that only one of the mother's parents suffered from myopia.

Task 302. Human height is controlled by several pairs of alleles of unlinked polymer genes. If we ignore environmental factors and assume that only three genes control height, then the shortest people will have only recessive alleles and a height of 150 cm, and the tallest ones – only dominant alleles and a height of 180 cm.

Determine the height of people who are heterozygous for all three pairs of alleles.

4. THE PENETRANCE AND EXPRESSIVITY

Task 303. Arachnodactyly ("spider fingers") is determined by the dominant allele of the autosomal gene with 30% penetrance. The ability to use the left hand is determined by the recessive allele of the autosomal gene with 100% penetrance.

Determine the probability of the birth of a left-handed child with arachnodactyly in a family where the parents are heterozygous for both pairs of alleles.

Task 304. A brown-eyed man suffering from retinoblastoma (a malignant tumor of the eye), whose mother was blue-eyed and came from a healthy family and whose father was brown-eyed and suffered from retinoblastoma, married a blue-eyed woman whose ancestors were all healthy.

Determine the probability of the birth of blue-eyed children with retinoblastoma in this family if the penetrance of its gene is 60%.

Task 305. Gout[10] is determined by the dominant allele of the autosomal gene, whose penetrance is 20% in men and 0% in women.

Determine the probability of developing the disease in a man if his parents are heterozygous.

Determine the probability of developing the disease in both sons in a family where one of the parents is heterozygous and the other is homozygous for a recessive allele.

Task 306. Craniofacial dysostosis (premature closure of the cranial sutures, unclosed anterior fontanelle) is determined by the dominant allele of the autosomal gene, whose penetrance is 50%.

Determine the probability of having sick children in a family where one parent is heterozygous and the other is homozygous for a recessive allele.

Task 307. Van der Hoeve syndrome is determined by the dominant allele of an autosomal gene with a pleiotropic effect. The main symptoms of the disease are bone fragility, congenital deafness and blue sclera. Blue sclera is found in 100% individuals with the mutant allele, fragile bones –

[10] Monogenic in its origin, the disease is characterized by the deposition of urate crystals in various tissues of the body in the form of monosodium urate or uric acid.

in 63%, deafness is typical for 60%. A man with blue sclera, normal hearing and showing no signs of bone fragility, married a healthy woman from a family with no past history of the syndrome.

Determine the probability of children being born with fragile bones if it is known that only one of the man's parents had manifestations of the syndrome.

Task 308. According to Swedish scientists, one of the forms of schizophrenia is determined by the dominant allele of the autosomal gene, whose penetrance is 100% in homozygotes and 20% in heterozygotes.

Determine the probability of giving birth to sick children in a family where one of the spouses is heterozygous and the other is homozygous for a recessive allele.

Task 309. Brown eyes are the dominant trait. Retinoblastoma, a malignant tumor of the eye, develops when the dominant allele of one of the autosomal genes with a penetrance of 60% is present in the genotype.

Calculate the probability of giving birth to blue-eyed children who may develop retinoblastoma and healthy brown-eyed children in a family where the parents are diheterozygotes.

Task 310. Angiomatosis (sudden dilation and proliferation of retinal vessels, degeneration of retinal nerve elements) occurs when the dominant allele of the autosomal gene is present in the genotype, the penetrance is 50%.

Determine the probability that the carriers of this allele will have a healthy child.

5. LINKED INHERITANCE

Algorithm of solving the task in sex-linked inheritance

Task (case study). In humans, the normal hearing gene (B) dominates the deafness gene (b) and is located in the autosome; the color blindness gene (d) is recessive and linked to the X chromosome. In a family where the mother suffered from deafness, but had normal color vision, and the father had normal hearing (homozygous), but was color blind, a girl was born with normal hearing and also color blind.

Draw up a scheme for solving the task. Determine the genotypes of parents, daughters, possible genotypes of children and their ratio. What patterns of inheritance are shown in this case?

The algorithm for solving the task is shown in table 7.

Table 7

Algorithm for solving the task of sex-linked inheritance

P	♀ **bbX^DX^d**	×	♂ **BBX^dY**
G	**bX^D, bX^d**		**BX^d, BY**
F_1	**BbX^DX^d** – a girl with normal hearing and vision 25%; **BbX^dX^d** – a girl with normal hearing, color blind 25%; **BbX^DY** – a boy with normal hearing and vision 25%; **BbX^dY** – a boy with normal hearing, color blind 25%.		

Ответ. The genotype of the mother– bbX^DX^d, the genotype of the father – BBX^dY, the genotype of the children – BbX^DX^d, BbX^dX^d, BbX^DY, BbX^dY in the ratio 1/4:1/4:1/4:1/4. The law of independent inheritance of traits and gender-linked inheritance of a trait manifests itself.

Task 311. In the laboratory, red-eyed Drosophila females were crossed with red-eyed males. The offspring included 69 red-eyed and white-eyed males and 71 red-eyed females.

Determine the genotypes of parents and offspring, if it is known that red eye color dominates white, and the gene that determines eye color is located on the X chromosome.

Task 312. The following offspring were obtained from crossing between red-eyed long-winged Drosophila: in females – 3/4 red-eyed long-winged and 1/4 red-eyed with rudimentary wings; in males – 3/8 red-eyed long-winged, 3/8 white-eyed long-winged, 1/8 red-eyed with rudimentary wings, 1/8 white-eyed with rudimentary wings.

Determine the inheritance of traits, explain their genetic determination, and specify the genotypes of the parents.

Task 313. A homozygous female Drosophila with a yellow body (y) and normal wings (vg+) was crossed with a homozygous male with a gray body (y+) and rudimentary wings (vg). In the offspring, all the females were gray with normal wings, and all the males were yellow with normal wings.

Determine the inheritance of traits, explain their genetic determination, and specify the genotypes of the parents.

Task 314. S.V. Maksimov, a bird lover from the city of Taganrog, mated a brown-crested Canary with a green male without a crest and got offspring in the ratio: 2 green-crested females, 1 brown-crested male and 1 brown male without a crest.

Determine the genotypes of the parents, given that the presence of a crest is an autosomal trait.

Task 315. In Canaries, alleles of the X-linked gene determine the color of the plumage: B is green, and b is brown. The presence of a crest (C) or its absence (c) determines the alleles of the autosomal gene. The green crested canary was crossed with a brown female without a crest. The first-generation canaries all had a crest.

Determine the color of the first-generation plumage.

Determine what the second generation will be like if we assume that the canary from the parent generation was homozygous for the dominant B allele.

Task 316. In some breeds of chickens, the striped plumage dominates

the white one. These traits are determined by a pair of alleles linked to the X chromosome gene. The heterogeneous gender of birds is female.

A) On a poultry farm, white hens were crossed with striped roosters and received striped plumage in the offspring: in both roosters and chickens. Striped birds of the new generation were crossed and the

offspring included 594 striped roosters and 607 striped and white hens.

Determine the genotypes of parents and descendants of the first and second generations.

B) When crossing striped roosters and white hens, 40 striped roosters and hens and 38 white roosters and hens were obtained.

Determine the genotypes of parents and offspring.

Task 317. Breeders in some cases can determine the sex of newly hatched chickens by color. Silver plumage is determined by the dominant allele. In birds, the female sex is heterogeneous.

Determine unambiguously the genotypes of the parents, if it is known that the alleles of the same gene that determine the golden and silver plumage are linked to the X chromosome.

Task 318. In birds, the female sex is heterogeneous. Striped plumage is determined by a dominant allele linked to the X chromosome gene, and the presence of comb is determined by a dominant allele of an autosomal gene. A striped rooster with a comb and a striped hen with a comb were crossed and their offspring were two chickens: a striped rooster with a comb and a unstriped chicken without a comb.

Determine the genotypes of parents and offspring.

Task 319. A black, dark-skinned rooster with a rose comb was crossed with a striped, dark-skinned hen with a leaf-like comb. Among the chickens are 12 striped dark-skinned roosters, 4 striped, white-skinned roosters, 10 black dark-skinned hens and 4 black white-skinned hens. All chickens with a rose comb.

Determine the genotypes of parents.

Task 320. In Plymouth Rock hens, the dominant allele of grey plumage color (B) is localized in the Z chromosome. Its recessive allele (b) causes black plumage.

Determine the phenotypes and genotypes of roosters and hens obtained: a) from crossing a gray hen with a black rooster;

b) from crossing a homozygous gray rooster with a black hen;

c) from crossing a heterozygous gray rooster with a black hen.

Task 321. In hens, a recessive allele of a single sex-linked gene causes chickens to die before hatching. From crossing a normal hen with a

heterozygous rooster, 120 live chickens were obtained.

Determine the theoretically expected number of males and females among them.

Task 322. After crossing a highbred curly feathered rooster with green legs with highbred hens that had normal plumage and yellow legs, in the first generation all the roosters were with curly feathers with yellow legs, and hens had curly feathers with green legs. In the second generation, there were hens and roosters of four phenotypes: 73 with curly feathers with yellow legs, 71 with curly feathers with green legs, 21 with normal plumage and yellow legs, 18 with normal plumage and green legs.

Determine the determination and inheritance of traits.

Determine the genotypes of parents and descendants of two generations.

Task 323. In bronze turkeys, body vibration (trembling) is transmitted by a sex-linked gene. When crossing vibrating turkey males and normal females, the offspring is obtained in which all the females were vibrating, and the males were normal.

Determine which of the two traits dominates, identify the genotypes of the parents.

Task 324. In bronze turkeys, there is an inherited characteristic of peculiar trembling ("vibrating"), due to a recessive allele of the sex-linked V gene. The viability of such a bird is normal. When crossing a normal female turkey with a "vibrating" turkey male, 36 offspring were obtained. All female descendants had the anomaly, and male descendants are normal.

Determine the genotypes of descendants and explain the distribution of the anomaly by sex.

Task 325. In sheep the allele K^1 determines hornless, and allele K – horned trait. The dominance of this pair of alleles depends on the sex. In rams, the horned character dominates the hornless, and in sheep the hornless dominates the horned trait.

Define:

a) splitting in the offspring when crossing a horned sheep with a hornless ram; inheritance of a trait (father or mother) for a daughter and sons;

b) splitting in offspring from crossing a horned ram with a hornless

sheep, if both parents are homozygous; inheritance of the trait (father or mother) for sons and daughters;

C) splitting in offspring from crossing a heterozygous horned ram with a heterozygous hornless sheep.

Task 326. The color of the cat (hair, skin, and eyes) is determined by the pigment melanin. Melanin is found in the form of microscopic granules that differ in shape, size, and quantity, which causes differences in color. There are two types of melanin: eumelanin and pheomelanin. Eumelanin granules are spherical and absorb almost all light, giving black pigmentation. Pheomelanin granules are oblong and reflect light in the red-yellow-orange range. Eumelanin is responsible for black color (and its derivatives – chocolate, cinnamon, blue, purple, faun), and pheomelanin – for red (cream). The genes that are responsible for displaying red (O – Orange) or black (o – not Orange) are located on the X chromosome, meaning that color inheritance is linked to gender.

Heterozygous individuals, which are almost always cats, and not tomcats, have a tortoiseshell color (random spots throughout the body of red and black colors). Hair color mosaicism is caused by the inactivation of the paternal or maternal X chromosome in different cell groups at an early stage of embryonic development.

Determine the probability of obtaining in the offspring of tortoiseshell kittens from crossing a tortoiseshell cat with a black tomcat.

Determine the offspring from crossing a black cat with a red tom-cat.

Explain the extremely rare birth of tortoiseshell kittens.

Task 327. The common type of baldness is determined by an autosomal allele, dominant in men and recessive in women. A normal man marries a bald woman, and they have an early balding son.

Determine the genotypes of all family members.

Task 328. Let us assume that in a person baldness dominates the absence of such in men, and in women it is recessive. A brown-eyed not bald right-handed man married a brown-eyed not bald left-handed woman. They had three children: a brown-eyed bald right-handed son, a blue-eyed not bald right-handed daughter, and a brown-eyed not bald left-handed son.

Determine the genotypes of parents and children.

Task 329. Hypertrichosis (the presence of hair on the ear auricle) is inherited linked to the Y chromosome.

Calculate the probability of having children with this abnormality in a family where the father has hypertrichosis.

Task № 330. Hypertrichosis is inherited as a Y-linked trait, and polydactyly is the dominant autosomal trait. In a family where the father had hypertrichosis and the mother had polydactyly, a daughter was born without abnormal traits.

Determine the probability that the next child in this family will also be without abnormal traits.

Task 331. Hypertrichosis is inherited as a Y-chromosome-linked trait that manifests itself only by the age of 17. One form of ichthyosis is a recessive trait linked to the X chromosome. In a family where the woman is healthy, and the husband has hypertrichosis, a boy with traits of ichthyosis was born.

Determine the probability of hypertrichosis in this boy.

Determine the probability of having children in this family without abnormal traits and determine the sex of the children.

Task 332. A color blind woman married a man with hairy ears (hypertrichosis).

Determine the inheritance of diseases in children, if the recessive allele of colorblindness is localized in the X chromosome, and the allele of hairy ears in the Y chromosome.

Task 333. Hypoplasia of tooth enamel is a dominant trait and is inherited linked to the X chromosome. In a family where both parents had hypoplasia of tooth enamel, a son with normal teeth was born.

Determine the inheritance of the disease by the second son.

Task 334. Classical hemophilia is a recessive trait linked to the X chromosome.

A) A man with hemophilia married a woman who was healthy. They had healthy daughters and sons who married healthy individuals.

Determine the appearance of hemophilia in grandchildren and calculate the probability of the appearance of individuals with hemophilia in the families of daughters and sons.

B) A man with hemophilia has married a healthy woman whose father has hemophilia.

Determine the probability of having healthy children in this family.

Task 335. In humans, the recessive allele of the gene localized in the X chromosome determines the development of one of the color blindness forms.

A) A girl with normal vision, whose father was color blind, married a normal man, whose father also had color blindness.

Determine the inheritance of color blindness in children from this marriage.

B) A man and a woman with normal color perception have: a color blind son who has a daughter with normal vision; a daughter who is healthy and has one son with normal vision and one son who is color blind; a daughter with normal vision who has five sons with normal vision.

Identify the genotypes of parents, children, and grandchildren.

Task 336. The spouses, who can distinguish the taste of phenylthiocarbamide and do not have color blindness, had a color blind son who does not distinguish the taste of phenylthiocarbamide. In humans, the ability to distinguish the taste of phenylthiocarbamide is determined by a dominant autosomal gene, and color blindness is determined by a recessive gene linked to the X chromosome.

Calculate the probability of having a child with color blindness in this family (expressed as a percentage).

Identify the phenotypes among the daughters and sons of this family.

Task 337. The Arabian Sheikh Mahmud, the owner of oil fields, was albino and had no sweat glands. His son Jalil and daughter Leila have a normal phenotype. After Mahmud's death, his younger brother Anis (also an albino without sweat glands) took over the management of the company, but he is not the heir to the company. According to the will left by Mahmud, all the property should be received by the one of his children who will give birth to an albino girl without sweat glands. Following the mother’s advice, Leila married her uncle Anis, and Jalil married his phenotypically normal daughter Saud.

Calculate the chances of inheritance, given that albinism is an autosomal trait, and the absence of sweat glands (anhidrotic ectodermal dysplasia) is linked to the X chromosome. Both traits are recessive.

Task 338. A brown-eyed woman with normal color vision, whose father had blue eyes and was color blind, married a blue-eyed man with normal color perception.

Determine what children can be expected from this pair if it is known that brown eyes are an autosomal dominant trait, and color blindness is recessive linked to the X chromosome.

Task 339. Darkening of teeth is determined by the dominant alleles of two genes, one of which is autosomal, and the second is linked to the X chromosome. In a family where parents have dark teeth, a girl and a boy with normal teeth color were born.

Determine the probability of birth in this family of a child without an anomaly, if it is established that the dark teeth of the mother are caused only by the allele linked to the X chromosome of the gene, and the dark teeth of the father – only by the allele of the autosomal gene.

Task 340. One form of Bruton agammaglobulinemia is determined by a recessive allele of an autosomal gene, and the other – by a recessive allele of a gene localized on the X chromosome.

Determine the probability of having sick children in a family where the mother is heterozygous for both genes, and the father is healthy and has only dominant alleles of these genes.

Task 341. In humans, color blindness is caused by a recessive allele of the X-linked gene. Thalassemia is an autosomal not completely dominant trait. Homozygotes often develop a severe, fatal form of the disease, while heterozygotes are less severe. A woman with normal color perception, but with a mild form of thalassemia married a healthy man, who is color blind, has a color blind son with a mild form of thalassemia.

Determine the probability of a healthy son born in this family.

Task 342. In humans, classical hemophilia is a recessive inherited trait with the X chromosome. Albinism is caused by a recessive allele of an autosomal gene. A healthy couple had a son with both traits.

Determine the probability that another son in this family will also have both traits.

Task 343. Retinitis pigmentosa (an inherited degenerative eye disease) is determined by recessive and dominant alleles of two different autosomal genes and a recessive allele of an X-linked gene.

Determine the probability of having sick children in a family where the mother has retinitis pigmentosa and is heterozygous for all three genes, and the father is healthy and homozygous.

Task 344. A right-handed woman with brown eyes and normal vision married a right-handed man with blue eyes and color blindness. They had a blue-eyed daughter who was left-handed and color blind. It is known that brown eye color and right-handedness are dominant autosomal, not linked traits, and color blindness is a recessive, linked to the X chromosome trait.

Determine the probability that the next child in this family will be left-handed and will have color blindness.

Identify the inheritance of eye color by sick children.

Task 345. Healthy parents with blood group B had a son who was a hemophiliac with blood group A. Hemophilia is inherited as an X-linked trait.

Determine the probability of having a healthy baby.

Task 346. A man with blue eyes and normal eyesight, both of whose parents had gray eyes and normal eyesight, married a normal-looking woman with gray eyes. The woman's parents had gray eyes and normal eyesight, and the blue-eyed brother was color blind. From this marriage was born a girl with gray eyes and normal eyesight and two blue-eyed boys, one of whom was color blind.

Determine the genotypes of all members of this family, given that color blindness is linked to the X-chromosome, a recessive trait.

Determine the probability of having a gray-eyed daughter with normal eyesight.

Task 347. A woman with blood group B and normal coagulation married a healthy man with blood group AB. They had three children: Kate is healthy with blood group B; Victor is healthy with blood group A; Gleb is a hemophiliac with blood group B. It is known that the woman's parents were healthy; the mother had blood group A, the father had blood group O. The man's father and mother were healthy and had blood group B and AB, respectively. Hemophilia is determined by the recessive allele of the X-linked gene.

Determine the genotypes of all family members.

Explain from whom Gleb inherited hemophilia.

Task 348. Polydactyly is an autosomal dominant trait, and color blindness is a recessive trait linked to the X chromosome. A color blind man with polydactyly and a healthy woman had a color blind son with

polydactyly and a healthy daughter.

Identify the genotypes of parents and children.

Task 349. In humans, aniridia (a type of blindness in which there is no iris) depends on the dominant allele of the autosomal gene (homozygotes for this allele die), and optical atrophy (another type of blindness) – from the recessive allele of the gene localized in the X chromosome. A man with optical atrophy and aniridia married a healthy girl who was homozygous for both pairs of alleles.

Determine the possible phenotypes of their children and their frequency.

Task 350. Hypoplasia of tooth enamel is a dominant trait and is inherited linked to the X chromosome, polydactyly is an autosomal dominant trait. In a family where the mother has got polydactyly and the father has hypoplasia of tooth enamel, a five-fingered healthy boy was born.

Determine the genotypes of all family members.

Explain why the son did not inherit the dominant characteristics of his parents.

Calculate the probability of having a child with two abnormalities in this family.

Task 351. In humans, albinism is caused by a recessive allele of an autosomal gene. Anhidrotic ectodermal dysplasia (absence of sweat glands) is a recessive trait linked to the X-chromosome. A healthy couple had a son with both abnormalities.

Calculate the probability that the second child in the family will be a normal girl.

Calculate the probability that the next child will be a normal son.

Task 352. A specific form of rickets that cannot be treated with vitamin D is accompanied by a absence of phosphorus in the blood. Among children from marriages 14 men with this form of rickets and healthy women, 21 girls and 16 boys were born. All the girls have rickets; all the boys are healthy.

Determine the type of disease inheritance.

Algorithm for solving the task of linked inheritance

Task (case study). When crossing maize plants with smooth colored seeds and plants with wrinkled uncolored seeds, all first-generation hybrids had smooth colored seeds. From the analyzing crossing of F1 hybrids, we obtained: 3,800 plants with smooth colored seeds; 150 – with wrinkled colored ones; 4,010 – with wrinkled uncolored ones; 149 – with smooth uncolored ones.

Determine the genotypes of parents and offspring obtained from the first and analyzing crosses. Draw up a scheme for solving the task. Explain the formation of four phenotypic groups in the offspring from the analyzing cross.

The algorithm for solving the task is shown in table 8.

Table 8

Algorithm for solving the task of linked inheritance

First crossing			
P	$\frac{\underline{\mathbf{AB}}}{\mathbf{AB}}$ Smooth colored	×	$\frac{\underline{\mathbf{ab}}}{\mathbf{ab}}$ Wrinkled uncolored
G	**AB**		**ab**
$\mathbf{F_1}$	$\frac{\underline{\mathbf{AB}}}{\mathbf{ab}}$		
Analyzing crossbreeding			
P	$\frac{\underline{\mathbf{AB}}}{\mathbf{ab}}$	×	$\frac{\underline{\mathbf{ab}}}{\mathbf{ab}}$
G	**AB, Ab, ab, ab**		**ab**
$\mathbf{F_2}$	$\frac{\underline{\mathbf{AB}}}{\mathbf{ab}}$ Smooth colored seeds (3,800) $\frac{\underline{\mathbf{Ab}}}{\mathbf{ab}}$ Smooth uncolored seeds (149) $\frac{\underline{\mathbf{aB}}}{\mathbf{ab}}$ Wrinkled colored seeds (150) $\frac{\underline{\mathbf{ab}}}{\mathbf{ab}}$ Wrinkled uncolored seeds (4,010)		

Answer. The linked inheritance of traits provides an explanation to the presence in the offspring of two groups of individuals with dominant and recessive traits in approximately equal proportions, a large phenotypic class (3,800 and 4,010). Two other phenotypic groups, the small phenotypic class (149 and 150) are formed as a result of crossing between allelic genes.

