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Genetics of production traits in animals

Module 1: Animal Genetics

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Erasmus+ project 2021-1-SK01-KA220-HED-000032068

Production traits

- ✓ Traits of economic importance.
- ✓ Mainly quantitative traits.
- ✓ Their mechanism of inheritance is complex and difficult to fully explain.
- ✓ Variation in these traits also depends on the impact of environmental factors.

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Quantitative traits

- ✓ Determined by many genes from different loci.
- ✓ These genes are called polygenes, polymeric genes, cumulative genes or additive genes.
- ✓ Polygenes act together to create a trait.
- ✓ The effects of individual polygenes add up and determine the magnitude of the trait.
- ✓ The number of polygenes controlling quantitative traits is unknown.

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- ✓ Each polygene has two alleles, between which partial dominance occurs.
- ✓ One of the alleles is positive, and the other is neutral.
- ✓ The effects of positive alleles from individual loci are equal.
- ✓ These effects add up in forming the phenotype.
- ✓ Examples of this type of trait include height, weight, weight gain, girth, and area – of parts of an animal or the entire animal – and yield, expressed using measurement units such as m, m^2, m^3, and kg.

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- ✓ The phenotypic manifestation of quantitative traits largely depends on environmental factors.
- ✓ These can enhance or attenuate the effect of polygenes.

genotype + **environment**

↓

phenotype

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- ✓ An important environmental effect is the effect of the mother.
- ✓ Although the number of chromosomes which an individual obtains from both of its parents is the same, the effect of the mother on the offspring is greater and has three sources:
  - Genetic background - extranuclear inheritance.
  - The effect of the mother’s environment during foetal life - prenatal effect.
  - The effect of the mother’s environment after birth - postnatal effect.

Continuous traits

- ✓ This type of trait in a population can take on any value between the maximum and minimum.
- ✓ The value of a trait in a given individual can fluctuate anywhere within this range.
- ✓ The number of possible phenotypes in practice is unlimited.
- ✓ An example is milk yield.

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Discrete traits

- ✓ The value of the trait is expressed as a number of defined units.
- ✓ In a population the trait takes on values from the minimum to the maximum.
- ✓ The value of the trait in a given individual must be expressed as an integral number of units.
- ✓ Examples are the number of eggs laid or the number of young in a litter…

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Threshold traits

- ✓ Traits determined by the effect of many genes and environmental factors
- ✓ They usually take on two or a very small number of phenotypic forms.
- ✓ Their genetic variation is continuous, and their phenotypic variation is similar to that of qualitative traits, very often binary.
- ✓ Examples of this type of trait include resistance to disease; survival or death; or litter size in animals that usually give birth to one offspring, but may sometimes have twins or triplets.
- ✓ A property of a threshold trait is the threshold for genes, beyond which there will be a fundamental change in phenotype.

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Distribution of a trait

- ✓ This is a parameter describing a population which defines what portion of individuals of the population exhibits each of the possible values of the trait (each possible phenotype).
- ✓ The description of the distribution of a trait depends on the number of phenotypic classes.
- ✓ The more phenotypes, the more difficult it is to describe the distribution of the trait.
- ✓ We distinguish three types of distribution:
  - continuous
  - discrete
  - threshold

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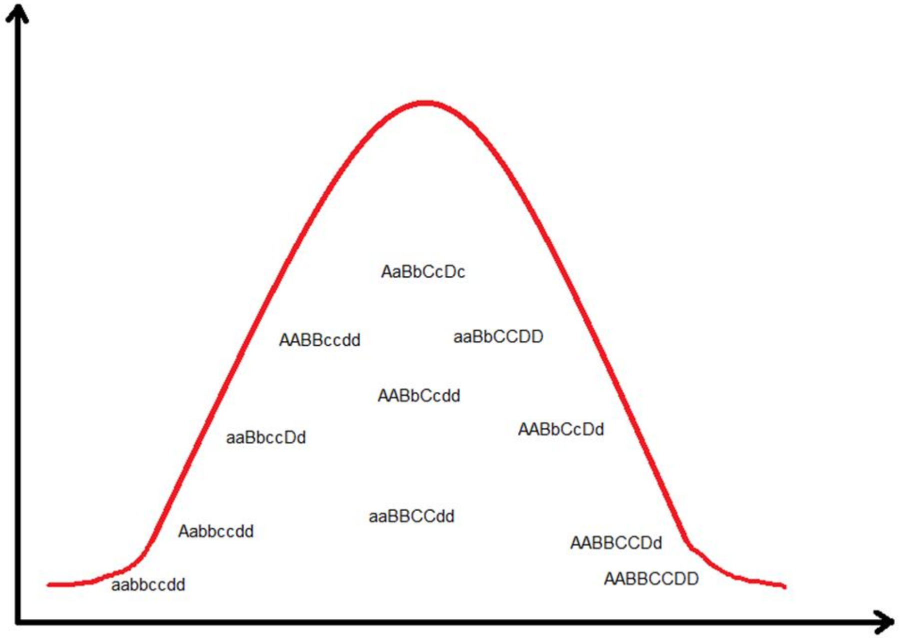
Continuous distribution

The distribution of phenotypes in the case of most quantitative traits corresponds to the Gaussian, or normal, distribution. This is a distribution in which the most individuals exhibit a value of the trait close to the mean, and the fewest exhibit extreme values above or below the mean. The normal distribution is symmetrical; the axis of symmetry passes through the mean for the trait. The parameters of normal distribution are the mean and standard deviation.



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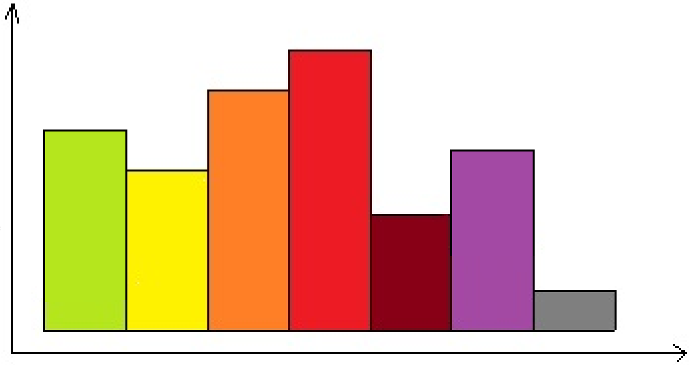
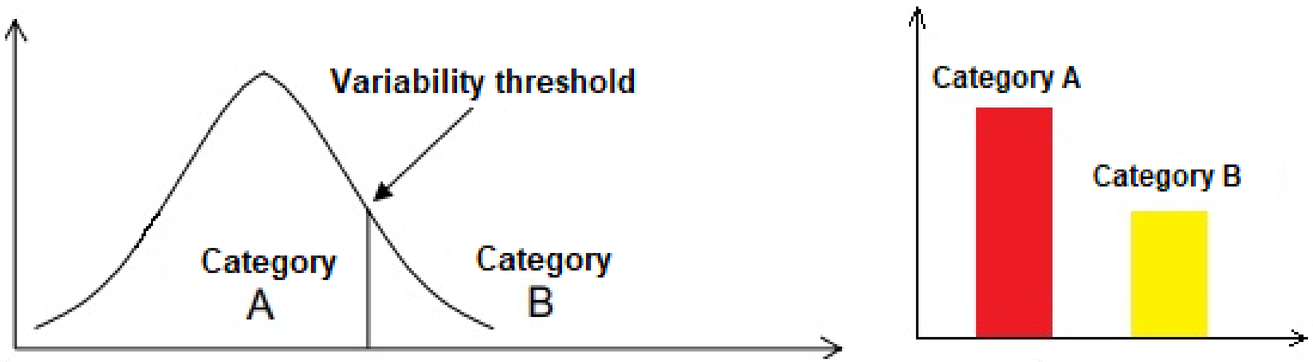
Discrete distribution

- The size of each phenotypic class is described



Threshold distribution

- The size of each phenotypic class (usually two categories) is described.