Task 353. In an individual, the gametes DE and de are several times larger than the gametes De and dE.

Determine the position of the dominant alleles in the diheterozygote DdEe (in the cis-position or trans-position).

Task 354. The distance between genes A and D is 5%, and between genes D and B is 6%.

Determine the distance between genes A and B, if it is known that the D gene lies at the end of the chromosome.

Task 355. Genes A, B, C, and D make up one coupling group. The distance between genes A and D is 2%, between genes D and C is 5.5%, between C and B is 1.5%, and between A and B is 6%.

Make a genetic map of the chromosome.

Task 356. Genes A, B, C, D, and E are located on the same chromosome. The distance between genes A and C is 2%, between B and C is 7%, between B and E is 3%, between D and E is 5%, between C and D is 9%, and between A and B is 5%.

Make a genetic map of the chromosome and determine the distance between genes A and D.

Task 357. The following results were obtained in the analyzing cross of the heterozygote AaBb: AB – 903; Ab – 101; aB – 98; ab – 898.

Based on the results of the analyzing cross, determine the phase of gene coupling and the distance between the genes.

Task 358. The following results were obtained in the analyzing cross of triheterozygotes: ABC – 255; ABc – 20; AbC – 128; Abc – 124; aBC – 136; aBc – 140; abC – 28; abc – 266.

Based on the results of the analyzing cross, determine the phase of gene coupling and the distance between the genes.

Task 359. The following results were obtained in the analyzing cross of triheterozygotes: ABC – 84; ABc – 76; AbC – 82; Abc –78; aBC – 86; aBc – 86; abC – 82; abc – 80.

Based on the results of the analyzing cross, determine the phase of gene coupling and the distance between the genes.

Task 360. The following results were obtained in the analyzing cross of triheterozygotes: ABC – 71; ABc – 3; AbC – 14; Abc – 17; aBC – 18; aBc – 11; abC – 2; abc – 64.

Based on the results of the analyzing cross, determine the phase of gene coupling and the distance between the genes.

Task 361. The following results were obtained in the analyzing cross of triheterozygotes: ABC – 126; ABc – 10; AbC – 64; Abc – 62; aBC – 68; aBc – 70; abC – 14; abc – 133.

Based on the results of the analyzing cross, determine the phase of gene coupling and the distance between the genes.

Task 362. The following results were obtained in the analyzing cross of triheterozygotes: ABC – 0; ABc – 164; AbC – 2; Abc – 1; aBC – 2; aBc – 3; abC – 172; abc – 0.

Based on the results of the analyzing cross, determine the phase of gene coupling and the distance between the genes.

Task 363. The following results were obtained in the analyzing cross of triheterozygotes: ABC – 29; ABc – 235; AbC –27; Abc – 210; aBC – 239; aBc – 24; abC – 215; abc – 21.

Based on the results of the analyzing cross, determine the phase of gene coupling and the distance between the genes.

Task 364. The following results were obtained in the analyzing cross of triheterozygotes: ABC – 1,270; ABc – 95; AbC – 6; Abc – 68; aBC – 65; aBc – 7; aвC – 86; abc – 1,275.

Based on the results of the analyzing cross, determine the phase of gene coupling and the distance between the genes.

Task 365. The following results were obtained in the analyzing cross of triheterozygotes: ABC – 151; ABc – 290; AbC – 37; Abc – 20; aBC – 21; aBc – 39; abC – 288; abc – 147.

Based on the results of the analyzing cross, determine the phase of gene coupling and the distance between the genes.

Task № 366. The following results were obtained in the analyzing cross of triheterozygotes: ABC – 19; ABc – 40; AbC – 289; Abc – 150; aBC – 148; aBc – 291; abC – 37; abc – 21.

Based on the results of the analyzing cross, determine the phase of gene coupling and the distance between the genes.

Task 367. It was found that the genes are linked and arranged in the chromosome in the following order: A–B–C. The distance between A and B is 8% of the crossover, and between B and C is 10%. The coefficient of coincidence (C) is 0.6.

Calculate the expected ratio of phenotypes in the offspring from the analyzing cross of an organism with the ABc/ abC genotype.

Task № 368. Presented 1 and 2 crosses (Fb):

1	+++	669	1	bcd	8
2	ab+	139	2	b++	441
3	a++	3	3	b+d	90
4	++c	121	4	+cd	376
5	+bc	2	5	+++	14
6	a+c	2,280	6	++d	153
7	abc	658	7	+c+	64
8	+b+	2,215	8	bc+	141

Determine the order of 4 genes and determine the distance between the genes.

Determine the genotype of the heterozygous parent.

Task 369. The following cleavage in the analyzing cross is presented:

1	AbC	104	5	aBC	5
2	abc	180	6	Abc	5
3	aBc	109	7	abC	191
4	ABc	221	8	ABC	169

Determine the genotype of the heterozygous parent.
Determine the frequency of the crossing.
Determine the order of the genes.

Task 370. Gametes of one parent are Ab, the other's gametes are aB.
Determine the gametes that form the resulting hybrid.
Determine the ratio of gametes if the genes are linked and located at a distance of 10%.

Task 371. Genes A and B are linked and the frequency of crossover

between them is 20%.

Calculate the correlation of genotypes in the second generation from crossing Ab/Ab and aB/aB.

Task 372. Genes A and B are linked and the frequency of crossover between them is 20%.

Calculate the correlation of genotypes from crossing AB/Ab and AB/Ab.

Task 373. Genes A and B are linked and the frequency of crossover between them is 40%.

Determine how many diheterozygous AB/ab will appear in the offspring if there is self-pollination of its forms aabb and A_bb.

Determine the result of crossing at a crossover frequency of 10%.

Task 374. Genotype of an individual A/a BC/bc. Genes B and C are linked, and the crossover frequency between them is 40%.

Determine the correlation of all types of gametes formed by this organism.

Task 375. Genes A and B are linked, the crossover frequency between them is 10%, and gene C is in a different coupling group.

Determine the type and correlation of gametes that will form heterozygotes AB/ab C/c and Ab/aB C/c.

Task 376. Chlamydomona triheterozygotes cells were formed because of copulation of two haploid cells with the ABC and abc genotype. For example, in the offspring of triheterozygotes, the proportion of recombinants for genes B and C is 20%, for genes A and C – 38%.

Calculate the types of daughter cells that may occur as a result of meiosis.

Determine the order of the genes on the chromosome.

Task 377. The smooth shape of corn seeds and anthocyanin pigment in the seeds are the dominant traits. Wrinkled seeds and absence of pigment in them are recessive traits. The shape and color of the seeds are inherited concatenated. After crossing two plants, diheterozygous and homozygous by recessive alleles, descendants with different seeds were obtained, including: 4,152 plants with colored smooth seeds, 149 plants

with colored wrinkled seeds, 152 plants with uncolored smooth seeds, and 4,163 plants with uncolored wrinkled seeds.

Identify the distance between the genes determining these traits.

Task 378. In maize the flour content of endosperm dominates the waxiness, the purple color of the seedlings dominates the green one. The genes that control these traits are linked and located 12% apart from each other.

Determine the phenotype and genotype for a first-generation individual from crossing two genetically different plants, each of which was homozygous for the dominant allele of one gene and the recessive allele of the other gene.

Calculate the phenotype cleavage that will occur among the descendants of the first-generation analyzing hybrid cross.

Task 379. In corn, the allele of normal chlorophyll content in seedlings dominates the allele of no chlorophyll, the allele of matte leaves dominates the allele of shiny leaves, the allele of normal fertility dominates the allele of reduced fertility. All three genes are located on the same chromosome. Two corn plants were crossed. One has chlorophyll-free sprouts, shiny leaves, low fertility; the other has sprouts with normal chlorophyll content, matte leaves, normal fertility. First-generation hybrids have sprouts with normal chlorophyll content, matte leaves, and normal fertility. These hybrids are crossed with the recessive parent form. The results of the analyzing cross are as follows:

Phenotypes of seedlings	Leaves	Fertility	Number of plants
Normal	Matte	Normal	235
Normal	Shiny	Reduced	62
Normal	Matte	Reduced	40
Chlorophyll-free	Matte	Reduced	4
Chlorophyll-free	Shiny	Reduced	270
Normal	Shiny	Normal	7
Chlorophyll-free	Shiny	Normal	48
Chlorophyll-free	Matte	Normal	70

Determine the distance between the genes and their order.

Task 380. Arne Müntzing published chromosome maps of all 10 groups of maize coupling in the book Genetics (1967). In one of them,

there are gene loci that determine striped leaves (sr), resistance to fillies (ag), male sterility (ms), and the color of the corncob sternum (p). The distance between the genes: the ag gene gives 11% of crossover gametes with the ms gene, 8% with the p gene, and 14% with the sr gene. In turn, the ms gene with the p gene gives 3% of the crossover, and with the sr gene – 25%.

Make a genetic map and determine the location of each locus.

Task 381. In lilac, the allele of double flowers is dominant over the norm allele, and the allele of seed color is dominant over the allele of uncolored seeds. Both genes are located on the same chromosome. The distance between them is equal to 27.6 %. As a result of the experiment, a crossover frequency of 26% was obtained.

Write the scheme of crossing diheterozygous plants with homozygous recessive plants.

Determine the amount of interference.

Determine the number of descendants of each phenotype if the total number of descendants is 300.

Task 382. In primula, the allele for purple flower color is dominant over the allele for red color and the allele for short pistil dominates the allele for long pistil. Both genes are located on the same chromosome. From crossing a heterozygous purple short-leaved plant, 9% of whose gametes were crossover, with a red long-leaved plant, 600 descendants were obtained.

Determine the number of descendants of each phenotype that should be among them and describe all their variants.

Task 383. In peas, when crossing a homozygous humifuse floccose plant with white flowers with a homozygous bushy non-floccose plant with red flowers, all descendants in the first generation were humifuse floccose plants with red flowers.

By crossing first generation hybrids with a beardless bushy plant with white flowers in analyzing hybridization the following splitting was obtained: 61 humifuse floccose red plants, 190 white humifuse floccose plants, 56 beardless humifuse red plants, 188 humifuse beardless white plants, 59 bushy white humifuse plants, 195 humifuse bushy red plants, 62 white bushy beardless plants, 193 bushy beardless red plants.

Write down the scheme of crosses and determine the distance between

genes, if A – gene is humifuse forms, and a – gene of bushy shape, B – floccose gene, b – beardless gene, C – gene for red flowers, c – gene of white flowers.

Task 384. In tomatoes (Solánum lycopérsicum) the high stem dominates the dwarf stem and the spherical shape of the fruit dominates the pear. The genes for the stem height and the fruit shape are linked and are located at a distance of 20% from each other. A plant that was heterozygous for both pairs of alleles (trans coupling phase) was crossed with a plant that was homozygous for recessive alleles of both pairs.

Determine the proportion of each phenotypic class among the descendants of this cross.

Task 385. In tomatoes the allele for tall plants is dominant over the allele for dwarf plants, and the allele for round fruit dominates the allele for pear-shaped fruit. A tall tomato plant with round fruits, crossed with a dwarf plant with pear-shaped fruits gave the following offspring: 81 tall round plants, 79 dwarf pear-shaped plants, 22 tall pear-shaped plants, 17 dwarf round plants. Another tall plant with round fruits crossed with a dwarf plant with pear-shaped fruits gave the following offspring: 21 tall pear-shaped plants, 18 dwarf round plants, 5 tall round plants, and 4 dwarf pear-shaped plants.

Determine the type of offspring and their ratio from tall round plants when crossing with each other.

Task 386. The tomato fruit can be round (O) and oval (o), floccose (P) and non-floccose (p), single flowers (S) and collected in inflorescences (s). the genes that determine The genes that determine them are localized in a single chromosome.

Phenotype	Number of plants
OPS	73
OPs	348
OpS	2
Ops	96
oPS	110
oPs	2
opS	306
ops	63

Determine the position of alleles in homologous chromosomes and the distance between genes based on the results of the analysis crossing.

Task 387. In the land snail Cepaea nemoralis, the color of the shell is determined by 3 alleles of the same gene: Y – brown allele, y^1 – pink allele, y – yellow allele. The brown allele is dominant over the allele for pink and yellow color, a pink color allele is dominant over the allele for yellow color. The color distribution gene (streakiness) is closely linked to the color locus.

Allele B determines the uniform distribution of color, allele b^1 – the appearance of a wide dark band on the general background, allele b – the appearance of several narrow bands. The B allele dominates the b^1 and b genes, and the b^1 allele dominates the b allele. In 4 different experiments, brown snails with uniform color were crossed with pink snails with a wide stripe. The snail genotypes were YyBb and y^1yb^1b. In the first variant of crossing, the offspring turned out: 2 brown uniform, 1 pink with a wide stripe and 1 yellow with narrow stripes. In the second version, it turned out: 2 brown uniforms, 1 pink with narrow stripes, 1 yellow with a wide stripe. In the other 2 crosses, 4 phenotypes were obtained in equal quantities: brown with a wide stripe, brown with narrow stripes, pink uniform and yellow uniform.

Determine the order in which the genes of the parents were linked in all 4 variants of crossing.

Task 388. In Drosophila cv+ determines the presence of a cross vein, cv – the absence of cross veins, ct+ is the absence of wing clipping, ct – the presence of wing clipping, v+ determines dark red eye color, v determines bright red eyes.

Results of analyzing crossbreeding are as follows:

Phenotypes		Number	Phenotypes		Number
1	$cv^+ ct^+ v$	73	5	$cv ct^+ v$	766
2	$cv^+ ct^+ v^+$	2	6	$cv ct v^+$	80
3	$cv^+ ct v^+$	759	7	$cv ct^+ v^+$	158
4	$cv^+ ct v$	140	8	cv ct v	2

Determine the genotype of triheterozygous female Drosophila, the order of genes and distance between them.

Task 389. Data on the frequency of crossover between genes b (black), cu (curved), pr (purple), sp (speck), S (star), vg (vestigial), which are localized in the II chromosome of Drosophila, are given below.

Genes	Number of flies	% of crossover
b-cu	62,679	22.7
b-pr	48,931	6.2
b-sp	685	47.0
b-S	16,507	37.0
b-vg	20,153	17.0
cu-pr	51,136	20.0
cu-sp	10,042	30.0
cu-S	19,870	46.0
cu-vg	1,720	8.2
pr-sp	11,985	46.0
pr-S	8,155	43.0
pr-vg	13,601	12.0
sp-S	7,135	48.0
sp-vg	2,054	36.0
S-vg	450	43.0

Based on these data, make a genetic map.

Task 390. In Drosophila, the gray body color and red eye color alleles dominate the black body color and brown eye color alleles. The two features are inherited concatenated.

Determine the results of crosses, each of which received 400 descendants:

a) a heterozygous grey female with red eyes with a homozygous black male with red eyes;

b) a heterozygous gray female with red eyes, 23% of whose gametes were crossover, with a black male with brown eyes;

c) a heterozygous gray female with red eyes, 17% of whose gametes were crossover, with a homozygous gray male with brown eyes.

Task 391. ec – size of the eye facets, cv – development of the cross vein on the wing, ct – wing clipping. The results of analyzing Drosophila crossing are presented.

1	ec cv+ ct	2,125
2	ec+ cv+ ct	265
3	ec cv ct	3
4	ec cv ct+	273
5	ec+ cv ct	223

6	ec+ cv ct+	2,207
7	ec cv+ ct+	217
8	ec+ cv+ ct+	5

Determine the genotype of the heterozygous parent.
Determine the order of the genes and the distance between them.

Task 392. In Drosophila, the allele of gray body color dominates the allele of yellow body color, and the allele of red eye color dominates the allele of crimson eyes. Both genes are located on the same chromosome. The distance between them is 33.8%. From crossing a heterozygous gray female with red eyes with a yellow male with crimson eyes, 49 gray flies with crimson eyes, 46 yellow flies with red eyes, 151 gray flies with red eyes, and 145 yellow flies with crimson eyes were obtained.

Write a diagram of crossing and determine the scope of interference.

Task 393. In Drosophila, the red eye gene dominates the cinnabaric eye gene, the gray body color gene dominates the black body color gene, and the normal wing gene dominates the rudimentary wing gene. All genes are located on the same chromosome. After crossing a homozygous female Drosophila with red eyes (cn+), gray body (b+) and normal wings (vg+) with a homozygous recessive male with cinnabaric eyes (cn), black body (b) and rudimentary wings (vg), heterozygous offspring were obtained. An analysis of crossbreeding was performed with a hybrid female from F_1.

As a result, 1,540 flies were obtained with 8 phenotypes: 631 red-eyed gray flies with normal wings, 575 black wingless flies with cinnabar eyes, 1 red-eyed black wingless flies, 2 gray flies with normal wings and cinnabar eyes, 91 red-eyed gray wingless flies, 80 black flies with normal wings and cinnabar eyes, 68 red-eyed black flies with normal wings, 56 gray wingless flies with cinnabar eyes.

Record the progress of the crosses.
Determine the distance between the genes and their order.

Task 394. As a result of crossing Drosophila females with a gray body and normal bristles with Drosophila males having a yellow body and split bristles, offspring with only a gray body and normal bristles are obtained. Then the first-generation females were crossed with the males of the parent generation and received numerous offspring, among which 1.5% of the individuals had a gray body and split bristles.

Determine the genotypes of parents and descendants, the position of alleles, the distance between the genes that determine the body color and the shape of the bristles.

Task 395. Drosophila has 4 groups of coupling. N.N. Medvedev described genetic maps of these coupling groups in 1968. Simplified information on 3 coupling groups is given below.

9 genes in the X chromosome located: b – length of bristles, cb – form wing (crumpled or straightened), cv – the development of cross veins on the wing, dy – color of the wing, ec – size of the eye facets, hw – development of additional bristles on the wing, oc – the development of simple eyes, s – body's color, sn – form of the bristles and hairs on the body. Crossing frequency: cv-ec 8.2%, cv-hw 13.7%, cv-cb 2.3%, cv-sn 7.3%, hw-ec 5.5%, hw-cb 16%, cb-sn 5%, cb-oc 7.1%, sn-oc 2.1%, sn-dy 15.2%, sn-s 22%, b-s 23%, b-dy 29.8%, b-oc 42.9%.

7 genes. Chromosome 2 contains the following genes: **ap** – development of beeflies, **al** – development of antennal bristles, **d** – number of segments on the legs, **dp** – surface relief of thoracic sclerites, **pys** – development of additional veins on the wing, **sm** – development of hairs on the abdomen, **sp** – number of bristles on the lateral sclerites of the chest. Crossover frequency: dp-sp 9%, dp-al 13%, dp-d 18%, sp-al 22%, sp-d 9%, sp-pys 30%, pys-d 21%, pys-ap 3.4%, pys-sm 39.5%, ap-sm 36.1%, ap – d 24.4%.

7 genes of the III chromosome are genes: bd – nature of the discontinuity of the main veins of the wing, cu – wing shape (straight or curved on the ends), and dl – form of veins at the wing edge, dv is the position of the wings, fz – the position of bristles on the breast, h – development of additional setae on scutellum, sz – development of dark strips on middle of back. Crossing frequency: cu-fz 6%, cu-sz 12%, cu-dl 16.2%, cu-bd 43.8%, sz-dl 4.2%, sz-bd 31.8%, sz-fz 16%, h-fz 17.5%, h-cu 23.5%, h-dv 6.5%, dv-fz 24%.

Make genetic maps for 3 groups of coupling.

Task 396. In Drosophila, the genes that determine the shape of the eyes and body length are in the same autosome, with the dominant allele of the first gene determining lobe eyes, and the recessive allele of the second – a shortened body. A homozygous female with a shortened body and lobe eyes was crossed with a normal male.

Determine the phenotype for first-generation hybrids.

Determine the splitting by phenotype and genotype in the offspring from the analyzing cross (in males, there is no crossing), if the distance between the genes is 0.5%.

Task 397. In Drosophila, white eyes and crumpled wings are caused by recessive alleles of two genes located in the sex chromosome at a distance of 15% from each other.

Identify first-generation hybrids from crossing a homozygous, red-eyed long-winged female Drosophila with a white-eyed male with crumpled wings.

Calculate the splitting by phenotype and genotype in the offspring from crossing a female F1 with a white-eyed male with crumpled wings.

Task 398. As a result of crossing a female Drosophila heterozygous for two pairs of alleles (MmNn) with a male homozygous for recessive alleles (mmnn), offspring were obtained, 47% of which had the MmNn genotype, 3% – Mmnn, 3% – mmNn and 47% – mmnn.

Determine the position of alleles in the chromosomes.

Determine the distance between the genes.

Task 399. In Drosophila, recessive alleles – cu and st – of two autosomal genes determine, respectively, the development of upturned wings and bright red eyes. The dominant alleles cu+ and st+ determine the development of straight wings and dark red eyes, respectively. After crossing a female diheterozygous on both pairs of alleles with a male homozygous on recessive alleles of both genes, the following offspring were obtained: 47.5% with dark red eyes and straight wings; 2.5% with bright red eyes and straight wings, 47.5% with bright red eyes and curved wings, 2.5% with dark red eyes and curved wings.

Determine the distance between the genes.

Determine the genotypes of descendants of all four phenotypic classes.