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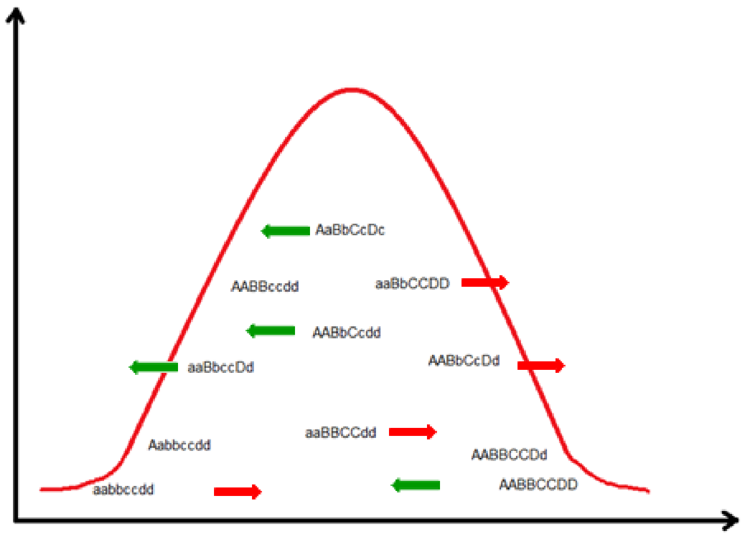
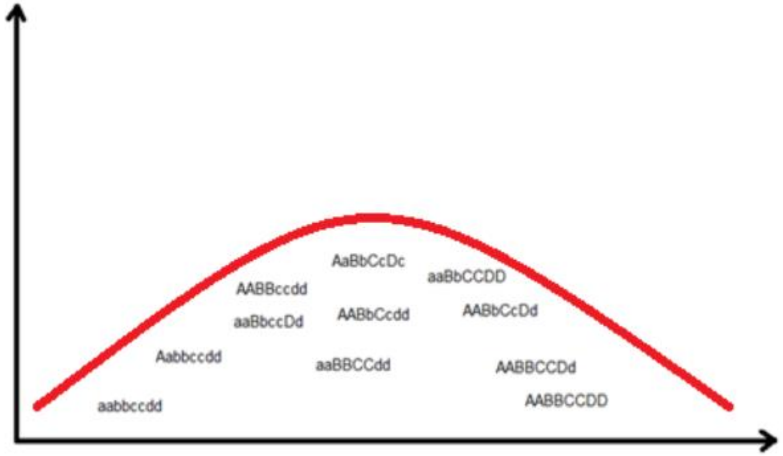
- *The environment can affect a trait in varying degrees and in both directions: increasing (→) and decreasing (←) the value of the trait.*

- The appearance of environmental influences results in increased variability of the trait and makes it more difficult to determine the genotypic value of individuals.





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Transgression

Farm animals are heterozygous for a large number of genes. Crossbreeding of such individuals may result in offspring showing higher or lower values of a trait than the parents. This phenomenon is called transgression and is widely exploited in breeding.

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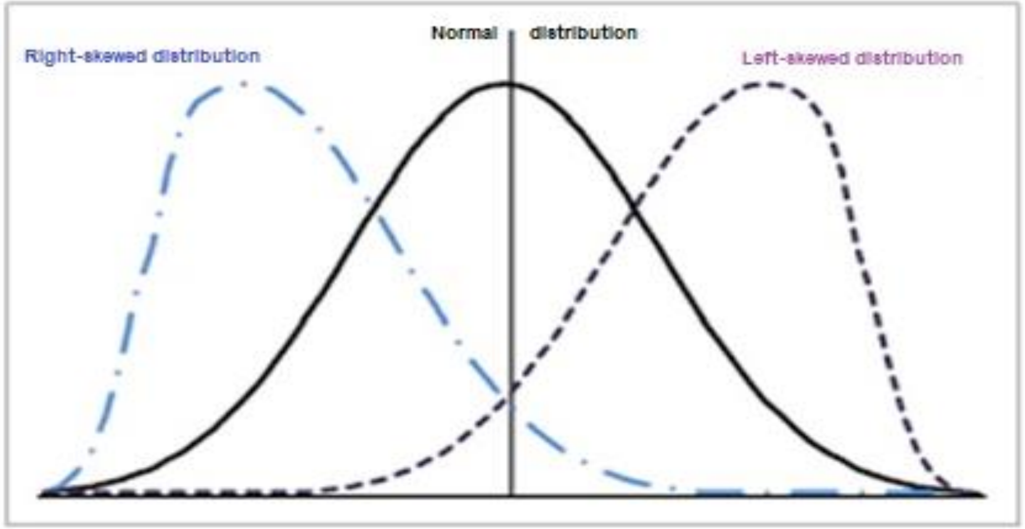
Genes of major effect (QTL - quantitative trait locus)

The graphic distribution of phenotypes of certain traits diverges significantly from the normal distribution curve. This is due to inheritance, when alongside polygenes there is a gene of major effect, called a major gene. It is identified when in opposite homozygotes differences in the value of the trait amount to at least one standard deviation.



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Examples of genes of major effect influencing various production traits in farm animals:

Cattle

Growth hormone (GH) gene, which influences the following:

- Growth hormone gene (*GH*), which influences the following:
- higher milk yield in comparison with homozygous AA individuals
- meat performance traits
- growth rate and carcass composition, together with the insulin-like growth factor 1 gene (*IGF-1*)
- chest length and circumference
- the ageing process, reproduction, and the body's immune response
- This gene is responsible for certain developmental disorders, such as dwarfism and acromegaly in poultry.