Task 400. In Drosophila, the gray-body allele (b+) dominates the black body allele (b), and the long-wing allele (vg+) dominates the rudimentarybwing allele (vg). From crossing a gray long-winged female with a black male with rudimentary wings offspring were obtained: 41.5% of gray long-wing flies; 41.5% of black flies with rudimentary wings; 8.5% of black long-wing flies; 8.5% of gray flies with rudimentary wings. In another case, from crossing phenotypically the same male and female,

offspring were obtained, among which 8.5% of flies had a gray body and long wings, 8.5% of flies had a black body and rudimentary wings, 41.5% of flies had a gray body and rudimentary wings, 41.5% of flies had a black body and long wings.

Determine the genotypes of the females used in both crosses.

Determine the distance between the genes determining body color and wing length.

Task 401. In Drosophila, alleles of red eyes (w+) and normal abdomen (A+) are dominant in relation to alleles that determine white eyes (w) and altered abdomen (A). Both pairs of allelomorphs are linked to the sex. The distance between these genes is 3%.

Determine the type and frequency of gametes: a) in a diheterozygous female; b) in a red-eyed male with a normal abdomen; c) in a white-eyed male with an altered abdomen.

Task 402. In hens, the golden plumage allele dominates the silver plumage allele, and the non-pock-marked plumage allele dominates the pock-marked plumage allele. By crossing golden pock-marked hens with silver non-pock-marked cocks got 34 pock-marked golden, 29 silver non-pock-marked, 32 golden non-pock-marked and 30 silver pock-marked descendants. The resulting silver pock-marked hens and golden non-pock-marked roosters were crossed. In the offspring from this crossing, 4 phenotypes of roosters and hens were obtained: 206 silver pock-marked, 382 golden pock-marked, 366 silver non-pock-marked, 212 golden non-pock-marked.

Write a crossing diagram and determine the crossover frequency.

Task 403. In Pskov hens with short legs, the short-leg allele dominates the normal-leg allele, and the rose comb allele dominates the leaf-like comb allele. Both genes are inherited concatenated. The heterozygous cock with short legs and rose comb was interbred with a long-legged hen with leaf-like comb and as a result there were 244 chickens with short legs and rose comb, 262 long-legged descendants with leaf-like comb, 35 normal leg with rose comb and 41 with short legs and leaf-like comb.

Write a crossing diagram and determine the frequency of the crossing-over.

Task 404. In hens, the golden plumage allele dominates the silver plumage allele, and the non-pock-marked plumage allele dominates the pock-marked plumage allele. Crossing golden pock-marked hens with silver non-pock-marked cocks resulted in 34 pock-marked gold, 29 silver non-pock-marked, 32 gold non-pock-marked and 30 silver pock-marked descendants. The resulting silver pock-marked hens and golden non-pock-marked roosters were crossed. In the offspring from this crossing, 4 phenotypes of roosters and hens were obtained: 206 silver pock-marked, 382 golden pock-marked, 366 silver non-pock-marked, 212 golden non-pock-marked.

Write a crossing diagram and determine the frequency of the crossing-over.

Task 405. In chickens, the allele of short legs dominates the allele of normal legs, and the allele of black plumage dominates the allele of white plumage. Both characteristics are inherited concatenated. From crossing a heterozygous rooster with short legs and black plumage and a hen with long legs and white plumage, 156 short-legged black descendants, 136 long-legged white descendants, 19 short-legged white descendants and 24 long-legged black descendants were obtained.

Write a crossbreeding scheme and determine the distance between the genes.

Task 406. In mice, the genes that determine coat color and color brightness are inherited concatenated. Yellow and bright coat color are dominant features, and pale wool and agouti color (each coat is divided into color zones: the main zone and the zone of coat tips) are recessive. From crossing yellow bright mice with agouti pale mice, the following offspring were obtained: 52 mice with bright agouti coat, 188 yellow bright mice, 41 yellow pale mice and 174 agouti pale mice.

Determine the genotypes of parents and descendants.

Determine the distance between the genes.

Task 407. In mice the allele for normal-length coat is dominant over the allele for long coat and the allele for curly coat – over the allele for straight fur. As a result of the analysis crossing, 27 mice with normal straight fur, 99 with normal curly coat, 98 with long straight coat, and 24 with long curly coat were obtained.

Write a crossing diagram and determine the frequency of the crossing.

Task 408. Rabbits have recessive alleles of two linked genes determine the white spotting of the coat and its long length (Angora type), and dominant alleles for the absence of spots on the coat and its short length. The distance between the genes is 14%. A homozygous spotted rabbit with short coat was crossed with a homozygous Angora non-spotted doe-rabbit.

Determine the phenotype and genotype for first-generation hybrids.

Calculate the possible number of non-spotted rabbits with long coat should be among 1,280 descendants from the analyzing cross of first-generation hybrids.

Task 409. In rabbits, the gene for black coat color gene is dominant over brown coat, the gene of the normal coat length over a genome of the short coat, the gene of white color of fat over the genome of the yellow color of fat. All 3 genes are located on the same chromosome. Two breeds of rabbits are crossed. One is characterized by black coat of normal length and white fat; the other is characterized by short brown coat and yellow fat.

First-generation hybrids have black coat of normal length and white fat. These hybrids are crossed with the recessive parent form. The results of the analyzing crossing are as follows:

Phenotypes The length of the hair	The color of fat	The color of the coat	Number of individuals
Normal	White	Black	188
Shot	Yellow	Black	50
Normal	Yellow	Black	6
Shot	White	Black	32
Normal	Yellow	Brown	38
Normal	White	Brown	56
Shot	Yellow	Brown	216
Shot	White	Brown	3

Make a diagram of crosses.

Determine the distance between the genes and their order.

Task 410. From crossing homozygous piebald rabbits with short coat with homozygous Angora rabbits without spots, piebald descendants with short coat were obtained. In the future, all individuals of the first generation were crossed with Angora without spots and received numerous

offspring: 72 piebald short-coat rabbits, 69 smooth-colored Angora, 11 piebald Angora, 13 smooth-colored short-coat rabbits.

Determine the genotypes of parents and descendants, the distance between the genes that determine the color and length of the fur.

Task 411. In rabbits, the genes for coat length and color are inherited concatenated. The allele for short coat is dominant over the allele for long coat, and the allele for spotted coloring – over the allele for white color. From crossing heterozygous English rabbits with short spotted coat with Angora rabbits with long white coat, 380 spotted short-coat, 380 white long-coat, 59 spotted long-coat and 66 white short-coat were obtained.

Write a crossbreeding scheme and determine the distance between the genes.

Task 412. In rats, the allele for black coat coloration is dominant over the allele for white coat coloration, and the allele for dark-colored eyes over the allele for light color eyes. Both characteristics are inherited concatenated. The distance between the genes is 54.7%. From crossing a heterozygous black female with dark eyes with a white male with light eyes, 66 black rats with light eyes, 61 white rats with dark eyes, 144 black rats with dark eyes, and 147 white rats with light eyes were obtained.

Write a crossing diagram and determine the amount of interference.

Task 413. In humans, Rhesus factor and elliptocytosis are linked signs. The genes that control these traits are 3% apart. Rh-positive and elliptocytosis (a disease associated with a change in the shape of red blood cells) are dominant autosomal traits, and Rh-negative and normal red blood cells are recessive. In the family, one spouse is diheterozygous, and Rh-positive inherited from the mother, and elliptocytosis from his father. The second spouse has normal red blood cells and Rh-negative blood.

Determine the probability of having children in this family with all possible genotypes and phenotypes.

Task 414. Classical hemophilia and color blindness, recessive traits, are inherited linked to the X chromosome. The distance between the genes controlling these traits is 9.8%.

A) A girl whose father suffers from both hemophilia and color blindness, and whose mother is healthy and comes from a well-off family for these diseases, married a healthy man.

Determine the phenotypes of children and their probability.

B) A woman whose mother was color blind and whose father had hemophilia married a man who had both abnormalities.

Determine the probability of children in this family who have both abnormalities at the same time.

Task 415. Genes that have recessive alleles that determine color and night-blindness are linked to the X chromosome and are 50% apart.

Determine the probability of children with two abnormalities at the same time in a family where wife and husband have normal eyesight, but the wife's mother had night-blindness, and the wife's father had color blindness.

Task 416. John Spock, second-in-command of the trans galactic starship Enterprise, was the son of two planets: Vulcan and Earth. His father was a Vulcan and had the characteristic pointed ears of his people, a heart on the right side, and small adrenal glands. All three attributes are dominant over the Earth ones. John Spock's mother was an Earthling. The genes that determine the heart position and size of the adrenal glands are inherited concatenated, and are spaced 20% apart, the gene of the ears is another group of adhesion. John marries a woman from Earth.

Identify the probability of the child inheriting a set of traits like his father.

Identify the probability that the first child will have small adrenal glands, but rounded ears and a heart on the left side.

Task 417. The nail-patella syndrome is a defect determined by a completely dominant allele of an autosomal gene. At a distance of 10% from it is the locus of blood groups of the ABO system. One of the spouses has blood group B, the other has blood group AB. The spouse with blood group B has a nail and kneecap defect. It is known that his father had blood group A and did not have these abnormalities, and his mother with blood group O had both defects. The spouse who has blood group AB is healthy and homozygous for both pairs of alleles.

Determine the probability of having children with nail and kneecap defects.

Establish the nature of their blood group inheritance.

Task 418. In humans, the genes that control blood clotting and color perception are located on the X chromosome at a distance of 10% and are recessive. A healthy woman, whose father had hemophilia and whose mother was color blind, married a normal man.

Calculate the probability of having a child with both abnormalities and the child's gender.

Task 419. Sensorineural deafness is determined by a recessive allele, which is located on the I chromosome, at a distance of 20% from the gene, whose recessive allele determines the development of papillary carcinoma (malignant tumor). In a family where the wife is healthy and the husband can hear well and was operated on for kidney carcinoma, a deaf boy was born with a malignant kidney tumor.

Determine the genotypes of the parents and the probability of the birth of such a child.

Task 420. The gene that determines blood groups in the Duffy system (D+) is located on the I chromosome. At a distance of about 5% from it is the glaucoma gene (a recessive trait that leads to the development of eye disease). The husband has excellent vision and blood group D+ (it is known that his mother had glaucoma, and his father had blood group D-). My wife has glaucoma and blood type D+ (her mother had blood type D-).

Calculate the probability of having a healthy baby with blood type D-.

Task 421. The allele of colon cancer and the allele of susceptibility to Mycobacterium infections are located at a distance of 18% from each other, in the II chromosome. Both abnormalities are recessive traits. A girl who inherited the allele of colon cancer from her father and the allele of susceptibility to Mycobacterium infections from her mother married a man who was susceptible to Mycobacterium infections and normal for colon cancer (this disease was not previously found in the family of this man).

Determine what children are likely to be born in this family and calculate their predisposition to diseases.

Task 422. The gene for small cell lung carcinoma (malignant tumor, recessive trait) is localized in the III chromosome, at a distance of about 25% from it is the gene for sensitivity to the herpes virus (dominant trait). The wife, who has small cell lung carcinoma, inherited a gene for sensitivity to the herpes virus from her mother. Her husband is

heterozygous for both genes, and he inherited both pathologies from his father.

Calculate the probability of having: a) a healthy child; b) a child with both pathologies; c) a child sensitive to the herpes virus.

Task 423. Cataract and polydactyly in humans are caused by the dominant alleles of two closely related autosomal genes. Recessive alleles of these genes control the development of normal traits.

A) The woman inherited cataract from her mother, and polydactyly from her father. Her husband does not have anomalies.

Calculate the probability of children born in this family: with cataract and polydactyly; without abnormal traits; with only one anomaly.

B) It is known that the wife's mother also had both abnormalities, and her father was healthy.

Calculate the predisposition of offspring to diseases in a family where the husband has normal traits, and the wife is heterozygous for both pairs of alleles.

Task 424. Recessive alleles of congenital cataract and papillary renal cell carcinoma (malignant tumor) are localized in the I chromosome at a distance of 20% from each other. The husband has from papillary renal cell carcinoma and has not got cataract, all his relatives are healthy. The wife inherited the allele of congenital cataract from her father, and the allele of papillary renal cell carcinoma from her mother.

Determine what children are likely to be born in this family and calculate their predisposition to diseases.

Task 425. The gene for congenital cataracts (the dominant trait) is located on the I chromosome. At a distance of about 15% from it is the gene that determines the blood group in the Duffy system (D+ and D-). The D+ allele is dominant. A woman with good eyesight and Duffy's blood type + (her father's blood type D-), married a man with congenital cataract who has blood type D-.

Determine what children are likely to be born in this family and calculate their predisposition to diseases.

Task 426. The colon cancer gene and the liver cancer gene are located on chromosome II at a distance of 18%. The husband inherited the recessive allele of colon cancer from the father, and the recessive allele of

liver cancer from the mother, the wife's mother died of colon cancer, according to the second gene, and the wife's second gene is normal.

Calculate the probability of having a healthy child in this family.

Task 427. The gene for wrinkly skin syndrome and the gene for susceptibility to Mycobacterium infections are located on the II chromosome at a distance of 25% from each other. The husband has wrinkly skin syndrome (recessive trait), and the wife is susceptible to Mycobacterium infections (recessive trait). A child with wrinkly skin syndrome was born in this family.

Determine the genotypes of the parents and the probability of a healthy child being born who will be a carrier of alleles of both diseases.

Task 428. The genes of small cell lung carcinoma and renal carcinoma are localized in the III chromosome at a distance of 19%. At a distance of 25% from the gene for small cell lung carcinoma, there is a gene for sensitivity to the herpes virus (the dominant trait). The husband inherited the recessive allele of small cell lung carcinoma and the dominant allele of sensitivity to the herpes virus from the mother, the wife inherited the recessive allele of renal carcinoma from the father, and the sensitivity to the herpes virus from the mother.

Determine which children are likely to be born in this family and calculate their predisposition to diseases.

Task 429. The gene for sensorineural deafness (recessive trait) and Waardenburg syndrome (partial albinism and deafness are determined by a dominant allele with a penetration of 67%) are localized in the first chromosome at a distance of 10% from each other. Both spouses are TRANS-diheterozygous on these genes.

Calculate the probability of a healthy child being born in this family.

Calculate the probability of having a child with two diseases.

Task 430. In humans, the gene that determines the nail-patella syndrome gene and the gene that determines the ABO blood group are linked together and are located at a distance of 10%. The gene determining Rh factor and the elliptocytosis gene are located on a different chromosome and are located at a distance of 3% from each other. The nail-patella syndrome, elliptocytosis, and Rh-positivity are determined by dominant alleles.

A) One spouse is heterozygous for all the analyzed genes and has blood group O. He inherited the nail-patella syndrome from his father along with the blood group B gene. The second spouse is homozygous for all recessive genes and has blood group A.

Calculate the probability of birth in this family of a child with Rh-positive blood group AB, without nail-patella syndrome, and normal red blood cells.

B) One spouse is heterozygous for all the analyzed genes and has blood group B. He inherited the nail-patella syndrome from his father along with the blood group B gene. The second spouse is homozygous for all recessive genes and has blood group A.

Calculate the probability of birth in this family of a child with Rh-negative blood group A, without nail-patella syndrome and normal red blood cells.

C) One spouse is heterozygous in all genes and has blood group AB. He inherited the nail-patella syndrome from his father along with the blood group AB gene. The second spouse is homozygous for all recessive genes and has blood group A.

Calculate the probability of birth in this family of a child with Rh-positive blood group AB, with nail-patella syndrome and elliptocytosis.

D) One of the spouses is heterozygous for nail-patella syndrome, has blood group O, Rh-negative and normal red blood cells. It is known that his father did not have nail-patella syndrome and had blood group AB. The second spouse had normal nail structure and blood group A and was heterozygous for Rh factor and elliptocytosis. His mother was Rh-positive and had elliptocytosis.

Determine the probability of having children in this family without elliptocytosis and nail-patella syndrome, Rh-positive and their possible blood groups.

Task 431. In humans, the Rh factor and elliptocytosis genes are located on the same chromosome at a distance of 3% from each other. The color blindness gene and the night-blindness gene are located 40% apart on the X chromosome. Rh-positivity and elliptocytes are dominant alleles, and night and color blindness is recessive.

A) A woman who is heterozygous in all respects, and whose ancestors did not have a crossover, marries a man who has night and color blindness, with Rh-negative blood and normal red blood cells.

Determine the probability of having a child with normal eyesight, Rh-positive blood and normal red blood cells.

B) A woman who was heterozygous for all genes, whose mother had

elliptocytosis and had Rh-negative blood, and whose father was night blind and color blind, married a man who had night and color blindness, with Rh-negative blood and normal red blood cells.

Determine the probability of having a child with night-blindness, Rh-negative blood and elliptocytosis.

C) A woman who was heterozygous in all her genes and whose ancestors did not have a crossover was married to a man who had night-blindness and color blindness, with Rh-negative blood and normal red blood cells.

Determine the probability of having a boy with color blindness, Rh-positive blood and normal red blood cells.

D) A woman who was heterozygous for all genes, whose mother had elliptocytosis and night-blindness, and whose father had Rh-negative blood and color blindness, married a man who had night-blindness and color blindness, with Rh-negative blood and normal red blood cells.

Determine the probability of having a girl with normal eyesight, Rh-negative blood and without elliptocytosis.

E) A Rh-positive woman with normal red blood cells and normal eyesight married a man with Rh-negative blood, elliptocytosis and night-blindness. It is known that the woman's father was Rh-negative and was color blind, and the mother was not color blind, but had night-blindness. The man’s father had elliptocytosis, and the mother had night-blindness.

Determine the probability of having Rh-positive children without other abnormalities.

F) A Rh-positive woman with normal red blood cells and normal eyesight married a man with Rh-negative blood, elliptocytosis and night-blindness. It is known that the woman's father was Rh-negative and was color blind, and the mother was not color blind, but had night-blindness. The man’s father had elliptocytosis, and the mother had night-blindness.

Determine the probability of having Rh-positive children with elliptocytosis and color blindness.

G) A Rh-positive woman with normal red blood cells and normal eyesight married a man with Rh-negative blood, elliptocytosis and night-blindness. It is known that the woman's father was Rh-negative and was color blind, and the mother was not color blind, but had night-blindness. The man’s father had elliptocytosis, and the mother had night-blindness.

Determine the probability of having a Rh-negative child with normal red blood cells, night and color blindness.

H) A Rh-positive woman with normal red blood cells and normal

eyesight married a man with Rh-negative blood, elliptocytosis and night-blindness. It is known that the woman's father was Rh-negative and was color blind, and the mother was not color blind, but had night-blindness. The man’s father had elliptocytosis, and the mother had night-blindness.

Determine the probability of having a Rh-negative boy with elliptocytosis, night and color blindness.

I) A woman who was heterozygous in all her genes married a Rh-negative man who was normal in all other respects. It is known that the woman's father was Rh-negative, had elliptocytosis and night-blindness, but was not color blind.

Determine the probability of having Rh-positive children with elliptocytosis and normal eyesight.

J) A woman who was heterozygous in all her genes married a Rh-negative man who was normal in all other respects. It is known that the woman's father was Rh-negative, had elliptocytosis, night blindness, but was not color blind.

Determine the probability of birth in this family of a Rh-negative son normal for all other traits.

K) A woman who was heterozygous in all her genes married a Rh-negative man who was normal in all other respects. It is known that the woman's father was Rh-negative, had elliptocytosis, night blindness, but was not color blind.

Determine the probability of having a Rh-positive daughter with elliptocytosis and normal eyesight.

Task 432. In humans, the hemophilia gene and the color blindness gene are located in the X chromosome at a distance of 9.8% and are inherited recessive. The gene for nail-patella syndrome is located in the autosome at a distance of 10% from the gene that determines the blood group according to the ABO system. The nail-patella syndrome is a defect of the nails and patella determined by the dominant allele.

A) A woman with blood group O and heterozygous in terms of other marries a man with blood group A and normal in terms of other. It is known that the woman's father had both hemophilia and night-blindness, had a nail-patella syndrome and blood group B.

Determine the probability of having children in this family without abnormalities and their blood groups.

B) A woman with blood group B and heterozygous for the rest of the analyzed traits marries a man with blood group AB, color blind and

normal in terms of other traits. It is known that the mothers of the spouses had blood group A and both suffered only from color blindness.

Determine the probability of having children in this family without abnormalities and their blood groups.

Task 433. V.N. Mikelsaar (1974) provided a map of 2 sections of the human X chromosome. In one section, there are the following genes linked: the genes of blood serum (**Xm**), 2 forms of blindness – deuteranopia (**d**) and protanopia (**p**), hemophilia (**h**) and the gene for glucose-6-phosphate dehydrogenase (**G**) deficiency. In another section, there are the following genes linked: the genes of blood group (**Xg**), ocular albinism (**a**), ichthyosis (**i**) and angiokeratoma (**ac**). For the first section is known, the gene **Xm** gives 7% crossing over with gene **d**, 11% – with gene **G**, 16% – with gene **p**. Gene **G** gives 4% crossing over with gene **d**, 5% from the genome of **p**. Gene **p** gives 3% crossing over with gene **h**. Gene **h** gives 6% crossing over with gene **d**. For the second section, it is known that the **Xg** and **ac** genes form 28% of crossover gametes, **Xg** and **i** – 11%, **Xg** and **a** – 18%, **a** and **ac** – 10%, **i** and **a** – 7%.

Build maps of both sections of the human X chromosome.

6. GENEALOGICAL AND TWIN METHODS OF GENETICS

In cases where it is not possible to apply hybridological analysis, for example, with a small number of offspring, other methods of genetic analysis are used, including genealogical analysis, which includes analysis of several generations of relatives. This method is usually used in humans and domestic animals, sometimes in plants.

The genealogical method consists of two stages:

– drawing up a pedigree and its graphic representation;

– genetic analysis of the obtained data.

The collection of information about the family begins with a **proband** – an individual who is the subject of interest of the doctor (researcher) in a particular pedigree. Most often, this is a patient or a carrier of the studied trait. The family tree includes known relatives both in the descending line (children, grandchildren, great-grandchildren, etc.) and in the ascending line (parents, grandparents, great-grandparents, etc.).