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Milk protein genes:

- **The κ-casein gene (*CSN3*)** is associated with milk performance traits (milk, protein and fat yield).
- Milk with the κ-casein type B gene has higher protein content and is more suitable for cheese production than milk with the A variant of κ-casein.
- **The β-lactoglobulin gene (*β-LG*)**, influences the yield of milk and its constituents.
- Milk containing β-lactoglobulin B differs from milk with the A variant in its higher content of dry matter, fat, and casein and better suitability for processing.
- **The diacylglycerol acyltransferase 1 gene (*DGAT1*)**, influences milk yield and the yield of protein and fat in milk, as well as intramuscular fat content.

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The muscular hypertrophy gene (*MH*), influences the following:

- increased lean meat content in the carcass
- better dietary properties, due to reduced content of fat and connective tissue
- This trait is preferred by breeders of pure breeds of cattle (Belgian Blue and Asturian) as well as their crosses.
- Unfortunately, this gene also has negative effects:
    - delayed sexual maturity in both sexes
    - reduced reproductive capacity – in bulls, lower plasma concentrations of sex hormones and lower testicular circumference and weight, and in cows, longer gestation and high foetal weight, causing problems during natural parturition.

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Pigs

The ryanodine receptor 1 gene (*RYR1*) influences the following:

- increased susceptibility to stress (porcine stress syndrome – PSS), e.g. induced by transport, temperature conditions, or chemical factors
- malignant hyperthermia
- stress myopathy results in unfavourable physicochemical changes in the body and deterioration of meat quality — discolouration, unpleasant odour, overly soft, watery meat
- This gene at the same time positively influences certain traits associated with meat performance, e.g. meat content in the carcass and loin eye area, which are most favourable in heterozygous individuals which are carriers of the mutated allele. These animals are also good fattening material.
- This gene is also found in cattle, horses, and people.

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The acid meat gene (*RN*), the gene of the AMP-activated protein kinase subunit γ (PRKAG3). Carriers of the mutated allele have twice as much glycogen in the muscles (especially in the ham).

The insulin-like growth factor 2 gene (IGF2), influences the following:

- meat performance traits
- increase in muscle mass
- reduced backfat content.

The oestrogen receptor gene (*ESR*) influencing litter size affects the following:

- prolificacy and litter size
- Sows with two copies of this gene in their genotype produce larger litters, with 1 to 1.4 more live-born piglets compared to sows without this gene.

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Sheep

The callipyge (muscle hypertrophy) gene (*CLPG*) causes:

- muscle hypertrophy, i.e. an increase in muscle mass by about 32%, lower fat content by about 8%, and better feed conversion

The high prolificacy gene (*BMPR-IB/ALK6*, *GDF9*, *BMP15*), causes:

- a high degree of ovulation in sows
- influences the development of Graafian follicles and corpora lutea
- reduced secretion of inhibitors influencing gonadotropic hormones
- The increased degree of ovulation increases prolificacy by about one lamb per litter.

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Heritability

- In breeding work it is particularly important to know the contribution of genetic variation to the phenotypic variation of a given quantitative trait.
- This contribution is estimated using heritability, which we can express with the following formula:

$$h^2 = \frac{\delta^2{}_G}{\delta^2{}_P}$$

where:
$\delta^2{}_G$ – genetic variation
$\delta^2{}_P = \delta^2{}_G + \delta^2{}_E$
$\delta^2{}_P$ - phenotypic variation (total variation of a given trait in the population)
$\delta^2{}_E$ - environmental variation

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- Heritability is defined as the strength of the relationship between an animal's phenotype and the value of the individual's genes for its offspring (breeding value).
- If a trait is highly heritable, the animal's phenotype is a very good source of information about its genes.
- When heritability is high, greater phenotypic similarity is observed between closely related individuals (full siblings; half siblings; parents and offspring).
- This is because these animals share a large proportion of the same genes (50%, 25% and 50%, respectively).
- When the contribution of genetic variation in the total variation in a trait is small, the phenotype tells us little about the value of the genes which the animal will pass on to its offspring.

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Heritability h^2 of some important performance traits in farm animals

Heritability h^2 for meat cattle traits

TRAIT	h^2 VALUE
Meat traits:	
Body weight at birth	0.40
Body weight at 120 days	0.49
Daily gains	0.40
Dressing percentage	0.60
Feed consumption per kg of growth	0.75
Height at withers	0.54
Carcass length	0.75
Loin eye area	0.18

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Heritability h^2 for dairy cattle traits

TRAIT	h^2 VALUE
Milk traits:	
Milk yield	0.30
Fat yield	0.25
Protein yield	0.25
% fat	0.50
% protein	0.50
Meat traits:	
Dressing percentage	0.45
Loin eye area	0.45
Conformation traits:	
Final conformation score	0.30
Height	0.40
Angularity	0.20
Rear leg angle	0.15
Rump angle	0.20
Rump width	0.25
Fore udder attachment	0.20
Udder width	0.25
Suspensory ligament	0.15
Teat spacing	0.20

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Heritability h^2 for sheep traits

TRAIT	h^2 VALUE
Body weight at birth	0.30
Body weight at weaning	0.30
Body weight at 100 days	0.61
Body weight at 10 months	0.27
Body weight at 12 months	0.14
Wool thickness	0.32
Fleece weight	0.43
Clean fibre weight	0.40
Wool yield	0.47
Milk yield	0.52
Body weight at birth	0.17

Heritability h^2 for pig traits

TRAIT	h^2 VALUE
Daily gains	0.30
Average daily gain 40-90 kg	0.26
Fat thickness on the back	0.50
Carcass length	0.50
Amount of fat in the basic cuts	0.39
Amount of meat in primary cuts	0.52
Area of the loin ,,eye”	0.74
Litter weight at 3 weeks	0.08
Litter weight at 8 weeks	0.03
Litter size after birth	0.07

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Heritability h^2 for chicken traits

CECHA	WARTOŚĆ h^2
Laying traits:	
wielkość jaj	0.45
masa jaj	0.30
masa ciała 20 tygodni	0.25
nieśność	0.27
barwa skorupy	0.70
płodność	0.03
Meat traits:	
wykorzystanie paszy	0.60
ciężar ciała 8 tygodni	0.3
kąt piersi	0.1
długość mostka	0.1
długość skoku	0.3

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Example 1

Assume that the fatback thickness in 100-kg fatteners is determined by two pairs of genes: A, a and B, b. The aabb genotype gives the lowest fatback thickness, equal to 2 cm. Genes designated with a capital letter (A, B) add an additional 0.5 cm to the thickness of the fatback. A pair of animals has genotypes AaBb and aaBb. Check whether transgression may occur in their offspring. If so, in what proportion of the offspring?