Children of the same parent pair (brothers and sisters) are called **sibs**. Usually, the pedigree is collected by one or more traits. The more generations traced in the pedigree, the more complete it is and the higher the chances of obtaining reliable information. Genetic information is collected through a survey, a questionnaire, and a personal family survey. Drawing a pedigree includes creating a brief record of each member of the genus with reference to their relationship to the proband, as well as the surname, name, patronymic, date of birth and death, age, nationality, place of residence, family, occupation, chronic diseases in the family, cause of death, etc.

After collecting information, researchers make a graphic image of the pedigree, using a system of symbols (figure 5).

When drawing up a graphic image of a pedigree, observe the following rules:

– Start the pedigree with a proband (the individual for whom the pedigree is compiled);

– Proband's siblings are arranged in order of birth from left to right, starting with the eldest;

– Representatives of each generation in the family tree are placed strictly in one row;

– Roman numbers indicate generations: to the left of the pedigree from top to bottom;

– Arabic numbers indicate the offspring of one generation (the entire

row) from left to right sequentially (under each representative, i.e. relative).

Thus, each member of the family tree has their own code, for example, II-3, III-6.

To get correct genetic conclusions, we must strive to obtain the most complete and objective primary material, which is the basis of statistical and genetic analysis.

The genealogical method is one of universal methods in medical genetics and is often called clinical genealogical, since it is about the study of pathological traits (diseases) in the family with the involvement of methods of clinical examination. It is widely used in solving theoretical and practical problems, such as:

– establishing the hereditary nature of the disease;

– defining the type of trait inheritance;

– evaluation of gene penetrance;

– decoding the mechanisms of gene interaction.

The genealogical method occupies a special place in medical and genetic counseling, being sometimes the only one when clarifying the nature of the disease, making a diagnosis of an inherited disease, evaluating the prognosis of the disease, calculating the risk for offspring, etc.

The purpose of genealogical analysis is to establish genetic patterns. The first task in the analysis of pedigree is to establish the hereditary character of the trait. If the same trait (or disease) occurs several times in the pedigree, you can think about its hereditary nature.

Once the hereditary nature of the trait or disease is established, the type of inheritance must be established. For this purpose, the principles of genetic analysis and various statistical methods of processing data obtained from the pedigree are used.

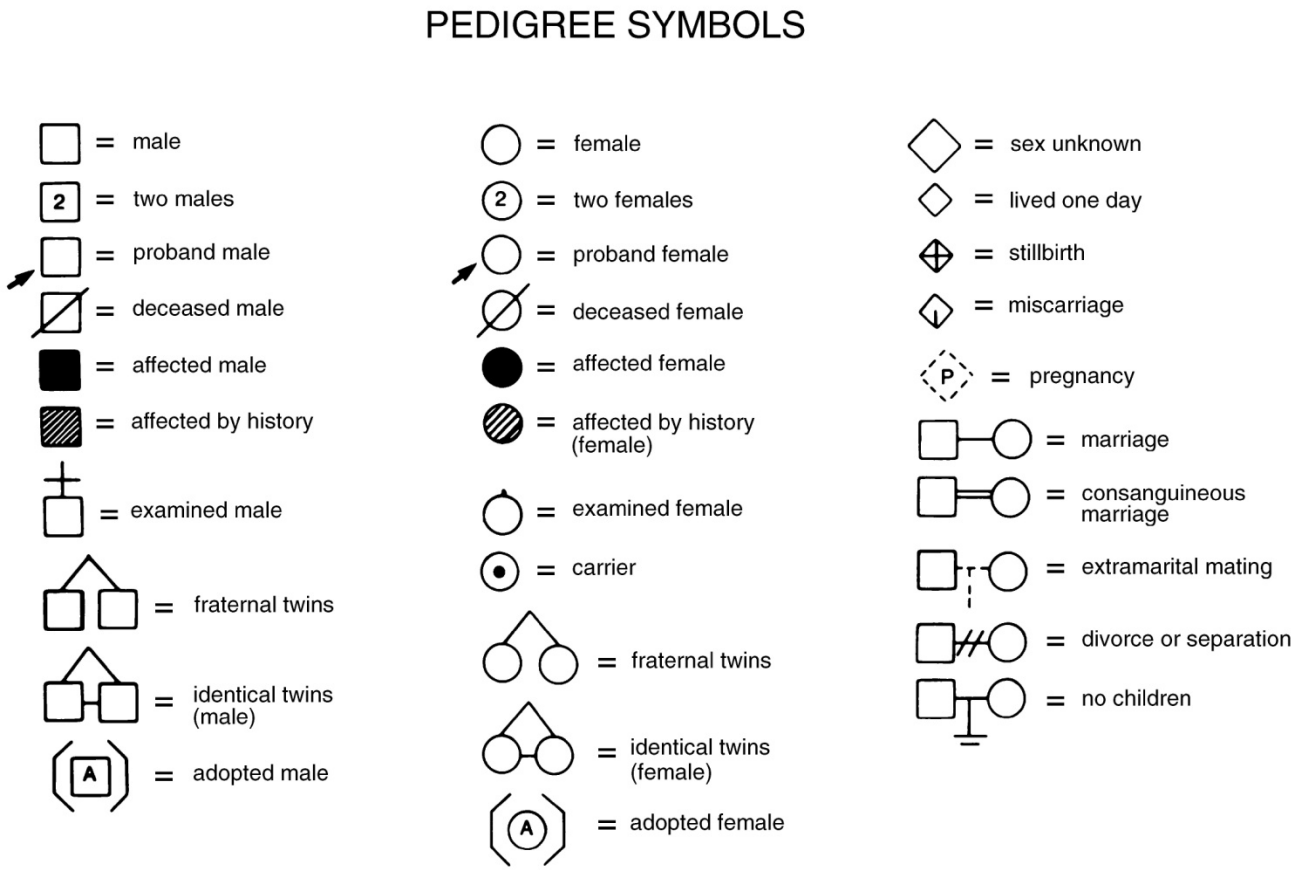


Figure 5. System of symbols for drawing up a pedigree

Only monogenic hereditary diseases, i.e. diseases whose etiological factor is a mutation of a single gene, are subject to the Mendelian laws of inheritance. Depending on the localization and properties of the gene, there are: **autosomal dominant and autosomal recessive types of inheritance**, when the gene is located in one of 22 pairs of autosomes (non-sex chromosomes), **X-linked dominant and recessive types of inheritance**, when the gene is located in the X chromosome, **Y-linked (holandric) inheritance**, when the gene is located in the Y chromosome.

The accuracy of the analysis will depend on the number of generations analyzed and the number of people in each generation, with an absolutely good knowledge of the patterns discussed in the previous chapters. Let's briefly consider the main patterns of inheritance of various types of deviant traits.

Inheritance of an autosomal dominant trait. If the disease is caused by a rare autosomal dominant gene, the absolute majority of patients in the population are born in marriages between the affected and healthy spouse. In this case, one of the parents is heterozygous for the autosomal dominant gene (Aa), and the other is homozygous for the normal allele (aa). In such

a marriage, the following variants of genotypes in the offspring are possible: Aa, Aa, aa, aa. Thus, every future child, regardless of gender, is 50% likely to receive both the A allele (and therefore be affected) and the normal a allele from a sick parent, and to be healthy. The ratio of the number of healthy children in the offspring to the number of affected is 1:1 and does not depend on the sex of the child.

The main criteria for assuming **an autosomal dominant type of inheritance** are:

— the disease manifests itself in every generation without omissions ("vertical" type);

— every child from a parent with an autosomal dominant disease has a 50% risk of inheriting this disease;

— unaffected children of sick parents are free of the mutant gene and have healthy children;

— the disease is inherited by men and women equally often and with a similar clinical picture.

To date, about 3,000 autosomal dominant human traits have been described. According to this type, a person inherits brachydactyly (shortened and partially reduced phalanges of fingers and toes), polydactyly (from 6 to 9 fingers on the hand or foot), arachnodactyly (abnormally long "spider" fingers), some forms of myopia, and other traits.

Autosomal recessive inheritance is characterized by the following features:

— parents of a sick child are usually healthy and are heterozygous carriers of the pathological allele;

— boys and girls are equally likely to get sick;

— the repeated risk of having a child with an autosomal recessive disease is 25%;

— "horizontal" distributions of patients, i.e. patients are more often found within the offspring of the same parent pair;

— an increase in the frequency of sick children in related marriages, and the rarer autosomal recessive diseases, the more often patients come from consanguineous marriages;

— in the marriage of two stricken parents, all the children are sick.

Autosomal recessive type inherited soft straight hair, snub nose, light eyes, thin skin and Rh-negative blood group A. The most frequent and clinically significant diseases with an autosomal recessive type of inheritance are: cystic fibrosis, phenylketonuria, many forms of visual and hearing disorders, and others.

Inheritance of an X-linked trait. X-linked recessive disease (or trait) always appears in men who have the corresponding gene, and in women – only in cases of homozygous condition (which is extremely rare).

The main features of **X-linked recessive inheritance** are as follows:

– the disease occurs mainly in men;

– this trait (disease) is transmitted from a sick father through his phenotypically healthy daughters to half of his grandchildren;

– the disease is never transmitted from father to son;

– subclinical signs of disease are sometimes revealed in female-carriers;

– married female-carriers with a sick man 50% of daughters will have the disease, 50% of daughters will be carriers, 50% of sons also will have the disease and 50% of sons will be healthy (diseases not reducing reproductive ability of male patients). This type of inherited hemophilia A, color blindness, and others.

Diseases with X-linked dominant type of inheritance are 2 times more common in women than in men. The main characteristic of X-linked dominant inheritance is that sick men pass the abnormal gene (or disease) to all their daughters and do not pass it to their sons. A sick woman passes the X-linked dominant gene to half of her children, regardless of gender.

The main features of X-linked dominant inheritance type are as follows:

– the disease occurs in men and women, but in women it is about twice as common;

– a sick man passes the mutant allele to all his daughters and does not pass it to his sons, since the latter receive the Y-chromosome from their father;

– sick women transmit the mutant allele to 50% of their children regardless of gender;

– women suffer less (they are heterozygous) than men when they are ill.

*Y-linked or holandric inheritance***.** For a long time, it was believed that the Y-chromosome contains only genetically inactive sections. Currently, about 20 genes have been identified in the Y chromosome, including genes that determine the development of testis responsible for spermatogenesis, controlling the intensity of growth, determining the hair of the ear auricles, middle phalanges of the hands, and some others. The trait, whose genes are localized in the Y chromosome, is transmitted from the father only to all boys.

Inheritance of a partially sex-linked recessive trait (alleles of the gene are present in the X and Y chromosomes) differs from autosomal recessive in that the trait, as a rule, appears in the lineage of descendants of the same sex, namely, the one who carried this trait.

Examples of solving tasks on pedigrees

A) The pedigree is given (Fig. 6). In the pedigree, obviously, inheritance of the trait is autosomal dominant, since it most often appears descendants of different sexes only in families where one of the parents (I-4) had the trait. In families where there were no parents with the trait, children also did not appear with this trait.

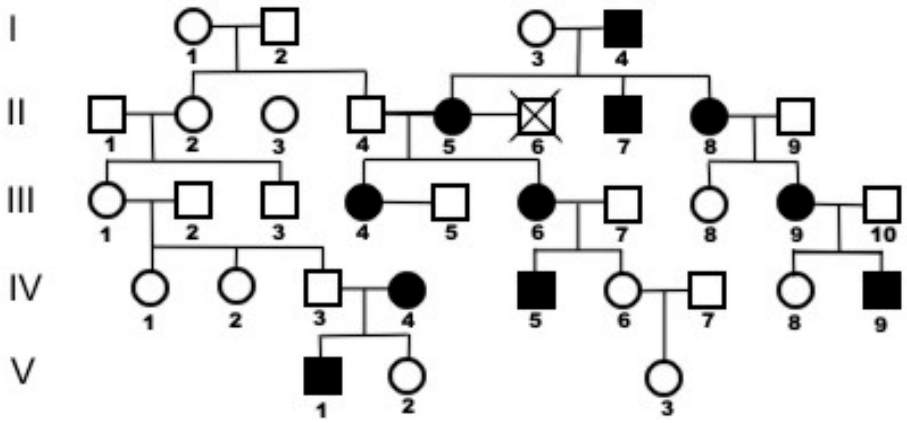


Figure 6. Pedigree to task A

B) The pedigree is given (Fig. 7). In this genealogy, the recessive trait is linked to the gender, since in the family, which does not have a parent trait, only male descendants appear with the trait (II-2, II-5, II-7, III-3, IV-1). Consequently, one of the mother's X chromosomes (I-1) has a recessive gene that determines this trait. The owner of the trait (III-7) appeared only in one family where the father (II-7) had the trait, and the mother, apparently, had a recessive gene on the same X-chromosome.

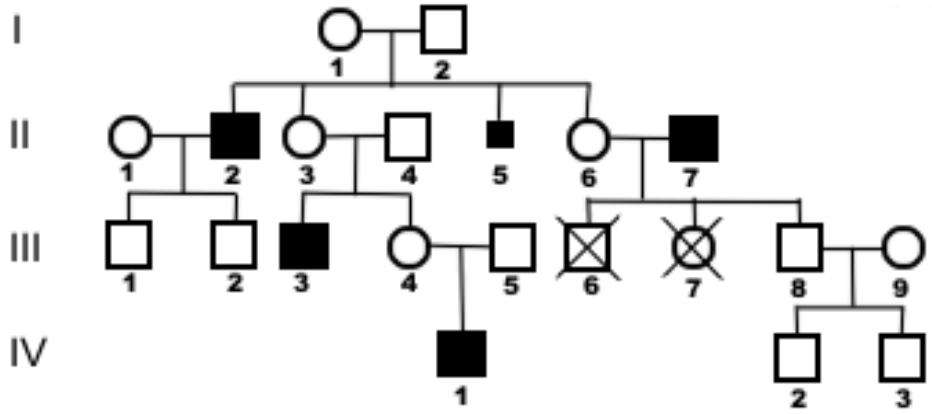


Figure 7. Pedigree to task B

C) The pedigree is given (Fig. 8). In this pedigree, only males appear in the offspring with the trait, so it could be assumed that the trait is holandric. However, a woman appeared in the same family with the sign (III-6). In this family, the father (II-8) had a trait, and the mother (II-7), apparently, was heterozygous, then the offspring may have a homozygous daughter. The trait in women is manifested only in homozygous, and in men in homozygous and heterozygous states, which is characteristic of a sex-dependent trait, i.e. in men it is dominant, in women it is recessive.

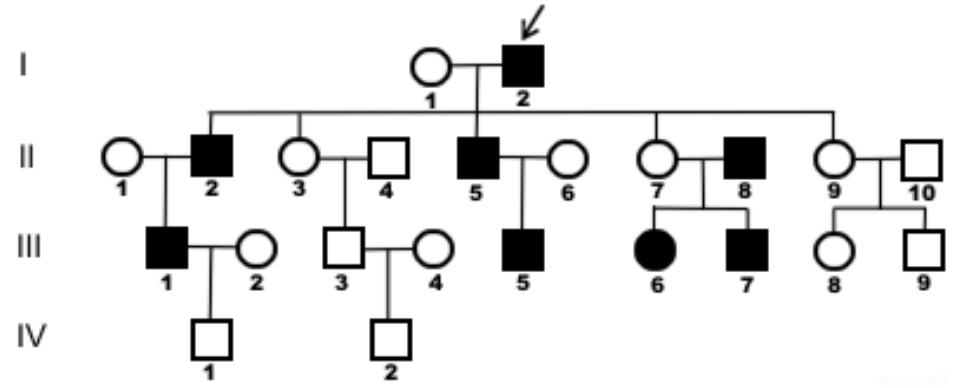


Figure 8. Pedigree to task C

D) The pedigree is given (Fig. 9). Here the inheritance is characteristic of a recessive trait partially linked to gender. In this case, there are descendants with the trait (V-2, V-3) of the same sex that originally had the trait (I-1) as a result of the fact that the great-granddaughter (IV-2) and her husband (IV-3) (great-grandson) on the X chromosome had a recessive gene for the trait being studied. However, the great-granddaughter (IV-8) also had a recessive gene on the X chromosome. She married a man (IV-9) who has the X and Y chromosome recessive gene of the trait being studied. As a result, all descendants (V-7, V-8, V-9) were born with the trait. In this family, all children with the trait appeared accidentally.

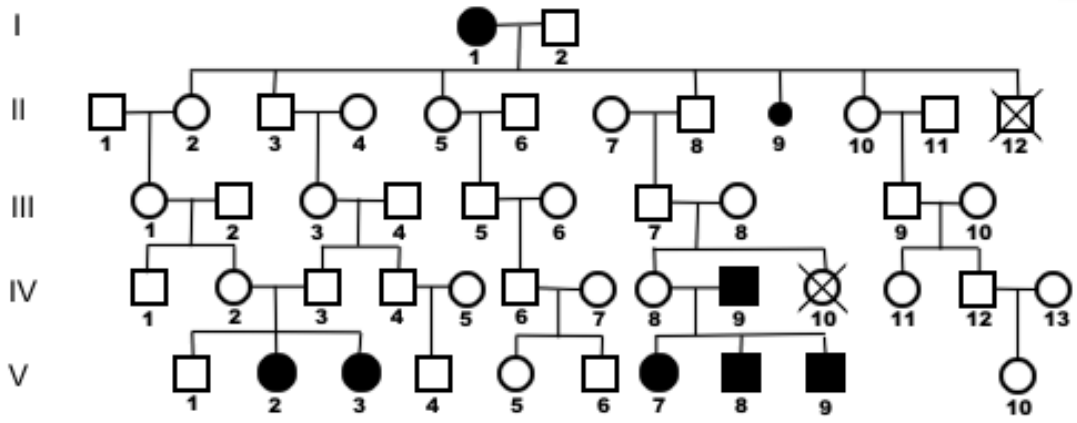


Figure 9. Pedigree to task D

E) The pedigree is given (Fig. 10). In the pedigree, both sexes have a trait. Its frequency is higher in those families where one of the parents has the trait, and the second is probably heterozygous. However, it does not appear in all branches of the family tree, for example, in the case where one of the parents has a trait (I-2). All this indicates that the trait is inherited by an autosomal recessive type, since such a trait can appear in the offspring if either parents are heterozygous or one of the parents is heterozygous (II-9), and the second (II-10) has this recessive trait.

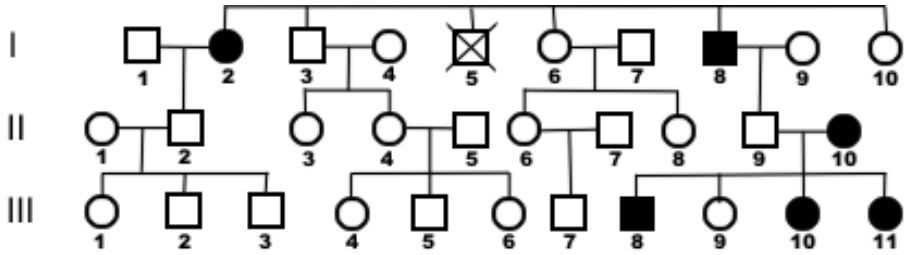


Figure 10. Pedigree to task E

F) The pedigree is given (Fig. 11). In this pedigree, there is a holandric trait since all sons (II-2, II-6, II-8) have the trait if their father (I-2) has it, i.e. the father with the Y chromosome passes this gene to his sons.

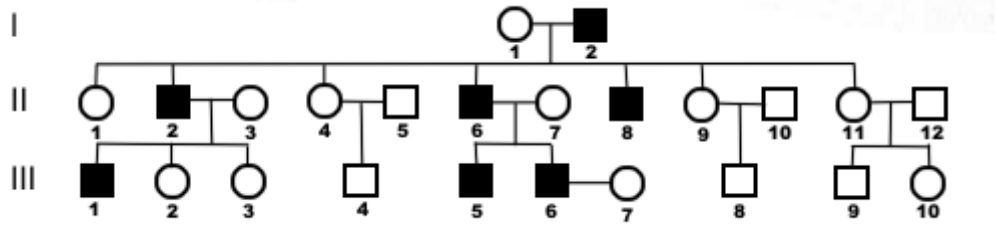


Figure 11. Pedigree to task F

G) The pedigree is presented (Fig. 12). In this pedigree, the inheritance of a trait is clearly characteristic of a sex-linked dominant gene, since if the father (I-2) has this gene on the X chromosome, then all the daughters (II-1, II-5, II-8, II-10) in the family appear with the trait. If the mother (II-1) has at least one X chromosome dominant gene, then both daughters (III-2) and sons (III-1) can appear with the trait, because both sexes receive the X chromosome from the mother.

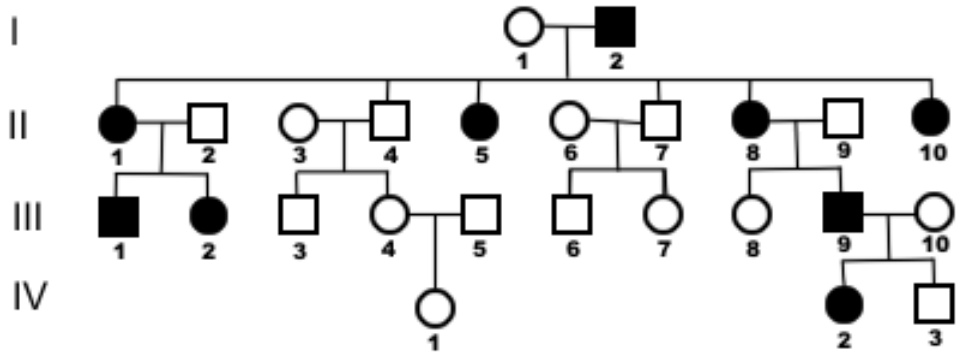


Figure 12. Pedigree to task G

Task 434 The pedigree (Fig. 13) shows the inheritance of familial epilepsy.

Analyze the type of disease inheritance.

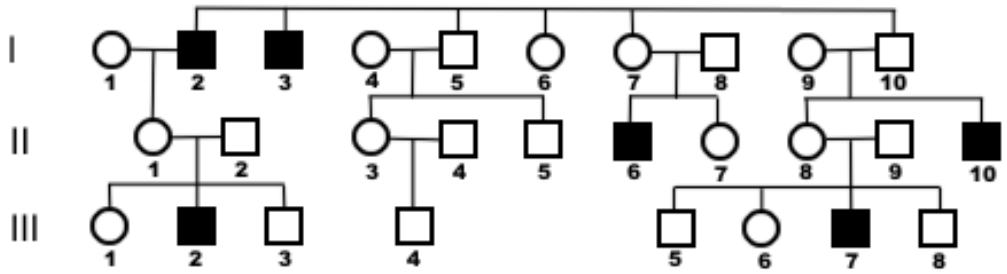


Figure 13. Pedigree to task 434

Task 435. The pedigree (Fig. 14) shows the inheritance of familial epilepsy.

Analyze the type of disease inheritance.

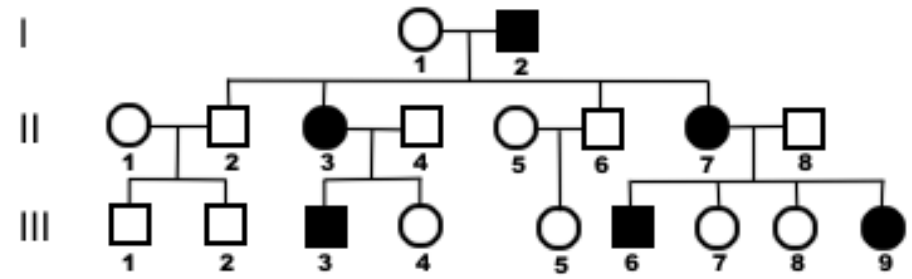


Figure 14. Pedigree to task 435

Task 436. Ayrshire cattle have a pedigree on inheritance of curly coat (Fig. 15).

Determine the type of inheritance of curly coat, if the nature of the coat of the ancestors is unknown.

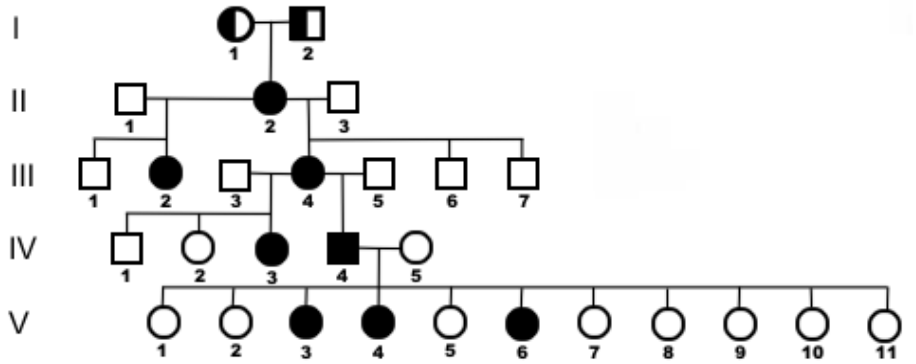


Figure 15. Pedigree to task 436

Task 437. The pedigree of Guernsey cattle is presented (Fig. 16).

Determine the nature of inheritance of hairlessness.

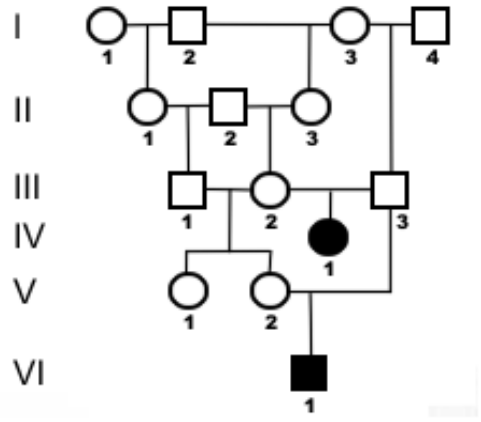


Figure 16. Pedigree to task 437

Task 438. The pedigree of dogs is presented (Fig. 17).

Analyze the pedigree of two puppies suffering from cerebellar ataxia, born in the same litter from normal parents.

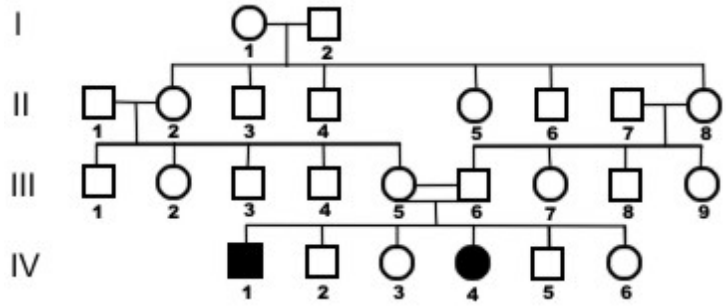


Figure 17. Pedigree to task 438

Task 439. Figure 18 shows the pedigree.

Analyze how the "curved little finger" trait is inherited in humans.

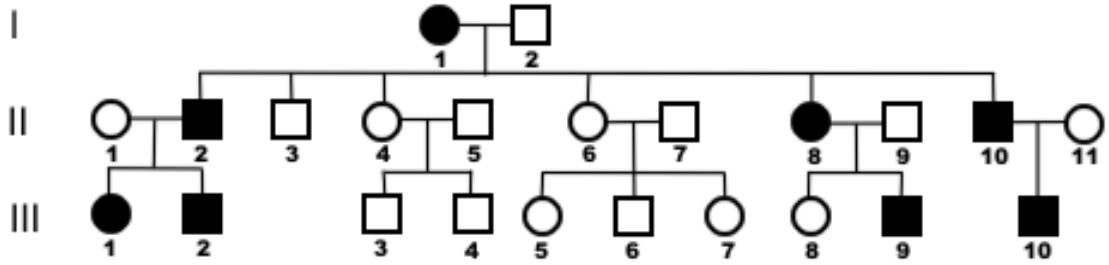


Figure 18. Pedigree to task 439

Task 440. The pedigree is presented (Fig. 19).

Analyze the inheritance of a person's "dimple on the cheek" trait. Set the parents (ancestors).

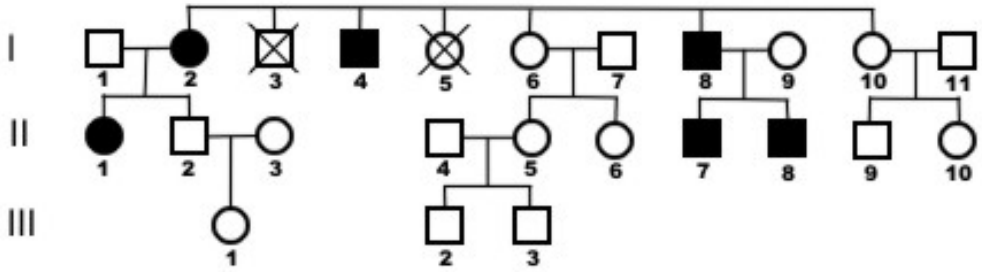


Figure 19. Pedigree to task 440

Task 441. The human pedigree is presented (Fig. 20).

Determine the nature of inheritance of the "small eyes" trait.

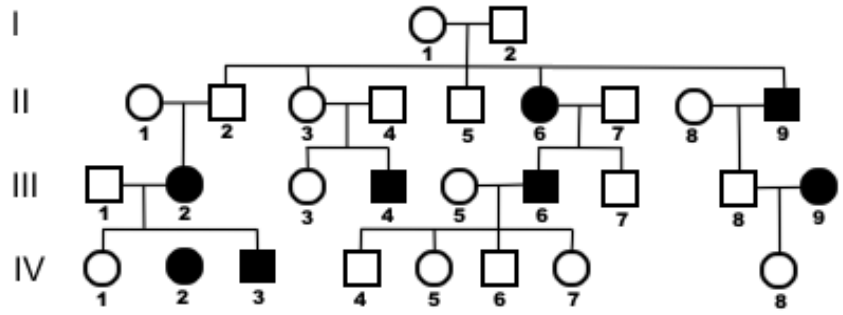


Figure 20. Pedigree to task 441

Task 442. The pedigree with hereditary albinism is presented (Fig. 21). Albino people have white hair, white skin, and colorless irises (the eyes appear red because the blood vessels in the fundus are visible). Albinism is known to be caused by a recessive gene.

Based on the presented pedigree, trace the transmission of this gene and determine the genotypes of as many individuals as possible.

Determine the frequency of albino children from the marriage of a woman (III-3) and a normal man (III-2) who is not related to her.

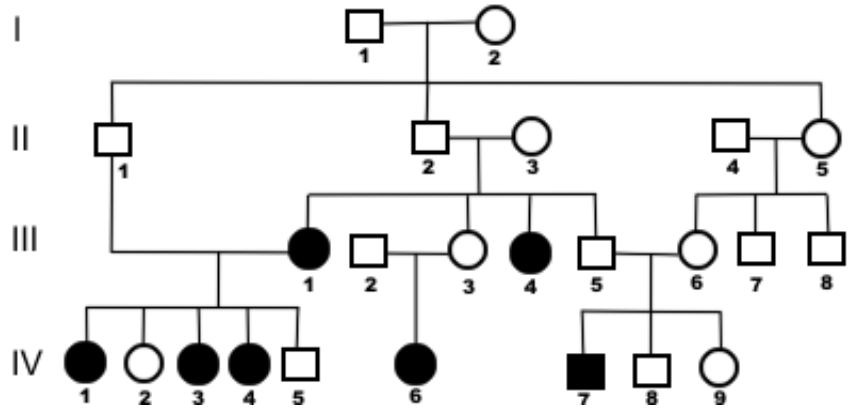


Figure 21. Pedigree to task 442

Task 443. In five human genealogies (Fig. 22 A, B, C, D, E), individuals marked in black carry the trait being studied.

Determine for each pedigree the method of inheritance of the studied trait (dominant or recessive).

Determine, if possible, the genotypes of each individual found in the presented pedigrees.

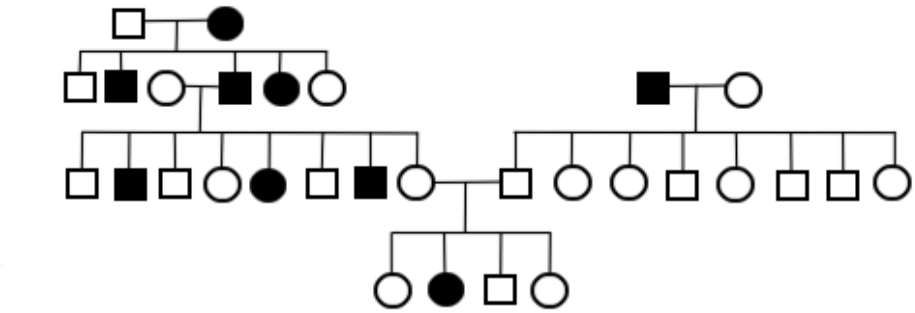


Figure 22 A. Pedigree of a family with left-handedness

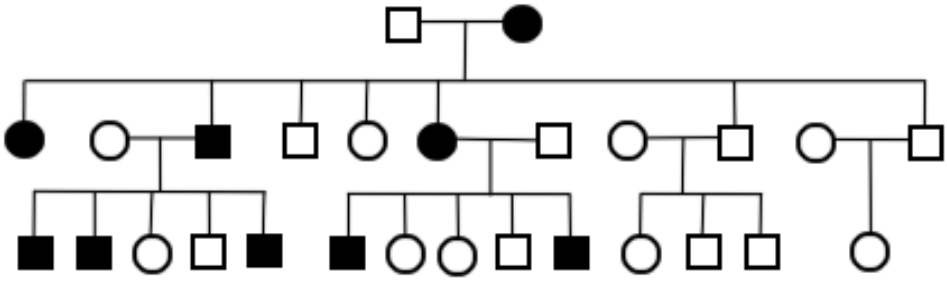


Figure 22 B. Pedigree of a family with polydactyly

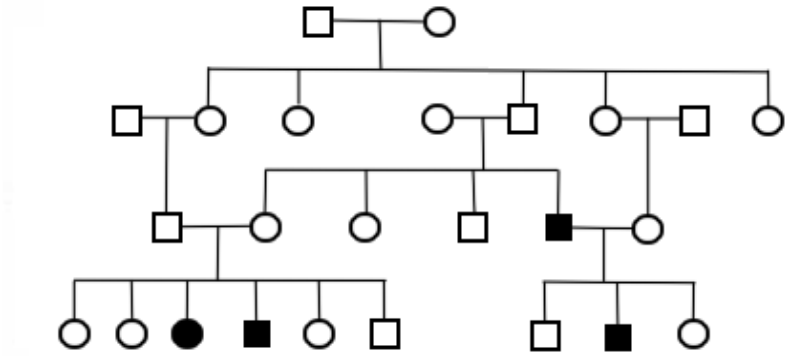


Figure 22 C. Pedigree of a family with muscular atrophy

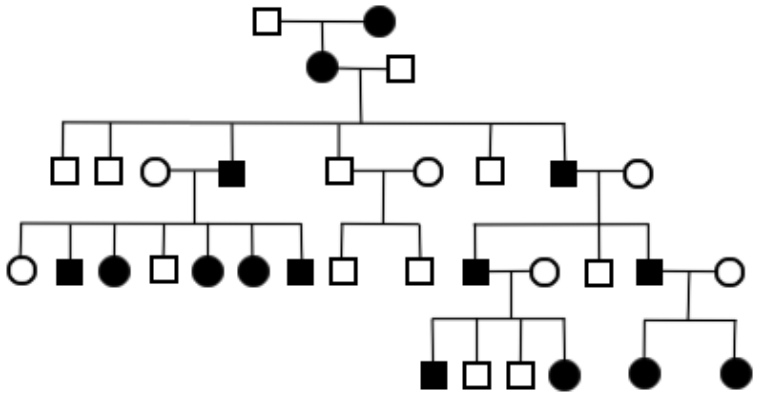


Figure 22 D. Pedigree of a family with an unknown trait

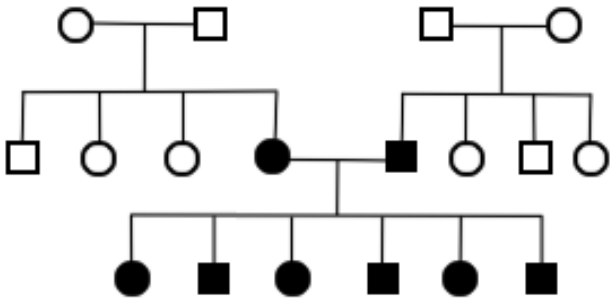


Figure 22 E. Pedigree of a family with an unknown trait

Task 444. Four human pedigrees show inheritance of dominant and recessive traits (Fig. 23 A, B, C, D). Let us assume that the crossed individuals do not have children and the only indication of their genotype is the nature of the distribution of the trait in the presented pedigree. Let us also assume that other individuals who marry members of this family and do not show a recessive trait do not carry the recessive genes that cause it.

Calculate the probability of showing the trait in the offspring of various crosses:

– In the pedigree A (with the dominant feature) – individuals III-1 and III-3; III-2 and III-4;

– In the pedigree B (with the dominant feature) – individuals III-1 and III-5; III-2 and III-4;

– In the pedigree C (with a recessive trait) – individuals III-1 and III-6; III-3 and III-4; III-1 and III-7; III-2 and III-9; III-6 and III-11;

– In the genealogy of D (with a recessive trait) – individuals III-1 and III-7; III-2 and III-4; III-6 and III-8.

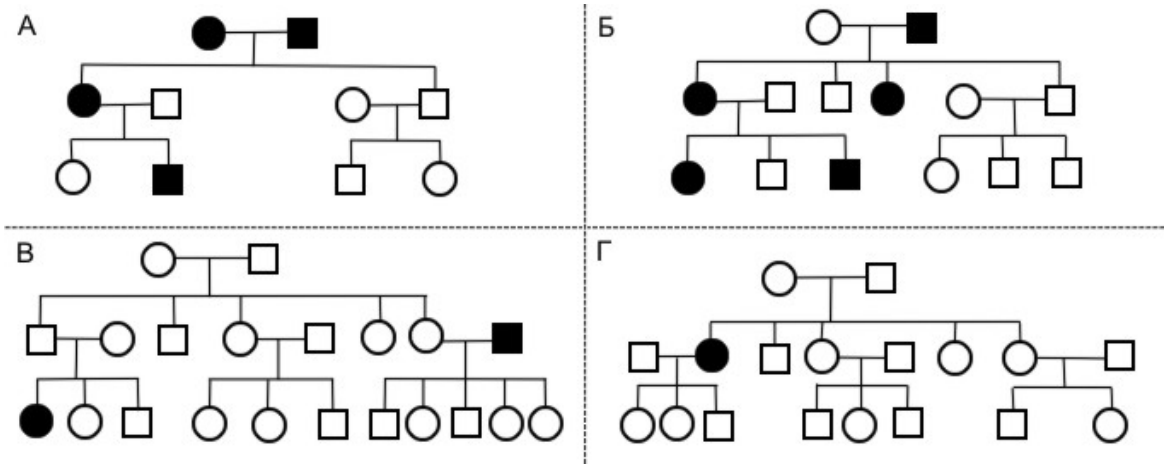


Figure 23. Pedigrees of four families with dominant and recessive traits

Task 445. A proband has a white streak. The proband's brother does not have a white streak. There was no abnormality on the side of proband's father. The proband's mother had a white streak. She has three sisters: two sisters with a white streak and one without it. The first aunt of the proband has a son with a white streak and a daughter without it. The second aunt has a son and a daughter with a white streak, and a daughter without it. The third aunt of the proband on the mother's side without a white streak has two sons and one daughter without it. The proband's maternal grandfather and two of his brothers had white streaks, and two others didn't have white streaks. The great-grandfather and great-great-grandfather also had a white streak over their foreheads.

Determine the probability of having children with a white streak over the forehead if the male proband marries his cousin who has this white streak.

Task 446. Newlyweds are right-handed. The woman has three right-handed sisters and three left-handed brothers. The woman's mother is right-handed, her father is left-handed. The father has a left-handed sister and a left-handed brother, and a right-handed sister and two right-handed brothers. The paternal grandfather is right-handed; the grandmother is left-handed. The mother of the woman has two brothers and a sister who are all right-handed. The husband's mother is right-handed, and the father is left-handed. The maternal and paternal grandparents of the man were right-handed.

Determine the probability of having left-handed children in this family.

Task 447. A proband is a healthy woman who had two healthy brothers and the two brothers with alkaptonuria (homogentisic acid is excreted in the urine). The proband's mother is healthy and has two healthy brothers. Proband's father has alkaptonuria and he is his wife's great-uncle. He has a healthy brother and a healthy sister. The paternal grandmother had alkaptonuria and was married to her healthy cousin. Proband's maternal grandparents were healthy, and his grandfather's father and mother were also healthy, while his grandfather's mother was a sister of proband's paternal grandfather.

Determine the probability of having children with alkaptonuria in a proband family, provided that she marries a healthy man whose mother had alkaptonuria.

Task 448. A proband is a healthy girl who has two healthy brothers and a sister who has alkaptonuria. The proband's mother and father are healthy. Two sisters of proband's mother are healthy. The maternal grandmother has alkaptonuria, and proband's grandfather is healthy. Two brothers and two sisters of the proband's father are healthy, a grandfather on the father's side and a grandmother are healthy. Both proband's aunts on his father's side were married to healthy men. All children in these families are healthy. The mother's aunt has a healthy husband and two healthy children.

Make a pedigree and determine the probability of the birth of a child with alkaptonuria, if proband marries a man with alkaptonuria.

Task 449. A proband is a normal woman, she has five sisters, two of whom are identical twins, two are fraternal twins. All sisters have six fingers. The proband's mother is normal, and his father is six-fingered. On the mother's side, all the ancestors are normal. The father has two brothers and four sisters, all five-fingered. The paternal grandmother is six-fingered. She had two six-fingered sisters and one five-fingered sister. The paternal grandfather and all his relatives are five-fingered.

Determine the probability of having six-fingered children in a proband's family, provided that she marries a normal man.

Task 450. Charlotte Auerbach (1969) described such a pedigree for six-fingered people. Two six-fingered sisters, Margaret and Mary, married normal men. Margaret had five children: James, Susanna, and David were six-fingered, and Ella and Richard were five-fingered. In the family, Mary had an only daughter, Jane, with a normal hand skeletal structure. From his first marriage to a normal woman, James had a six-fingered daughter Sarah, and from his second marriage to a normal woman, he had six children: one daughter and two sons were five-fingered, two daughters and one son were six-fingered. Ella married a normal man. They had two sons and four daughters, all were five-fingered. David married a normal woman. Their only son Charles was six-fingered. Richard married his cousin Jane. Their two daughters and three sons were five-fingered.

Determine the probability of having six-fingered children if a normal daughter of James is married to one of Richard's sons; if Sarah is married to David's son.

Task 451. Brachydactyly is characterized by shortening of fingers. A proband is a woman with brachydactyly. One of her sisters and one of her brothers also have brachydactyly, and two of her sisters are healthy with respect to the analyzed disease. The proband's mother is ill and his father is healthy. The father's brother and two sisters are healthy. The proband's paternal grandparents are healthy. In addition, the grandmother has a healthy brother and sister. All their relatives are healthy. The proband's mother has a brother with brachydactyly and two healthy sisters. Their father is ill and their mother is healthy. The proband married a healthy man whose relatives are all healthy.

Determine the genotype of proband and all her relatives, as well as the probability of the birth of children with brachydactyly in proband.