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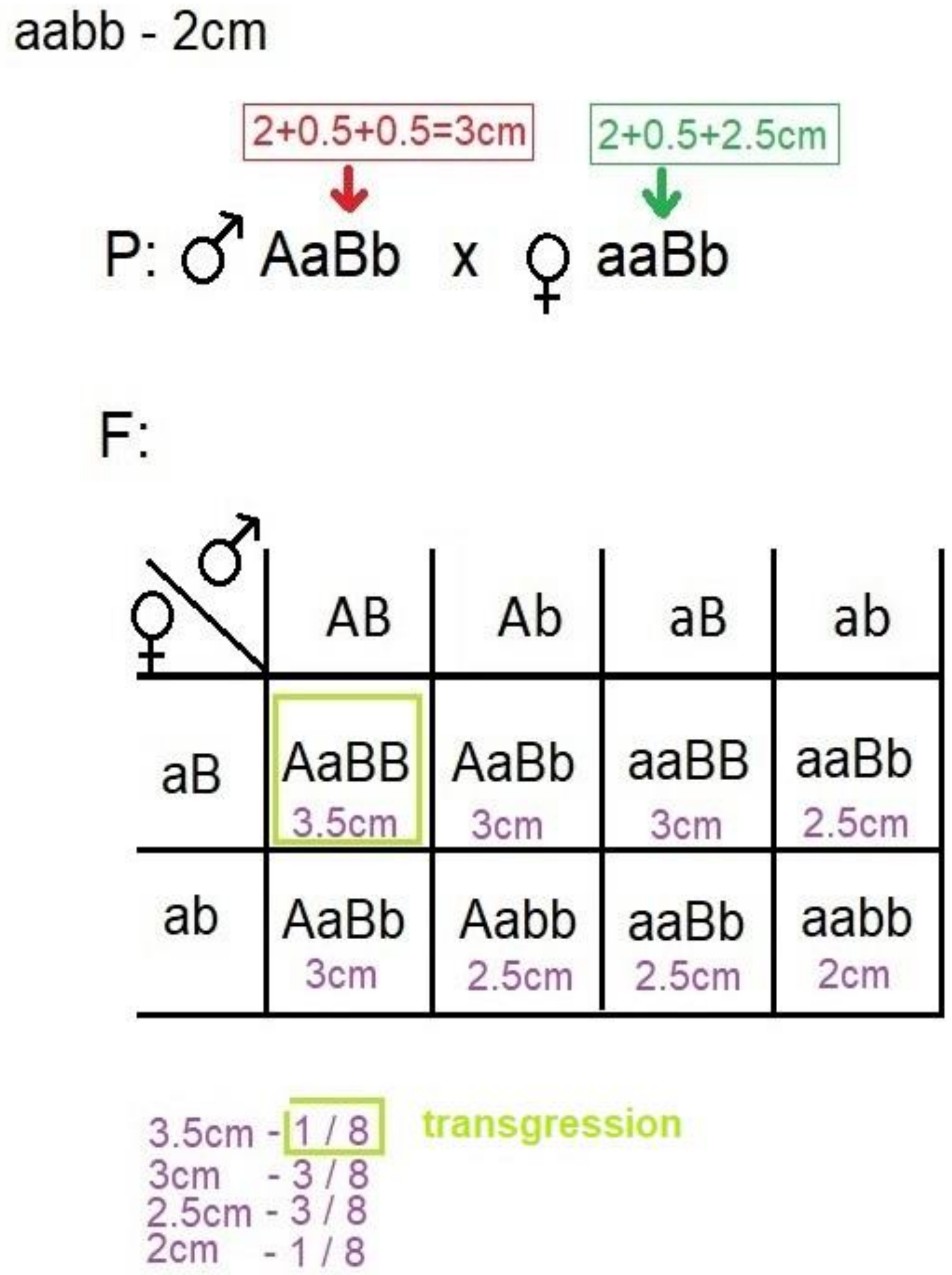
- We assume that AB alleles have a ‘favourable’ effect, whereas ab alleles have an ‘unfavourable’ effect on fatback thickness, and that we are dealing only with the additive effect of the genes.
- Each gene designated with a capital A or B increases fatback thickness by 0.5 cm.
- The aabb genotype gives fatback thickness of 2 cm.
- We write out the genotypes of the parents and then all types of gametes which the parents can produce.
- We combine the male and female gametes to create the F1 generation.
- We determine the phenotypes and check whether we are dealing with the phenomenon of transgression.



aabb - 2cm

2+0.5+0.5=3cm

2+0.5+2.5cm

P: ♂ AaBb x ♀ aaBb

F:

♀ \ ♂	AB	Ab	aB	ab
aB	AaBB 3.5cm	AaBb 3cm	aaBB 3cm	aaBb 2.5cm
ab	AaBb 3cm	Aabb 2.5cm	aaBb 2.5cm	aabb 2cm

3.5cm - 1 / 8 transgression
3cm - 3 / 8
2.5cm - 3 / 8
2cm - 1 / 8

Example 2

Assume that we are crossing two homozygous rabbits, one weighing 1000 g and the other 1900 g. If the difference in weight is caused by three pairs of cumulative genes, and each gene causes a 150 g increase in weight relative to rabbits weighing 1000 g, what can we say about the possible weights of the rabbits of the F1 and F2 generation?

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- We assume that A, B, and C alleles have a ‘favourable’ effect, while a, b, c alleles have an ‘unfavourable’ effect on the body weight of the rabbit, and that we are dealing with only the additive effect of the genes.
- Each gene designated with a capital A, B, or C increases body weight by 150 g.
- The aabbcc genotype gives a body weight of 1000 g.
- The AABBCC genotype gives a weight of 1900 g.
- We write out the genotypes of the parents and then all types of gametes which the parents can produce.
- We combine the male and female gametes to create the F1 generation.
- We determine the phenotypes and check whether we are dealing with the phenomenon of transgression.
- We check whether the data have a normal distribution.