Task 452. A proband is a healthy girl who has a healthy brother and a sister with syndactyly (fused or webbed fingers). The proband's father is healthy, and his mother is ill. The father's relatives are all healthy. The proband's mother has a healthy brother and sister and a sick sister. Both sisters were married to healthy men. A healthy sister gave birth to a healthy son, and a sister with syndactyly gave birth to a healthy daughter and a sick son. The proband's maternal grandfather has syndactyly, but he has a healthy sister and a healthy brother. The maternal grandmother is healthy and has two healthy brothers.

Determine the probability of having a sick child in a proband family if she marries a heterozygous man relative to the analyzed trait.

Task 453. A proband (male) has polydactyly. His father also has polydactyly, and his mother has a normal hand structure. Further pedigree is known only on the father's side. The father has a brother and sister with normal hand structure, as well as a brother and a sister with polydactyly. The proband's uncle with polydactyly was twice married to women with normal hand structure.

From one marriage the proband’s uncle had a daughter with polydactyly, from the second marriage he had six children: two daughters and one son with polydactyly and two sons and one daughter with normal hand structure. The aunt of the proband with a normal hand was married to a man with no analyzed abnormality. They had three boys and three girls with normal hand structure. The proband’s grandfather has no anomalies, and the grandmother has polydactyly.

Calculate the probability of having multi-fingered children in a proband’s family if he marries a woman with a normal hand structure.

Task 454. A proband is a girl with normal finger structure. Her mother and father also have normal finger structure. The proband's father has a sister with brachydactyly and a brother with normal fingers. The proband's paternal aunt, who has brachydactyly, is married to a man without the abnormality being analyzed. Their son with brachydactyly. The Grandmother of the proband on the father's side has brachydactyly, grandfather doesn't have it. The proband's paternal grandmother had a sister with brachydactyly. The great-grandparents (father and mother of proband's paternal grandmother) had brachydactyly.

The great-grandfather was married twice. His second wife had brachydactyly. In the second marriage the great-grandfather had two daughters without abnormalities and four sons with brachydactyly. All the children of the great-grandfather from the second marriage were married to persons who do not have an anomaly. One of his daughters had two girls and a boy without brachydactyly, the other daughter had a boy without an anomaly, one of his sons had a girl with brachydactyly, the other son had one normal girl and two twin girls with brachydactyly, the other two sons had one boy each without an anomaly.

Determine the probability of having children with an anomaly in the proband's family, provided that she marries a man of the same genotype as herself.

Task 455. A proband is a girl with brachydactyly. She has three brothers and one sister with the normal structure of the fingers. The father of the proband has brachydactyly, a mother without anomalies. The proband's father has a brother with brachydactyly and two sisters: one with normal finger structure and the other with brachydactyly. The brother of proband's father is married to a woman without an anomaly. They have four sons and six daughters, of whom one son and two daughters have normal finger structure, the others have brachydactyly. The proband's paternal grandmother had brachydactyly, grandfather didn't have it. The proband's paternal grandmother had seven sisters and four brothers, including three sisters and one brother with normal finger structure, the others had brachydactyly. Two brothers and three sisters of proband's grandmother, who had brachydactyly, were married to people with normal finger structure.

One brother of proband's grandmother had two daughters with brachydactyly who were married to men who had normal finger structure. The first daughter of brother of proband's grandmother has three sons with

normal finger structure, one son with brachydactyly, one daughter with normal finger structure, and two daughters with brachydactyly. The second daughter has two boys with an abnormality and two with normal hand structure, one girl with brachydactyly and one with normal hand structure. Another brother of proband's paternal grandmother has a daughter without an anomaly and a daughter with brachydactyly.

The daughter of one of brothers of proband's grandmother with brachydactyly from a man with normal finger structure and has a son without an anomaly and a son with brachydactyly. One of sisters of a proband's paternal grandmother had two daughters without this anomaly. The second sister of proband's grandmother has a son without an anomaly and two daughters with brachydactyly, one of whom married a normal man and has a son with a normal finger structure. The third sister of proband's paternal grandmother has two daughters without an anomaly and a son with brachydactyly, who married a woman with normal finger structure and has a daughter with the analyzed anomaly and a daughter with normal finger structure. Great-grandfather (father of proband's paternal grandmother) with brachydactyly, his wife without an anomaly. This great-grandfather had six brothers without an anomaly and three sisters with brachydactyly. Mother of a great-grandfather with brachydactyly, father without an anomaly.

Determine the genotypes of all the persons mentioned in the pedigree and calculate the ratio of healthy and affected by the anomaly direct descendants of the mother of proband's paternal grandfather.

Compare this relation to the Mendelian law of segregation.

Task 456. A proband is a short-fingered woman with three healthy brothers and one healthy sister. The proband's father has short fingers. On the father's side, the uncle and one aunt are short-fingered, and the second aunt has a normal hand. The uncle has seven children with short fingers (three sons and four daughters), and one son and two daughters with a normal hand. The paternal grandmother was short-fingered, and all maternal relatives are normal.

Make a family pedigree according to the trait specified, determine the nature of inheritance of this trait and the genotypes of the individuals indicated in the pedigree.

Task 457. A proband is a healthy woman. Her sister is also healthy, and her two brothers are color blind. The proband's mother and father are

healthy. The four sisters of proband's mother are healthy, and their husbands are also healthy. The following is known about cousins on the mother's side of the proband: in one family there are one sick son, two healthy daughters and a healthy son; in two other families there are one sick son and one healthy daughter; in the fourth family there is one healthy daughter. Proband's maternal grandmother is healthy, and his grandfather was color blind. There were no color blind people in the family of the proband's father.

Determine the probability that proband will have children with color blindness if she marries a healthy man.

Task 458. A proband (male) suffers from night-blindness. His two brothers are also ill. There were no night-blind people in the family of the proband's father. The proband's mother has night-blindness. Two sisters and two brothers of the proband's mother are healthy. They only have healthy children. On the maternal side, the following is known: grandmother with night-blindness and healthy grandfather; grandmother's sister is ill and her brother is healthy; great-grandfather, who was the grandmother's father, had night-blindness; grandfather's sister and brother had night-blindness; great-great-grandfather and his brother had night-blindness; the brother of the great-grandfather has a daughter and two sons with night-blindness. Proband's wife, her parents and relatives are healthy.

Determine the probability of having sick children in a proband's family.

Task 459. In proband's blood, normal hemoglobin A is replaced by hemoglobin S and hemoglobin Hopkins-2. Proband has two sisters and two brothers with hemoglobin S, one brother with hemoglobin Hopkins-2 and one brother with hemoglobin S and hemoglobin Hopkins-2 at the same time. The proband's father is normal in terms of hemoglobin (hemoglobin A), and his mother has both hemoglobin S and hemoglobin Hopkins-2. The proband's mother and her two brothers and one sister have the same hemoglobin; in addition to them, proband's mother has a sister with hemoglobin S and a brother whose hemoglobin has not been studied. The proband's maternal grandmother with hemoglobin S and hemoglobin Hopkins-2 at the same time, and his grandfather with normal hemoglobin A. the proband's maternal uncle, who was not tested for hemoglobin, was married to a woman who had hemoglobin S.

Their two daughters have both hemoglobin S and hemoglobin

Hopkins-2. These two cousins of the proband are married to men with normal hemoglobin A. One of them has a girl with normal hemoglobin and a girl with hemoglobin S and hemoglobin Hopkins-2 at the same time, the other has two sons: one with hemoglobin S, the other with hemoglobin Hopkins-2. Aunt of proband on her mother's side was married twice. She was married to a man whose hemoglobin was not tested due to his death, she has a daughter with hemoglobin Hopkins-2. Then she was married to a man with normal hemoglobin A, she has a son and a daughter – both with hemoglobin Hopkins-2.

Determine the nature of inheritance of abnormal hemoglobin. Calculate the probability of having children at the same time with two abnormal hemoglobin in the proband's family, if she marries a man of the same genotype.

Task 460. A proband is a healthy young man with a healthy sister and a hemophiliac brother. The disease is characterized by bleeding and hemarthrosis. The proband's father and his parents are healthy. The proband's mother is healthy, has a sick brother and a healthy sister who married a healthy man. They had a healthy daughter and a son with hemophilia. The proband's mother has a sister who is married to a man whose parents are healthy. The proband's maternal grandparents are healthy. The proband married a healthy woman who has the same genotype as his mother. They had a healthy girl.

Make a pedigree and analyze it.

Determine the probability of birth of a boy with hemophilia.

Task 461. A proband has a mild form of sickle cell anemia. His wife is healthy. They have a daughter with a mild form of sickle cell anemia; her mother's siblings and her father are healthy. The proband's wife has a sister with a mild form of anemia, and her other sister died of anemia. The mother and father of proband's wife had anemia, in addition, it is known that the father had two brothers and a sister with a mild form of anemia, and that in the family of the father's sister, two children died of sickle cell anemia.

Determine the probability of having children with severe anemia in the family of proband's daughter, if she marries the same man as her father.

Task 462. A proband is ill with a mild form of elliptocytosis (oval-shaped red blood cells). In heterozygotes, the disease occurs in a mild form, in homozygotes, severe hemolytic anemia develops. The proband is married to a healthy woman and has a sick daughter and a healthy son. The proband's father is ill and his mother is healthy. The proband's mother has a healthy sister and healthy parents. The paternal grandfather is ill, and my grandmother is healthy. The proband has a healthy aunt and uncle on his father's side. The uncle is married to a healthy woman. Their three sons (proband's paternal cousins) are healthy.

Calculate the probability of a proband daughter having sick grandchildren in her family if she marries a man who is heterozygous for elliptocytosis.

Task 463. A proband (a man) and his five brothers are healthy. Proband's mother and father are deaf and dumb. Two uncles and an aunt on the father's side are also deaf and dumb. On the mother's side, four aunts and an uncle are healthy, and one aunt and one uncle are deaf and dumb. The maternal grandmother and grandfather are healthy. The paternal grandmother and grandfather are deaf and dumb. The paternal grandmother has a deaf and dumb brother and two deaf and dumb sisters.

The paternal grandfather has two brothers, one of whom is healthy, the other is deaf and dumb, and five sisters, two of whom are deaf and dumb. The paternal grandfather’s mother and father are healthy, the paternal grandmother’s mother and father were deaf and dumb.

Determine the probability of having children with deaf and dumb in the proband family, if he marries a woman who is not deaf and dumb and has no history of this disease in the family.

Task 464. A proband is a normal woman, one of her sisters and one of her brothers have otosclerosis (deafness), and two of her sisters and two of her brothers are healthy. The proband's mother is ill and his father is healthy. The father's brother is ill and his sister is healthy. The paternal grandfather and grandmother are healthy. The grandmother has one sick brother, two healthy sisters, and one healthy brother. The grandmother's father is ill, and the mother and her parents are healthy. The proband's mother has a sick brother and three healthy sisters. The proband's maternal grandparents are healthy, his maternal grandfather has a brother with otosclerosis, while his other brother and sister are healthy.

Make a pedigree and determine the probability of having children with otosclerosis in proband, if she marries a healthy man.

Task 465. A proband is a healthy girl with two healthy brothers and a sister with congenital deafness. The proband's mother and father are healthy. Two sisters and parents of proband's mother are also healthy in terms of the analyzed disease. The proband's father has a healthy brother, one deaf sister and one healthy sister. The father's deaf sister married a healthy man and they had a healthy son and daughter. The healthy sister of the proband's father was married to a healthy man and had two healthy girls. The proband's paternal grandparents are healthy, and his grandmother has a healthy sister and a deaf brother.

Determine the probability of having a sick child, if proband marries a healthy man.

Task 466. A proband is a young man who has deafness. His sister is healthy. The proband's mother has five sisters with normal hearing and one deaf brother. Three sisters of proband's mother are married to healthy men. One sister of proband's mother has a healthy daughter, the second one has a healthy son, the third sister has a healthy daughter and a deaf son. The proband's maternal grandmother and her husband are healthy.

The proband's maternal grandmother has three healthy sisters, one healthy brother and one deaf brother. The maternal grandmother's healthy sisters had healthy husbands, and her healthy brother was married to a healthy woman. The first sister of the proband's grandmother has four healthy daughters and one deaf son. The second sister of the proband's grandmother has a healthy daughter and a deaf son. The third sister of the proband's grandmother has a healthy daughter, one healthy and one deaf son. Maternal The father and mother of proband's maternal grandmother are healthy.

Determine the probability of having deaf children in proband's family, provided that his wife has the same genotype as proband's mother.

Task 467. A proband (male) is healthy. The proband's father has epidermolysis bullosa. The mother and her relatives are healthy. Two of proband's sisters are healthy, and one of his brothers is ill. Three paternal uncles and their children are healthy, and three uncles and one aunt are ill. One sick uncle with his first wife had a sick son and a healthy daughter, and in his second marriage a sick daughter and son were born. The second sick uncle has two healthy daughters and a sick son. The third sick uncle has two sick sons and two sick daughters. The paternal grandmother is ill, and the paternal grandfather is healthy; the grandmother's three sisters and two brothers were healthy.

Determine the probability of having sick children in the family of the proband under the condition that he marries with a healthy woman.

Task 468. A proband has normal color of teeth. His sister's teeth are brown. The teeth of proband's mother are brown, and his father's teeth are normal. Seven of sister of the proband's mother have brown teeth, and four of her brothers have normal teeth. One of the proband's aunts (sisters of his mother) with brown teeth married a man with normal teeth. They have three children: a daughter and a son with brown teeth and a daughter with normal teeth.

Two of proband's uncles on his mother's side are married to women with normal teeth. One of them has two sons and a daughter, the other has two daughters and a son. All of them have normal teeth. The proband's maternal grandfather had brown teeth, and the maternal grandmother had normal teeth. Two brothers of the maternal grandfather had teeth with normal color. The great-grandmother (mother of the maternal grandfather) and the great-great-grandmother (mother of this great-grandmother) had brown teeth, and their husbands had normal teeth.

Determine what children proband might have if he marries a woman with the same genotype as his sister.

Task 469. In Northern Ireland, the inheritance of deaf-mutes was studied in several families. In one of these families, 8 children were born to healthy parents, four of whom (two sons and two daughters) were deaf and dumb. In another family, deaf and dumb parents had three daughters and one son, all deaf and dumb. A deaf and dumb son from the first family married one of the daughters from the second family and all their children, a daughter and three sons, were deaf and dumb. One of these three sons married a deaf and dumb girl who was not related to these families, and their six sons were healthy.

Make a family tree.

Explain the above facts.

Task 470. Aroband is a healthy young man has two sisters with tooth enamel hypoplasia. Proband's mother is healthy and his father had tooth enamel hypoplasia. The mother has two healthy sisters and a healthy brother. The mother's parents are also healthy. The father has a healthy sister and a sister with the anomaly. Both sisters have healthy husbands. The healthy sister has a healthy son, and the sister with the anomaly has a

son and daughter both with tooth enamel hypoplasia. The proband's paternal grandfather is healthy, and his grandmother has got the anomaly. The grandmother has two sick sisters and a healthy brother.

The father of the sick proband's grandmother had this anomaly and the mother, i.e. proband's great-grandmother, was healthy. The proband marries a girl who has hypoplasia of tooth enamel. The girl's older brother is ill and has a healthy wife and a sick daughter. The younger brother is healthy, and has a healthy wife. He has no children. The mother of proband's wife has tooth enamel hypoplasia, and the father is healthy. The proband's mother-in-law has a sick sister and a healthy brother. His wife's maternal grandfather is ill, and the grandmother is healthy.

Determine the probability of having sick children in proband's family, as well as in the families of his relatives.

Task 471. A proband is a healthy young man with two sisters and a healthy brother who have vitiligo syndrome (focal skin depigmentation). Proband's mother and her brother are healthy. On the mother's side, her grandfather, grandmother and two of her sisters are healthy. The parents of the proband's grandmother were also healthy. The proband's father is healthy and has a sick sister and a healthy brother. The proband's paternal grandfather has vitiligo, and his two sisters and brother are healthy, and the proband's grandmother is healthy. Proband's brother has a sick son and a healthy daughter.

Determine the probability of having healthy and sick children in the proband family if he marries a healthy girl.

Make a pedigree and analyze it.

Task 472. A healthy woman turned to medical and genetic counseling in order to find out the prognosis for intestinal polyposis for her offspring. Her brother is ill, and her mother and father are healthy. Relatives of the father: two sisters, father and mother are healthy. The proband's mother has two brothers who are healthy and one brother with intestinal polyposis. The proband's maternal grandmother is healthy. Brother, sister and the parents of the grandmother are healthy. The proband's maternal grandfather and one sister have intestinal polyposis, and another brother and sister are healthy. The proband's maternal great-grandmother and great-grandfather are healthy.

Make a pedigree and analyze it. Determine the prognosis of proband's offspring if she marries a healthy man.

Task 473. Ichthyosis is a change in the skin. A proband and his two sisters are healthy, and his two brothers have ichthyosis. The proband's mother and her sister are healthy. In the family of a healthy proband's aunt, on the mother's side, there is a healthy daughter and a sick son. The proband's maternal grandfather is ill, and his two sisters are healthy. The proband's maternal grandmother is healthy and has a healthy brother and sister. The proband's father is healthy and has a healthy brother and sister. The proband's paternal grandmother and grandfather are healthy.

Determine the type of inheritance of the disease, the genotypes of relatives and the forecast of offspring if a proband is married to a heterozygous girl.

Task 474. A proband is a young man with Aarskog–Scott syndrome. This syndrome is characterized by stunting (90%), hypertelorism, ptosis, as well as loose joints, brachydactyly, etc. The proband has two healthy sisters and a healthy brother. The proband's father, his two sisters and their parents are absolutely healthy with respect to the analyzed disease. The proband's mother is healthy and has a healthy brother and sister, and one brother with Aarskog–Scott syndrome. Brothers and sisters of the proband's mother are married to healthy people.

The brothers of the proband's mother have one healthy daughter each, and the sister has a son with Aarskog–Scott syndrome. The proband's maternal grandparents are healthy. His grandfather has a healthy sister and a healthy brother. The grandmother has a sick brother and a healthy sister.

Determine the probability of having sick children in the proband's family and the families of his cousins, if they have healthy spouses.

Task 475. A proband is a healthy young man, he has a healthy sister and a brother with Hartnup disease. This disease is a condition caused by the body's inability to absorb certain protein building blocks (amino acids) from the diet. Patients suffer from stunting, irritability, and constipation. The proband's father and his sisters are healthy, and their parents are also healthy. The proband's paternal grandfather has a healthy brother, and his grandmother has a healthy sister.

The proband's mother is healthy and has healthy siblings. The proband's maternal grandmother is healthy, and his grandfather has Hartnup disease. The proband's maternal grandfather has two healthy sisters; their mother and father are healthy.

Give a forecast of proband's offspring if he marries a heterozygous woman relative to the analyzed disease.

Task 476. Mandibular prognathism is characterized by excessive development of the lower jaw and underdevelopment of the upper one. Healthy newlyweds who have this disease in their families have turned to medical and genetic counseling. The woman has two healthy brothers and one sick sister. Her mother is healthy. The mother's parents are also healthy.

The woman's father is ill; he has two sisters and one healthy brother. The paternal grandfather is ill, and the grandmother is healthy. The woman's husband is healthy and has a healthy sister. His mother is ill, and his mother's sister is healthy. The husband's aunt on the mother's side has three children: one son is ill, and another son and daughter are healthy. The husband's maternal grandmother is ill, and his grandfather is healthy. The husband's father is healthy. All his relatives are healthy.

Determine the probability of having a sick child in this family.

Task 477. A proband has nail-patella syndrome, and his brother is normal. The proband's father had this syndrome, and his mother was healthy. The proband's paternal grandfather had the syndrome, and his grandmother is healthy. The proband's father has three brothers and four sisters, including two brothers and two sisters with nail-patella syndrome. A sick paternal uncle is married to a healthy woman and has two daughters and a son. They are all healthy.

Determine the probability of having children with the disease in the proband's family, if his wife does not have this disease.

Task 478. A proband is a woman with cerebellar ataxia. Her husband is healthy. They have six sons and three daughters. One son and one daughter have cerebellar ataxia, and the other children are healthy. The proband has a healthy sister and three brothers with cerebellar ataxia. A healthy sister is married to a healthy man and has a healthy daughter.

Three brothers of the proband are married to healthy women. The first brother had two healthy sons and one healthy daughter. The second brother has a healthy son and a with cerebellar ataxia daughter. The third brother has two sons and two daughters who are all healthy. The proband's father is not healthy and his mother is healthy.

Calculate the probability of proband's sick daughter having sick children, if she marries a healthy man.

Task 479. A proband is a healthy young man and has four brothers who have Duchenne muscular dystrophy (DMD). The proband's mother and father are healthy. The proband's mother has two healthy sisters, one healthy brother, and two brothers with DMD. The proband's maternal grandparents are healthy. The grandmother had three healthy sisters, two healthy brothers, and one brother with DMD.

All healthy brothers and sisters of the grandmother had healthy spouses. Both brothers had five children – all girls and boys are healthy. One of the grandmother's sisters had a son with DMD, the second grandmother's sister had three healthy sons and one healthy daughter. The third grandmother's sister married healthy men several times. She and her first husband had a son with DMD, in the second marriage she gave birth to a healthy boy and a boy with DMD, in her third marriage she gave birth to a healthy son and a healthy daughter and two sons with DMD. The parent of the proband's maternal grandmother were healthy.

Determine the probability of having sick children in the proband's family if the spouse has the same genotype as the proband's mother.