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A, B, C - 150g

1900g ↓ 1000g ↓

P1: ♂ AABBCC x ♀ aabbcc

G: ABC x abc

F1: AaBbCc → 1000+150+150+150=1450g

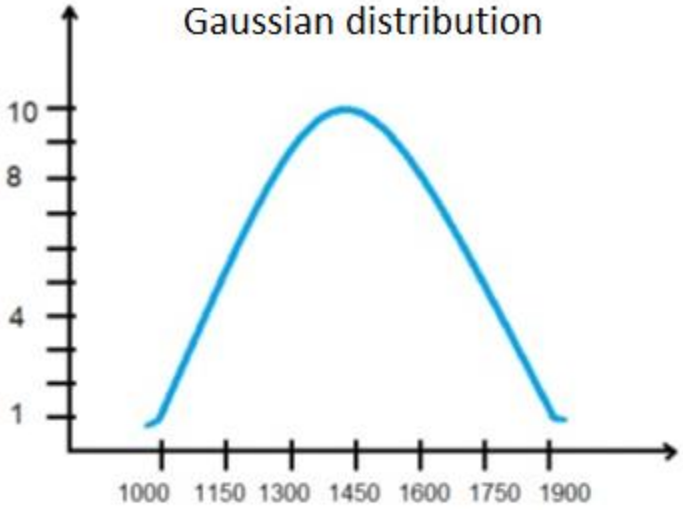
1450g 1450g

P2: ♂ AaBbCc x ♀ AaBbCc

♀ \ ♂	ABC	ABc	Abc	aBC	aBc	abc
ABC	AABBCC 1900g	AABBCc 1750g	AABbCc 1600g	AaBBCC 1750g	AaBBCc 1600g	AaBbCc 1450g
ABc	AABBCc 1750g	AABBcc 1600g	AABbcc 1450g	AaBBCc 1600g	AaBBcc 1450g	AaBbcc 1300g
Abc	AABbCc 1600g	AABbcc 1450g	AAbbcc 1300g	AaBbCc 1450g	AaBbcc 1300g	Aabbcc 1150g
aBC	AaBBCC 1750g	AaBBCc 1600g	AaBbCc 1450g	aaBBCC 1600g	aaBBCc 1450g	aaBbCc 1300g
aBc	AaBBCc 1600g	AaBBcc 1450g	AaBbcc 1300g	aaBBCc 1450g	aaBBcc 1300g	aaBbcc 1150g
abc	AaBbCc 1450g	AaBbcc 1300g	Aabbcc 1150g	aaBbCc 1300g	aaBbcc 1150g	aabbcc 1000g

🟨 transgression

1900g - 1 / 36
1750g - 4 / 36
1600g - 8 / 36
1450g - 10 / 36
1300g - 8 / 36
1150g - 4 / 36
1000g - 1 / 36



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Example 3

Assume that egg weight in chickens depends on two pairs of genes with a cumulative effect. A flock of hens laying eggs with an average weight of 54 g was mated with a rooster from a large family in which the average egg weight was 58 g. Assume that each gene designated with a capital letter increases egg weight by 1 g. Write the likely genotypes of the hen and rooster. Which genotypes and phenotypes can we expect to obtain from these pairings in the F1 and F2 generations? What is the ratio of genotypes and the ratio of phenotypes in the F2 generation? Present the distribution of phenotypes in graphic form. Does transgression occur in the offspring? If so, in which individuals? Apart from the polygenes determining egg weight, does a gene of major effect have an influence?

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- We assume that A and B alleles have a 'favourable' effect, while a and b alleles have an 'unfavourable' effect on egg weight.
- Each gene designated with a capital A or B increases egg weight by 1 g.
- The aabb genotype determines egg weight of 54 g.
- The AABB genotype determines egg weight of 58 g.
- We write out the genotypes of the parents (P1) and then the types of gametes produced by the father and mother.
- We combine the male and female gametes to create the F1 generation.
- We use individuals from the F1 generation for mating to obtain the F2 generation.
- We write out the types of gametes produced by the father and mother.
- We determine the phenotypes and check whether we are dealing with the phenomenon of transgression.
- We check whether the data have a normal distribution.

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A, B - 1g

58g 54g

P1: ♂ AABB x ♀ aabb

G: AB x ab

F1: AaBb → 54+1+1=56g

56g 56g

P2: ♂ AaBb x ♀ AaBb

♀ \ ♂	AB	Ab	aB	ab
AB	AABB 58g	AABb 57g	AaBB 57g	AaBb 56g
Ab	AABb 57g	AAbb 56g	AaBb 56g	Aabb 55g
aB	AaBB 57g	AaBb 56g	aaBB 56g	aaBb 55g
ab	AaBb 56g	Aabb 55g	aaBb 55g	aabb 54g