Task 480. One form of rickets is not cured by regular doses of vitamin D. A proband is a young man with this form of rickets. His sister is healthy. The proband's mother has rickets, and his father is healthy. The proband's mother had three brothers, who were all healthy. The proband's maternal grandfather is ill, and his grandmother is healthy. The grandfather had two healthy brothers and a sick one. The grandfather's healthy brothers had five healthy sons from healthy wives (one had four sons, the other had one). The grandfather's sick brother married a healthy woman. They had three sick daughters and two healthy sons. Two women with rickets whose father was the brother of the proband's grandfather, were married to healthy men and they had one healthy daughter each. One sick woman whose father was the brother of the proband's grandfather married a healthy man and had a healthy son, a son with rickets and a daughter with rickets. The healthy men whose father was the brother of the proband's grandfather had healthy wives, and their children are healthy.

Determine the probability of having children with rickets in the proband's family, if he marries his second cousin with rickets.

Task 481. Make a family tree with a case of diabetes. A healthy husband and wife (cousins) have a child with diabetes. The husband's mother and the wife's father who are siblings are healthy. The husband's

brother, the wife's two sisters, their uncle and grandmother are healthy. The grandfather was diabetic. All relatives of the husband's father (two uncles, a cousin, a grandfather and grandmother) and the wife's mother (an aunt, a cousin, a grandfather and grandmother) are healthy.

Determine the nature of the disease inheritance and mark those family members who are definitely heterozygous for the diabetes gene.

Task 482. Make a family tree with a case of schizophrenia. A proband is a woman with schizophrenia. Her brother, sister and father are healthy. Her paternal relatives are an uncle with schizophrenia, and two healthy aunts. One of the aunts has three healthy children, the second one has a healthy son. The father's grandparents are healthy; the grandmother's sister had schizophrenia. The proband's mother, uncle, and maternal grandparents are healthy; the uncle has two healthy children.

Determine the nature of the disease inheritance and specify the genotypes of as many people as possible.

Task 483. Make a family tree with the rare disease epiloia, which is determined by a gene with a lethal effect. Most people with congenital epiloia (abnormal skin growth, mental retardation, convulsive seizures, tumors of the heart, kidneys, and other organs) die before reaching puberty. With a weak manifestation of the syndrome some of these patients survive and have offspring.

A proband is a woman with epiloia, married to a healthy man had three children: a healthy son and daughter, and a sick daughter. The sick daughter later had five children: healthy two sons and two daughters and one daughter with epiloia. It is known that this sick woman who is the proband's daughter had two stillborn children.

Determine which gene, dominant or recessive, determines this disease and explain the different effects of this gene.

Task 484. A proband of normal height has a sister with achondroplasia. The proband's mother is normal, and his father suffers from achondroplasia. On his father's side, the proband has two normal aunts, one aunt with achondroplasia and one uncle with achondroplasia. An aunt who has achondroplasia married a healthy man. They have a son with dwarfism. A healthy aunt and her healthy husband have healthy children: two boys and two girls. The uncle with dwarfism married a healthy woman. He has two normal girls and a son with dwarfism. The

paternal grandfather has dwarfism, and the grandmother is normal.

Determine the probability of the appearance of dwarfs in the proband's family if his wife will have the same genotype as himself.

Calculate the probability of dwarfs in the family of proband's sister, if she marries a healthy man.

Task 485. A proband is a young man with night-blindness. He has a sister and a brother with normal vision. The proband's mother has five brothers and one sister. The mother's sister has normal vision. She is married to a man with normal vision and has a son with color blindness. Three of the mother's brothers have both night-blindness and color blindness, one brother has only night-blindness and one brother is only color blind. The proband's maternal grandmother has normal vision and is married to a man with normal vision. The grandmother has one brother with night-blindness and one more brother and five sisters with normal vision. All grandmother's sisters are married to men with normal vision.

The grandmother's two sisters have one son each, both with night-blindness and color blindness. The third sister has two sons with color blindness and a daughter with normal vision who is married to a healthy man and has a healthy son. The fifth sister has one son with night-blindness and two healthy daughters. Both daughters of the fifth sister are married to healthy men and have two healthy sons. The great-grandmother (mother of the proband's maternal grandmother) and her husband were healthy.

A healthy sister of the great-grandmother was married to a healthy man and had a healthy daughter, who is married to a man with normal vision and had a color blind and a healthy girl. The great-grandmother's parents had normal vision.

Determine the genotypes of the great-grandmother's parents.

Calculate the probability of having children with visual impairment in the proband family, provided that he marries a woman who comes from a family with no history of the analyzed diseases.

Task 486. Rosa and Alla are sisters and like their parents suffer from night-blindness. They also have a healthy sister, a sister and brother who suffer from night-blindness. Rosa and Alla married men with normal vision. Alla had two girls and four boys who all have night-blindness. Rosa has two sons and a daughter with normal vision and a son with night-blindness.

Determine the genotypes of Rosa and Alla, their parents and children.

Calculate the probability that Rosa and Alla will have grandchildren who are night blind, provided that all their children marry people who are normal with respect to vision.

Task 487. A proband has congenital cataract (an ophthalmic disease associated with clouding of the lens of the eye and causing various degrees of visual impairment). He married a healthy woman and has a sick daughter and a healthy son. The proband's father has cataracts and his mother is healthy. The proband's mother has a healthy sister and healthy parents. The paternal grandfather has cataract, and his grandmother is healthy. The proband has a healthy aunt and uncle on his father's side. The uncle married a healthy woman. Their three sons (the proband's paternal cousins) are healthy.

Calculate the probability of a proband's daughter having sick children in her family if she marries a man who is heterozygous for cataracts of this type.

Task 488. A proband suffers from glaucoma (pathological changes in the eyes that lead to blindness) and has two healthy sisters. The proband's wife and her parents are healthy with respect to the analyzed disease. The proband's parents are healthy. The parents and sister of the proband's father are healthy, too. The proband's mother has a sick sister who married a healthy man and they had a healthy boy and a girl with glaucoma. The proband's maternal grandfather is ill, and his grandmother is healthy.

Determine the probability of having a sick child in a proband's family.

Task 489. A proband is a girl who suffers from high (-5.0 D or more) myopia. Her brother has moderate (-2.0 D to -4.0 D) myopia. The proband's father has normal vision, and his mother had high myopia. The proband's mother has a sister with moderate myopia. The sister of proband's mother is married to a healthy man and has two daughters with moderate myopia. The man who is married to the sister of the proband's mother has a brother and sister with normal vision, their parents are also with normal vision. The proband's maternal grandmother has moderate myopia, her husband (the proband's maternal grandfather) has high myopia.

The proband's maternal grandmother has three brothers with normal vision. The proband's maternal great-grandmother had moderate myopia,

and her husband had normal vision. The proband's maternal grandfather had three brothers: one with moderate myopia, the other with high vision; the third brother's health is unknown.

The brother of the proband's maternal grandfather who has moderate myopia is married to a woman with normal vision. Another brother of the proband's maternal grandfather, who has high myopia, is married to a woman with normal vision. The father of the proband's maternal grandfather was with normal vision, his wife had high myopia. The proband's paternal grandparents had normal vision, and all their relatives and parents are healthy.

Determine the probability of having children with myopia and the nature of myopia in a proband's family if she marries a man with the same genotype as her mother.

7. POPULATION-STATISTICAL METHOD OF GENETICS

Task 490. The Lutheran blood group system is defined by two alleles: Lu^a (Lutheran-positive) and Lu^b (Lutheran-negative). Heterozygotes Lu^a Lu^b are Lutheran-positive. Among the English, Lutheran-positive people make up 8% of the population, and among the population of Cracow – 11.5% (by V. Socha, 1979).

Determine the frequency of alleles Lu^a and Lu^b of English and residents of Cracow.

Task 491. The Duffy blood group system defines three alleles of the same gene: Fy^a, Fy^b, and Fy^c. However, the Fy^c allele is found only in negroes. Fy^a dominates Fy^b, and individuals with the Fy^a gene are Duffy-positive. According to V. Sokha (1970) and L.O. Badalyan (1971), the Fy^a gene in homo or heterozygous state occurs in 74.53% of Russians, 66.46% of Italians, and 69.9% of Poles.

Determine the frequency of the Fy^a and Fy^b genes in the specified Russians, Italians, and Poles.

Task 492. The Kidd blood group is determined by two alleles of the Ik^a and Ik^b. The Ik^a allele is dominant in relation to Ik^b, and those with it, Kidd-positive. The frequency of the Ik^a gene among the population of Cracow is 0.458 (V. Socha, 1970). The frequency of Kidd-positive people among negroes is 80% (K. Stern, 1965).

Determine the genetic structure of the population of Cracow and negroes according to the Kidd system.

Task 493. The population consists of 9,000 individuals. 3,000 individuals have the AA genotype, 4,500 individuals have the Aa genotype, and 1,500 individuals have the aa genotype.

Determine the allele frequency for A and a in this population.

Task 494. In a population, 1,000 individuals have the CC genotype, 2,000 individuals have the Cc genotype, and 7,000 individuals have the cc genotype.

Determine the frequency of C and C alleles.

Task 495. Two populations have the following structures: the first is 0.33AA:0.14Aa:0.53 aa; the second is 0.24 AA:0.32 Aa:0.44 aa.

Calculate the ratio of genotypes in the next generation in both populations under the condition of panmixia.

Task 496. There are three groups of individuals with the following genotype frequency: 60% EE and 40% ee; 50% EE, 30% eE and 20% ee; 30% EE, 40% eE and 30% ee.

Determine which genotype frequencies will be established in the second generation in each of the three groups under the condition of panmixia.

Task 497. The initial ratio of genotypes in a certain panmyctic population is 2AA:1Aa:3aa.

Determine the genotypic structure of this population in F3.

Task 498. In a panmyctic population, the ratio of three pairs of alleles is as follows: 1A:1a, 99B:1b, 1D:99d.

Determine the frequency of different genotypes for each pair of alleles.

Task 499. The population consists of individuals with three genotype variants in the ratio 9AA:6Aa:1aa.

Determine whether the population is in a state of genetic equilibrium.

Calculate the genotypic composition of the next-generation population in panmixia.

Task 500. The proportion of AA individuals in a large free-crossing population is 0.09.

Calculate the part of the population that should be heterozygous for a gene.

Task 501. Homozygous aa individuals make up 1% of the population.

Calculate (in %) the frequency of the AA, Aa, and aa genotypes.

Task 502. The genotype frequencies are given, respectively: AA, Aa, aa.

a) 0.5:0:0.5;
b) 25:10:1;
C) 0.36:0.15:0.49;
d) 0.09:0.10:0.81;
e) 1:1:0.25;

e) 0.45:0.45:0.10;
g) 0.22:0.36:0.42;
h) 0.5625:0.3750:0.0625.

Specify which of the populations listed below are in equilibrium and which are not.

Task 503. The proportion of AA individuals in a large crossbreeding population is 0.09.

Determine the part of the population that should be heterozygous for A, if all genotypes have the same reproductive potentials relative to this gene.

Task 504. The original ratio of genotypes is 25% AA, 25% aa, and 50% Aa.

Determine the state of the population obeying the Hardy–Weinberg principle for 10 generations.

Task 505. The following samples from the population are presented:
a) 400 AA individuals and 100 aa individuals;
b) 700 SS individuals and 300 ss individuals;
C) 60 individuals MM and 40 individuals mm.

Calculate the dominant and recessive alleles frequency.

Task 506. Two populations have the following genotypic frequencies: the first – 0.24 AA, 0.32 Aa, 0.44 aa; the second – 0.33 AA, 0.14 Aa, 0.53 aa.

Calculate the ratio of genotypes in the next generation in panmixia.

Task 507. In population A, the recessive allele frequency is 20%; in population B, which has the same number of individuals, the frequency of this allele is 4%.

Calculate the genotype frequencies if you combine the populations and panmixia occurs in the new population.

Task 508. In the panmyctic population, the ratios of alleles, in each of the three pairs, are as follows: 1A:1a, 99B:1b, 1D:99d.

Determine the frequency of all genotypes in this population for each pair of alleles separately.

Task 509. In one panmyctic population, the frequency of the recessive allele b is equal to 0.1, and in another – 0.9.

Determine the population where the frequency of heterozygotes is higher.

Task 510. The ratio in the sample is 10aa:1AA:10Aa.

Determine the genotypic structure of F3 in self-pollination and panmixia.

Task 511. The population consists of 80% of individuals with the AA genotype and 20% with the aa genotype.

Determine the frequency units of the AA, Aa, and aa genotypes after establishing equilibrium in the population.

Task 512. In one population, there are three genotypes for the autosomal locus in the ratio 9AA:6Aa:1aa.

Determine whether the population is in a state of genetic equilibrium. Calculate the genotypic composition of the next-generation population in panmixia.

Task 513. The ratio of genotypes in the sample is as follows: 1 AA to 1 aa.

Determine the genotypic structure of populations in the fifth generation in self-pollination and panmixia.

Task 514. The ratio of genotypes in the sample is as follows: 7 aa, 1 AA, 1 Aa.

Determine the genotypic structure of the population in the fifth generation in the case of self-pollination and panmixia.

Task 515. The original plant is heterozygote Bb.

Determine the frequency of genotypes in F_8 during self-pollination.

Task 516. In the maize variety, albino plants (aa) occur with a frequency of 0.0025.

Calculate the frequency of alleles A and a and the frequency of genotypes AA and Aa in this variety.

Task 517. In the first generation of the hordeum hybrid, the number of heterozygous forms for a pair of alleles is 100%.

Determine the proportion of homozygous forms in the offspring of this plant after self-pollination in the fifth generation.

Task 518. Rye is a cross-pollinated plant, and wheat is self-pollinated.

Identify plants with a higher proportion of heterozygotes for many genes.

Task 519. Chlorophyll breakdown is the recessive allele, the mutants are viable, pea is only self-pollinated.

Determine the ratio of green plants and chlorophyll pea mutants that can be expected in the fifth generation from self-pollination of a heterozygous plant.

Task 520. A single grain of wheat, which is heterozygous for a certain B gene, accidentally landed on a deserted island. It sprang up and gave rise to a series of generations of self-pollinators.

Calculate the proportion of heterozygous plants among the representatives of the sixth generation.

Task 521. On an island, the wind brought a seed of a yearling which is self-pollinating, heterozygous for one gene.

Determine the vegetation cover on the island after three years, if all individuals survive by producing one generation per year.

Calculate the probability of finding a plant in five years that is identical in genotype to the parent plant.

Task 522. Albinism in rye is inherited as an autosomal trait. In the surveyed area, 210 albinos were found among 84,000 plants.

Determine the frequency of the albinism gene in rye.

Task 523. Albinism in maize is inherited as an autosomal recessive allele. In some varieties of maize, albino plants occur with a frequency of 25:10 000.

Determine the frequency of the albinism gene in these varieties of maize.

Task 524. Seeds of red-grain wheat (AA and Aa) and white-grain wheat (aa) were sown in equal quantities.

Calculate the ratio of red and white seeds in 10 years.

Task 525. Seeds of red-grain wheat (AA and Aa) and white-grain wheat (aa) were sown in equal quantities.

Calculate the ratio of red-grain and white-grain plants in 5 years, provided that during these years the plants only self-pollinated.

Task 526. Albinism in sunflower is inherited as a recessive allele. At an experimental site, 39 out of 17,385 plants were albino in one of the varieties of sunflower.

Determine the frequency of the albinism allele and the genotypic structure of this variety.

Task 527. In an experiment, 4 plants of red-flowered heterozygous peas (Aa) and 1 plant of red-flowered homozygous (AA) were used.

Determine the ratio of genotypes and phenotypes in the population in the fourth generation, subject to self- and cross-pollination.

Task 528. The initial group of animals, consisting of 10% of individuals with the AA genotype and 90% with the aa genotype.

Identify the frequencies of AA, Aa, and aa genotypes in this population to F3 in panmixia.

Task 529. 10 pairs of Drosophila flies from the line with recessive brown eyes and 50 pairs from the wild type line with dominant red eyes were placed in one vessel.

Calculate the ratio of phenotypes in the fifth generation in panmixia.

Task 530. In the Shorthorn breed of cattle, the red color does not completely dominate the white color. Hybrids from crosses of red and white cattle are roan. 4,169 red animals, 3,780 roan animals and 756 white animals were registered in the area that specializes in breeding the Shorthorn cattle.

Determine the frequency of alleles of red and white coat coloration of cattle in this area.

Task 531. In the cattle population, 4,169 individuals were red, 3,780 individuals were roan, and 756 individuals were white.

Determine the ratio of alleles and genotypes in F3 of this population in panmixia (individuals heterozygous for alleles of red and white colors are roan).

Task 532. In a mice population, 2% of albinos were born within one year (recessive allele).

Determine the allele frequency and the proportion of heterozygotes in this population in panmixia.

Task 533. On one of the islands, 10,000 foxes were shot, of which 9,991 were red and 9 were white. Red coat coloration dominates white.

Determine the frequency of red and white alleles and the genetic structure of the population.

Task 534. Romashov and Ilyinaya studied14,345 foxes: 12 foxes were black, 678 were of blended color and 13,655 foxes were red.

Find the frequency of alleles of black and red fur color in the population of foxes.

Task 535. Albinism is a recessive autosomal allele. The disease occurs with a frequency of 1:20 000.

Determine the genetic structure of the population.

Task 536. Aniridia (the absence of the iris in humans) is inherited as an autosomal dominant trait and occurs with a frequency of 1:20 000.

Determine the frequency of the aniridia gene and the genotypic structure of the isolated population.

Task 537. Aniridia is inherited as a dominant autosomal trait and occurs in some populations with a frequency of 1:10 000 (V.P. Efroimson, 1969).

Determine the genetic structure of the population.

Task 538. Phenylketonuria in humans is inherited as a recessive autosomal trait and occurs with a frequency of 1:40 000.

Determine the frequency of alleles and the genotypic structure of the population

Task 539. In one city with a well-established population composition, 2 newborns were diagnosed with phenylketonuria, which is determined by a recessive allele of an autosomal gene, among 25,000 newborns within five years.

Determine the theoretically expected number of heterozygotes among the 500,000 population of a given city.

Task 540. Among the Caucasian population of North America, the proportion of Rh-negative individuals (pp) is 15%.

Taking into account that the choice of spouses is not determined by their blood antigens, calculate the average probability that a rhesus-negative girl will become a man's wife: a) pp; b) Pp; c) PP.

Task 541. Alkaptonuria is determined by a recessive allele of an autosomal gene. In old age, arthritis develops in patients with this abnormality. The disease occurs with a frequency of 1:1 000 000 (V.P. Efroimson, 1968).

Calculate the theoretically expected number of heterozygotes in a population of 1 million people.

Task 542. In an area with a population of 500,000 people, 5 patients with alkaptonuria (autosomal recessive inheritance) were registered.

Determine the number of heterozygotes based on the analyzed trait in this population.

Task 543. The average incidence of autosomal recessive deafness in European countries is 2:10 000.

Determine the possible number of heterozygous deaf and dumb people in an area that includes 8 million inhabitants.

Task 544. In a population of 500,000, the incidence of recessive disease is 1 per 400 people.

Determine the number of carriers of the mutant allele in this population.

Task 545. Arachnodactyly ("spider fingers") is determined by the dominant allele of an autosomal gene, whose penetrance is 30%. In Europe, patients with arachnodactyly occur with a frequency of 0.04 per 1,000.

Determine the allele frequency in a population of 300,000 people.

Task 546. Retinoblastoma and arachnodactyly are autosomal dominant traits. The penetrance of alleles that determine them is 60% and 30%, respectively. In Europe, patients with retinoblastoma occur with a frequency of 0.03, and arachnodactyly 0.04 per 1,000.

Determine the frequency of alleles that determine these diseases among Europeans.

Task 547. In a complete survey of the population (280,000 people), 7 cases of Spielmeyer-Vogt-Sjogren-Batten disease (a juvenile form of amaurotic idiocy) were registered in one of the regions of Europe. The disease is determined by a recessive allele of an autosomal gene.

Determine the theoretically expected number of heterozygous carriers of this allele among 1 million people.

Task 548. In European populations, the incidence of Tay–Sachs disease (a childhood form of amaurotic idiocy), inherited by recessive type, is 4:1000.

Calculate the number of individuals in the population per one host.

Task 549. 210 children were found to have a pathological recessive trait out of 84,000 children born within 10 years in maternity hospitals in one city.

Determine the genetic structure of the population.

Task 550. The release of aminobutyric acid in the urine is caused by a recessive allele of an autosomal gene. Patients among the Caucasian population of the United States make up 10%.

Determine the genetic structure of the population.

Task 551. Hereditary methemoglobinemia (increased content of methemoglobin in the blood due to a defect in the enzyme diaphorase) is inherited as a recessive trait. In the population of Alaskan Eskimos, the disease occurs with a frequency of 0.09% (P.B. Gofman-Kadoshnikov, 1969).

Determine the genetic structure of the analyzed population by methemoglobinemia.

Task 552. Gout occurs in 2% of people and is caused by the dominant allele of the autosomal gene. In women, the gout gene does not appear, in men, its penetrance is equal to 20% (V.P. Efroimson).

Determine the genetic structure of the population based on the analyzed trait, based on these data.

Task 553. In an American city in a part where only Italian immigrants lived, in the period from 1928 to 1942, among 26,000 newborns, 11 were found to have a severe form of thalassemia – the TT genotype (K. Stern).

Determine the number of heterozygotes among the Italian immigrants of this city.

Task 554. Congenital hip dislocation is inherited as an autosomal dominant trait, with an average penetrance of 25%. Pain occurs with a frequency of 6:10 000 (V.P. Efroimson, 1968).

Determine the number of homozygous individuals by recessive alley. Determine the theoretically expected number of heterozygotes in a population of 250,000.

Task 555. In a population consisting of 100 million people, 40,000 are affected by a disease caused by a recessive gene.

Determine the number of affected people in the next generation, provided that these individuals are prevented from reproducing their offspring and if the population size does not change.

Task 556. 210 children were found to have a pathological recessive trait out of 84,000 children born in maternity hospitals for 10 years in the city of K. The population of this city meets the conditions of panmixia and genotypic equilibrium for a two-allelic genetic system.

Determine the frequency of the recessive allele in this population and its genetic structure.

Task 557. Fructosuria (a rare, recessive inherited defect of carbohydrate metabolism), occurs in a population of people with a frequency of 7:1 000 000.

Determine the frequency of alleles and genotypes in this population. Calculate the number of individuals per one carrier of the disease.

Task 558. In the population, the incidence of a disease associated with homozygosity by a recessive gene is 1 per 400 people.

Determine the proportion of carriers of the disease and the frequency of different genotypes in this population, assuming a two-parallel mechanism of gene control of the studied trait.

Task 559. 32 newborns had a pathological recessive trait out of the 27,312 children born in the city.

Determine the frequency of alleles in the population and identify the number of newborns per carrier of the disease.

Task 560. Women who have a harmless recessive trait linked to the X chromosome are found in the population: 1 in 10,000.

Determine the frequency of men affected by this sign.

Task 561. The frequency of occurrence of a recessive allele that causes the inability to turn the tongue into a "longitudinal tube" is 0.6.

Determine the frequency of occurrence of individuals who can curl the tongue into a "tube" and do not have it.

Task 562. In population I, the frequency of occurrence of a sex-linked recessive gene is 20%, and in population II, the frequency is 4%.

Determine the frequency of possible genotypes after a multi-generational panmixia in which both populations participated in equal numbers.

Task 563. In the population, the frequency of occurrence of the Rh-allele is equal to 0.1.

Calculate the percentage of pregnancies that can be subjected to selection directed against heterozygotes.

Task 564. All Chinese have a blood type Rh+, and among negroes, such persons make up only 91%.

What proportion of individuals Rh+ and Rh- should be expected if equal populations of negroes and Chinese marry, and panmixia will prevail for many generations?

Task 565. Let us assume that the frequency of occurrence of some recessive disease linked to gender is equal to 1 in 10,000 for men, and 1 in 5,000 for women-carriers.

Calculate the frequency of occurrence of sick men in the next generation, if the affected individuals are not able to recover.

Determine the frequency of female carriers.

Task 566. General Albinism (milky-white skin color, absence of melanin in the skin, hair follicles and retinal epithelium) is inherited as a recessive autosomal trait. The disease occurs with a frequency of 1:20 000 (A. Stern, 1965).

Calculate the number of heterozygotes in the population.

Task 567. One of the forms of fructosuria (an increase in its content in the urine) is manifested subclinically. Metabolic defects are reduced when fructose is excluded from food. The disease is inherited autosomal recessive and occurs with a frequency of 7: 1 000 000 (V.P. Efroimson).

Determine the number of heterozygotes in the population.

Task 568. The ability to taste phenylthiocarbamide (a white crystalline substance that some people (about 70 %) consider bitter, and others – tasteless) is a recessive trait. 31.5% of Englishmen, 16% of Malays, and 7.1% of Japanese were found to be unable to taste phenylthiocarbamide.

Determine the genetic structure of three different populations.

Task 569. J. Neel and W. Shell (1958) provide the following data on the frequency of the recessive gene of insensitivity to phenylthiocarbamide among various groups of the world population.

Ancient European	0.5
Caucasian	0.65
Negroid	0.45

Calculate the frequency of occurrence of individuals sensitive to phenylthiocarbamide among the populations of each of these groups.

Task 570. The frequency of individuals who feel phenylthiocarbamide in one population is 70%. In the selected group of 150 people, there were 135 people who felt phenylthiocarbamide.

Specify whether the found deviation from the norm is statistically significant.

Task 571. Essential pentosuria is inherited as an autosomal recessive trait and occurs with a frequency of 1:50 000 (L. O. Badalyan).

Determine the frequency of dominant and recessive alleles in populations.

Task 572. The release of β-aminoisobutyric acid in the urine is caused by a recessive allele of the autosomal gene. According to V.P. Efroimson (1968), "excretors" are found: among the Caucasian population of the United States – 10%, black population of the USA – 30%, Chinese and Japanese – 40%.

Determine the genetic structure of these populations.

Task 573. In one of the American Indian populations, the frequency of homozygotes with blood group A is 0.986, and the frequency of homozygotes and heterozygotes with blood group B is 0.014. The frequency of the O and A alleles is 0.993 and 0.007, respectively. People with blood groups AB and O are not registered in the population.

Determine whether the population is in equilibrium.

Task 574. Among the world population, blood group genes are distributed unevenly in the ABO system. There are populations in which only two of the three alleles are found. So, in the reports of J. Neel, W. Shell (1958) and V.P. Efroimson (1969), it is indicated that the American Indians of the Ute, Toba, Najvalo, Blackfoot and aborigines of Western Australia have only blood groups A and B (OO, AO, AA), the Bushmen have only blood groups A and AB (OO, OB, BB). The number of individuals with blood group A in the population is determined (in %):

Ute	97.4
Blackfeet	23.5
Toba	98.5
Aboriginal Australians	48.1
Najvalo	77.7
Bushmen	83

Based on the presented data, determine the genetic structure of these populations.

Task 575. The diversity of blood groups in the MN system is due to the combination of M and N antigens. They correspond to the genotypes L^ML^M, L^ML^N, L^NL^N.

Caucasian population of the USA	54	Eskimos of East Greenland	91.3
African Americans	53.2	Ainu people	43
Native Americans	77.6	Aboriginal Australians	17.8

Determine the genetic structure of these populations if Stern's summary (1965) shows the following frequency rates of the L^M allele among different population groups (in %).

Task 576. In the reference book of L.O. Badalyan (1971), the structure of populations by the gene "system of blood groups MN" is defined (%) among:

Population of the USSR	Europeans	Papuans of New Guinea
MM – 36	MM – 30	MM – 1.1
MN – 48	MN – 50	MN – 15.9
NN – 16	NN – 20	NN – 83

Determine the genetic structure of populations.

Task 577. An examination of the population of southern Poland identified the following: with the blood group MM – 11,163 people, MN – 15,267, and NN – 5,134 (V. Sokha, 1970).

Determine the frequency of alleles in the population of southern Poland.

Task 578. 730 indigenous people in Australia had the following blood group distribution: blood of group M (genotype MM) was found in 22 people, blood of group MN (genotype MN) – in 216, and blood of group N (genotype NN) – in 492.

Determine the genetic structure of the population.

Task 579. Diego's blood group system is defined by two alleles of the autosomal gene – D and d. Diego-positive persons (DD, Dd) are found among representatives of the Mongoloid race. The frequency of occurrence of Diego-positive among some tribes of South American Indians is 36%, and the Japanese – 10%.

Determine the frequency of alleles D and d in the mentioned populations.

LIST OF RECOMMENDED LITERATURE

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GLOSSARY

ALLELE, one of two or more alternative forms of a gene.

ALLELOMORPH, variant of a single trait.

ANALYZING CROSSING, crossing of an individual with a dominant trait, in order to determine its genotype, with an individual homozygous for a recessive allele (analyzer); if two classes of individuals are identified in the offspring in equal shares, the analyzed individual is heterozygous; if all descendants will have a dominant trait, the analyzed individual is homozygous.

ANEUPLOIDY, change in the number of individual chromosomes in a cell or organ; most often an increase or a decrease of one or two chromosomes; that does not affect the entire main set, i.e. a non-repeated change.

ANTIGEN, foreign molecule whose presence in the body may trigger an immune response (the synthesis of an antibody, immunoglobulin)

AUTOSOME, chromosome that is the same in males and females; a nonsex chromosome.

BACK CROSS, mating individuals of the first generation with individuals of both parent lines.

BIVALENT, homologous pair of synapsed chromosomes of four chromatids that conjugate in the prophase of reductive division.

CELL CYCLE (MITOTIC), stages through which a cell passes during mitosis and interphase.

CENTIMORGAN, unit of recombination frequency of linked genes (rf); 1% of crossovers in the offspring from the analyzing cross of the diheterozygotes; unit of measure for distances on a genetic map (d).

CENTROMERE, primary binding of the chromosome, the region of the chromosome where the sister chromatids are connected to each other.

CHIASM, X-shaped structure that occurs as a result of crossing after the beginning of the divergence of homologous chromosomes in the prophase of the first meiotic division.

CHROMATID, each of the two longitudinal structures of the mitotic chromosome formed during replication in the interphase.

CHROMATIN, material that consists of DNA and histone proteins in the nuclei of interphase cells; it is detected by its ability to be stained with DNA-specific dyes.

CHROMOMERE, intensely colored granule; it can be distinguished as a component of a chromosome under certain conditions (especially in the early stages of meiosis).

CHROMOSOME, nucleoprotein body.

CODOMINANCE, type of allelic interaction in which the heterozygote simultaneously expresses the phenotypes of both homozygotes.

CODON, triplet of nucleotides that encodes one amino acid in a protein.

COMPLEMENTATION, one of the types of interaction of genes, in which the dominant alleles of all interacting genes, being part of a single genotype, complement each other's phenotypic effect, and forms a new variant of the trait, usually normal, that is, wild type.

CONCORDANCE, similarity between mono- and dizygotic twins by some attribute. The measure of concordance (coefficient of coincidence) is the percentage of twin pairs that are similar in the analyzed trait from the total number of studied twin pairs.

COUPLING GROUP, set of genes (alleles) that are localized on the same chromosome and are inherited primarily together.

CROSSING, reciprocal exchange of identical segments of homologous chromosomes, leading to recombination of linked genes (alleles).

CROSSOVER, individual recombinant by linked genes (alleles).

CYTOKINESIS, process by which the cytoplasm of a cell divides during mitosis, usually it begins in late anaphase or telophase;

DEGENERATE GENETIC CODE, fact that the genetic code contains more codons than are needed to specify all 20 common amino acids. Replacement in the third base of the codon does not always lead to the replacement of the amino acid.

DIPLOID, possessing two sets of chromosomes (2 genomes).

DISCORDANCE, difference between twins in relation to the analyzed trait.

DOMINANCE, one of the types of allele relationships in which only one allele from a pair in heterozygotes has a phenotypic effect.

DOMINANT ALLELE, allele that determines the phenotype of a heterozygote.

DOMINANT TRAIT, trait (of a parent) which heterozygotes have (hybrids of first generation); the trait of a parent, which three-quarters of the individuals of the second generation monohybrid crossing have.

ENDOMITOSIS, multiple increase in the number of chromosomes in the cell nucleus or an increase in the number of nuclei without cell division; leads to polyploidy.

EPISTASIS, type of gene interaction in which the mutant allele of one gene masks or suppresses the phenotypic effects of the mutant allele of another gene, which does not lead to wild-type recovery.

EQUATIONAL division (equalization), one of the two divisions of meiosis, usually the second one, before which there is no doubling of chromosomes and which leads to equalization of the number of chromosomes and the amount of DNA (1n 2c 1n 1c).

EXPRESSIVITY, variation in a group of individuals by the degree to which a trait is expressed.

FRAMESHIFT MUTATIONS, deletions or inserts whose dimensions are not multiples of the three bases, they cause the reading frame to change when translating triplets into a protein.

G1 PERIOD, period of the cell cycle between the last mitosis and the beginning of DNA replication.

G2 PERIOD, period of the cell cycle after the end of DNA replication and before the beginning of the next mitosis.

GAMETE, sex cell (egg, sperm).

GAMETOGENESIS, process of formation of germ cells (oogenesis and spermatogenesis).

GENDER, set of characteristics and properties of an organism that ensure reproduction and inheritance based on specialized gametes.

GENE, functional unit of heredity, materially represented by a sequence of nucleotides of a genomic nucleus acid that determines a specific functionally significant sequence of amino acids in a polypeptide or RNA nucleotides (transport or ribosomal).

GENE INTERACTION, interaction of products of two different or many genes in the formation of a trait (phenotype).

GENE PENETRANCE, ability of a gene to produce a phenotypic effect, i.e. to "break into a trait". Quantitative assessment of penetrance consists in determining the proportion of individuals with a trait determined by this allele among all individuals with this allele in the genotype.

GENE POOL, collection of alleles of all genes in all individuals that make up a population or species, their frequencies and combinations.

GENE POSITION EFFECT, change in the activity of a gene due to its movement to a different region of the chromosome.

GENOME, haploid set of chromosomes of the type (n) or the entire DNA of the haploid set.

GENOTYPE, genetic constitution of an organism (genes, the nature of their coupling, the set of alleles of all genes, the presence of changes).

GONOSOMES, sex chromosomes (heterochromosomes).

HAPLOID, possessing a single set of chromosomes (n).

HEMIZYGOSITY, absence of an allele of any partner gene in the genotype of a diploid organism.

HEREDITY, program of development of traits and characteristics of an organism that is passed down in a number of generations, ensuring material and functional continuity between ancestors and descendants, i.e. the continuity of life of biological species.

HETEROCHROMATIN, genetically inactive areas of chromosome that remains in a highly condensed state throughout the cell cycle.

HETEROCHROMOSOMES, sex chromosomes.

HETEROGAMETIC SEX, representatives of which produce two types of gametes with respect to sex chromosomes.

HETEROGAMOUS INDIVIDUAL, individual of any sex that produces gametes of different types in relation to sex chromosomes.

HETEROZYGOTE, individual whose gene(s) are represented in the genotype by different alleles.

HOMOGAMETIC SEX, representatives of which produce gametes that are all alike with respect to sex chromosomes.

HOMOGAMOUS INDIVIDUAL, individual of any sex that has gametes of the same type with respect to sex chromosomes.

HOMOLOGOUS CHROMOSOMES (HOMOLOGS), chromosomes that are alike in structure and size and that carry the same set of genes.

HOMOZYGOTE, individual has two identical alleles at a locus.

INCOMPLETE DOMINANCE, type of dominance in which differences of heterozygotes and homozygotes in the phenotype are caused by different doses (different number) of incompletely dominant allele in the genotype of individuals.

INDEPENDENT INHERITANCE, transfer from parents to descendants of genes localized in different non-homologous chromosomes.

INHERITANCE, transfer of information that provides material and functional continuity between ancestors and descendants in a number of generations.

INTERALLELIC RELATIONS, relations between different variants of the same gene associated with different activity (complete and

incomplete dominance) or qualitative differences in polypeptides, the synthesis of which is determined by different alleles (codominance, interallelic complementation).

INTERPHASE, major phase of the cell cycle between mitotic divisions; it consists of pre-synthetic (G1), synthetic (S), and post-synthetic (G2) periods.

INTERKINESIS, short period between reduction and equation divisions, during which there is no doubling of DNA.

KARYOKINESIS, processes that occur with nuclear material during mitosis and lead to the formation of genetically equivalent nuclei of daughter cells.

KARYOTYPE, the complete set of chromosomes possessed by an organism: the number of chromosomes (2n), the number of chromatid arms (NF), the size and shape of the chromosomes of each pair.

LEADING STRAND, DNA strand that is replicated continuously in the 5'-3' direction.

LETHAL MUTATION, mutation that causes the premature death of an organism at one or another stage of ontogenesis.

LINKED INHERITANCE, exclusive or preferable transmission of two or a group of alleles localized on the same chromosome together.

LOCUS, position on a chromosome where a specific gene is located.

MEIOSIS, process by which the chromosomes of a eukaryotic cell divide which leads to the transition of diploid cells to haploid ones. It consists of two consecutive divisions, during which DNA division occurs once. As a result of meiosis, four haploid genetically distinct cells are formed.

MENDELIAN INHERITANCE, inheritance of genes with monogenic determination; genes are localized in different pairs of autosomes.

MENDEL's LAW 1 (law of dominance and uniformity), hybrids of the first generation, obtained from crossing contrasting forms that differ in one feature, are phenotypically identical.

MENDEL's LAW 2 (law of segregation) – among the second-generation hybrids in strict numerical correlations, there are individuals with the phenotypes of the original parent forms and hybrids of the first generation; with complete dominance, the second generation consists of individuals with a dominant trait and individuals with a recessive trait in the proportions of ¾ : ¼, and among individuals with a dominant trait, with a probability of ⅓ there are homozygotes for the dominant allele and with a probability of ⅔ – heterozygotes; the second generation consists of

individuals of three genotypic classes: with the genotype of the first parent form, with the genotype of hybrids of the first generation and with the genotype of the second parent form in the proportions of ¼ : ½ : ¼, respectively.

MENDEL's LAW 3 (law of independent assortment), each pair of allelomorphs is inherited independently, with complete dominance and accounting for two pairs of allelomorphs in the second generation, individuals of four phenotypic classes are identified in the proportions $\frac{9}{16}$: $\frac{3}{16}$: $\frac{3}{16}$: $\frac{1}{16}$. There are limitations to this law: such a number of traits can be inherited independently that does not exceed the number of chromosomes of the haploid set.

MITOSIS, indirect cell division; the main process by which the nucleus of a eukaryotic cell divides, which results in an equivalent distribution of reduplicated chromosomes between two daughter cells, which ensures the genetic equivalence of daughter cells.

MITOSIS ANAPHASE, stage of mitosis during which sister chromatids connected in the centromere region separate from each other and move to different poles.

MITOSIS METAPHASE, stage of mitosis in the eukaryotic cell cycle which begins from the moment chromosomes line up on the metaphase plate to the division of chromatids and the moment they begin to align from the equator to the poles.

MITOSIS PROPHASE, initial and longest stage of mitosis; it is characterized by nucleus swelling, condensation of diffuse interphase chromatin into clearly visible chromosomes, and the formation of division poles. The end of prophase marks the disappearance of the nucleolus and the disintegration of the nuclear membrane into fragments.

MODIFIER GENE, gene that affects the phenotypic effect of other genes.

MUTAGENS, factors that increase the frequency of mutations, causing changes in the DNA.

MUTATION, any sudden abrupt change in the inherited material; sudden transition of a gene or chromosome to a new stable form that is reproduced in new generations.

NONCROSSOVER, individual non-recombinant in coupled genes (alleles).

NONDIVERGENCE, inability of a chromatid (duplicated chromosomes) to align to opposite poles during mitosis or meiosis.

NUCLEOLAR ORGANIZER, region of the chromosome containing rRNA encoding genes.

NUCLEOLUS, separate region of the nucleus formed during transcription of rRNA genes.

NUCLEOSOME, basic repeating unit of chromatin, consisting of ≈ 200 nucleotide pairs of DNA and an octamer of histone proteins.

PHENOTYPE, set of all characteristics (external and internal) of an organism.

PLASMID, small, usually circular extra-chromosomal DNA that is capable of autonomous replication.

PLEIOTROPY, multiple phenotypic manifestation of a gene based on the fact that the gene product takes part in the formation of several or many traits (the pleiotropic effect of genes was first discovered by G. Mendel, who established that plants with purple flowers always had red spots in the leaf axils, and the seed rind was gray or brown).

POLYMERY, one of the types of interaction of genes which can be cumulative and non-cumulative. In cumulative polymery, the phenotype of an individual depends on the number of interacting genes (alleles). The more alleles, the more pronounced the trait. In non-cumulative polymery, the phenotype depends on the presence of dominant alleles in the individual's genotype (the number does not matter) of interacting genes or their complete absence.

POLYMORPHISM, simultaneous existence of a population of several allelic variants of a gene; it is detected either by differences in phenotypes corresponding to different alleles, or by the nature of restriction of DNA carrying different alleles.

POLYTENE CHROMOSOMES, chromosomes formed as a result of successive replication of chromosomes without their subsequent separation.

PROKARYOTES, organisms (bacteria) that do not have a nucleus.

PROMETAPHASE MITOSIS, stage of mitosis which begins when the nuclear membrane breaks apart into numerous small fragments; kinetochore microtubules emerging from the centrosomes at the poles (ends) of the spindle reach the chromosomes and attach to the kinetochores, other spindle microtubules make contact with microtubules coming from the opposite pole; lasts in mammalian cells for 10-20 minutes and ends with the formation of a metaphase plate.

RECESSIVE, property of an allele not to show its phenotypic effect in the presence of another allele of the same gene in the genotype of an individual.

RECESSIVE ALLELE, allele that does not participate in the formation of the phenotype in heterozygotes.

RECESSIVE TRAIT, trait of a parent individual that is absent in first-generation hybrids.

RECIPROCAL CROSSES, two direct and reverse crosses mutual in the direction with respect to the sex of individuals of the crossed forms.

RECOMBINATION, process of transferring units of heredity or their groups (genes, gene blocks, chromosomes, groups of chromosomes) into new combinations.

REDUCTIONAL DIVISION, one of the divisions of meiosis, usually the first division, resulting in a halving of the number of chromosomes in the daughter cell nuclei compared to the parent cell nucleus.

SEMICONSERVATIVE REPLICATION, replication in which the two nucleotide strands of DNA separate, and each serves as a template for the synthesis of a new strand.

SEX CHROMOSOMES, chromosomes that differ in number or morphology in males and females. Usually, such chromosomes are designated as X and Y (or W and Z), one sex has an XX or WW-set, the other – XY or WZ-set. They play the main role in initiating processes of gender differentiation.

SEX-LINKED INHERITANCE, inheritance of traits determined by genes located either on the X chromosome (full sex-linked), or on the Y chromosome (holandric inheritance), or in both heterochromosomes (incomplete sex-linked).

SISTER CHROMATIDS, two copies of a chromosome that are formed during its replication.

SOMATIC CELLS, all cells of the body, excluding germ cells.

SYNAPTONEMAL COMPLEX, structure that appears during chromosome conjugation.

SYNAPSIS, conjugation of two pairs of sister chromatids of homologous chromosomes that occurs during meiosis; the resulting structure is called a bivalent.

TELOMERE, stable end of a chromosome.

TELOPHASE, final stage of mitosis in which the chromosomes arrive at the spindle poles, the nuclear membrane re-forms; which leads to the

decondensation of chromosomes, the appearance of nucleoli and the formation of daughter nuclei; cytokinesis begins.

UNEQUAL CROSSING, recombination event in which the recombination points are not located at identical loci of two parent molecules.

ZYGOTE, cell with which a new organism appears during sexual reproduction; it is formed because of the fusion of an egg and a sperm.

Educational and methodological manual

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