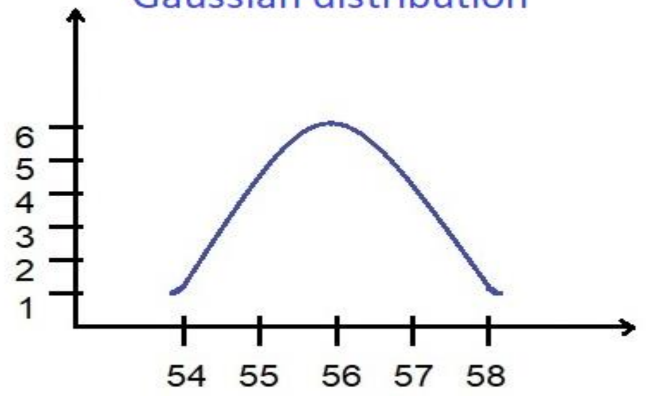
🟩 **transgression**

F2:

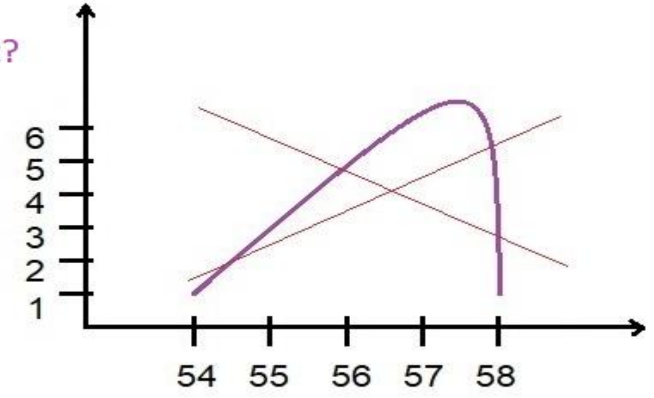
Number of phenotypes	
58g	1 / 16
57g	4 / 16
56g	6 / 16
55g	4 / 16
54g	1 / 16

Number of genotypes	
AABB	1 / 16
AABb	2 / 16
AaBB	2 / 16
AaBb	4 / 16
AAbb	1 / 16
Aabb	2 / 16
aaBB	1 / 16
aaBb	2 / 16
aabb	1 / 16

Gaussian distribution



gene of major effect?



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This presentation has been supported by the Erasmus+ KA2 Cooperation Partnerships grant no. ***2021-1-SK01-KA220-HED-000032068 “Innovation of the structure and content of study programs in the field of animal genetic and food resources management with the use of digitalisation - Inovácia obsahu a štruktúry študijných programov v oblasti manažmentu živočíšnych genetických a potravinových zdrojov s využitím digitalizácie”****. The European Commission support for the production of this presentation does not constitute an endorsement of the contents which reflects the views only of the authors, and the Commission cannot be held responsible for any use which may be made of the information contained therein.*

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References

- Charon K.M., Świtoński M. 2012. Genetyka i genomika zwierząt. Wydawnictwo PWN, Warszawa.
- Jeżewska-Witkowska G. 2014. Zbiór zadań i pytań z genetyki. Wydawnictwo Uniwersytetu Przyrodniczego w Lublinie.
- Nowicki B., Kosowska B. 1995. Genetyka i podstawy hodowli zierząt. Wydawnictwo PWRiL, Warszawa.
- Piątkowska B., Goc A., Dąbrowska G. 1998. Zbiór zadań i pytań z genetyki. Wydawnictwo Uniwersytetu Mikołaja Kopernika w Toruniu.
- Strabel T. 2006. Genetyka cech ilościowych zwierząt w praktyce. Wydawnictwo Akademii Rolniczej im. Augusta Cieszkowskiego w Poznaniu, http://jay.au.poznan.pl/~strabel/dydaktyka.
- Żuk B., Wierzbicki H., Zatoń-Dobrowolska M., Kulisiewicz Z. 2011. Genetyka populacji i metody hodowlane. Wydawnictwo PWRiL, Warszawa.
- https://onlinestores.factorysale2023outlet.ru/category?name=hodowla%20zwierz%C4%85t%20gospodarskich
- https://www.kwestiasmaku.com/blog-kulinarny/tag/jajka
- ttps://www.google.com/search?q=cechy+ilościowe++zwierząt&tbm=isch&ved=2ahUKEwjZr7fh_uaDAxX6h_0HHacYCpsQ2-cCegQIABAA&oq=cechy+ilościowe++zwierząt
- https://wiescirolnicze.pl/hodowla/czy-produkcja-polskich-prosiat-ma-szanse/

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