**Animal Genetics and Breeding**

**Chapter- 4: Genetic properties of population**

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1. Which of the following is not a factor that can affect the frequencies of genotypes in a population?
(a) Natural selection
(b) Genetic drift
(c) Mutation
**(d) Gene flow**
2. Which of the following is not a type of genetic variation?
(a) Allelic variation
(b) Chromosomal variation
(c) Epigenetic variation
**(d) Mitochondrial variation**
3. Assuming you are studying a single autosomal gene with two alleles (A1 and A2), how many distinct genotypes are possible within a population?

(a) 1

(b) 2

**(c) 3**

(e) Depends on the population size.

1. What is the genetic constitution of a population described by?
**(a) The array of gene frequencies**
(b) The genotypes of the individuals
(c) The phenotypes of the individuals
(d) The number of genes in the population
2. During the transmission of genes from one generation to the next, what happens to the parent genotypes?
3. They remain unchanged in the progeny
4. **They are broken down and reconstituted in the progeny**
5. They are passed on directly to the progeny
6. They are irrelevant to the progeny's genotypes
7. What term describes the proportion of all genes at a specific locus that are a particular allele?

(a) Genotype frequency

(b) Chromosome number

**(c) Gene frequency**

(d) Allelic ratio

1. Which statement BEST defines the genetic constitution of a population?

(a) The total number of individuals within the population.

(b) The sum of all individual genotypes within the population.

**(c) The frequencies of different alleles at all gene loci.**

(d) The specific DNA sequences of all individuals in the population

1. When studying non-ideal populations, what measures can be used to assess the impact of breeding structure on genetic variation?

(a) Mutation rates and gene flow between populations.

(b) Selection coefficients and environmental changes.

**(c) Variance of gene frequencies and rate of inbreeding.**

(d) Phenotypic expression and individual fitness differences.

1. The relationship between the actual population size (N) and the effective size (Ne) depends on:
2. The environment in which the population lives and its resources.
3. **The specific deviations from the idealized population structure.**
4. The rate of gene flow from neighbouring populations.
5. The presence of genetic bottlenecks or founder effects.
6. In the idealized population, how is the rate of inbreeding (ΔF) related to the population size (N) according to equation?

(a) ΔF = N

(b) ΔF = N/(N-1)

**(c) ΔF = 1/2N**

(d) ΔF = 1/N

1. What can be evaluated by either the variance of gene frequencies or the rate of inbreeding in a population?
2. The genetic diversity of the population
3. **The breeding structure of the population**
4. The physical traits of the population
5. The environmental impact on the population
6. What term describes the observed value of a measurable trait in an individual?

(a) Genotypic value

(b) Environmental deviation

**(c) Phenotypic value**

(d) Genotype frequency

1. The symbolic equation P = G + E represents the division of phenotypic value into:

(a) Additive and non-additive gene action.

**(b) Genotypic value and environmental deviation.**

(c) Phenotypic variance and heritability.

(d) Mean genotypic value and genotypic variance.

1. In a stable population with constant environment, the mean phenotypic value is equal to:

(a) The average environmental deviation.

**(b) The mean genotypic value.**

(c) The value of the most common genotype.

(d) The difference between G and E.

1. In a single-locus system with two alleles (A1 and A2), the genotypic values are assigned as +a, -a, and d for the respective genotypes. What does the value of "d" represent?

(a) The frequency of the A1 allele in the population.

(b) The difference in mean values between the two homozygotes.

**(c) The degree of dominance of A1 over A2.**

(d) The average environmental deviation for all genotypes.

1. Which value indicates complete dominance of A1 over A2 in this single-locus system?

(a) d = 0

(b) d = -a

**(c) d = a**

(d) d is negative but less than -a.

1. Overdominance occurs when the heterozygote has a:

(a) Lower genotypic value than both homozygotes.

(b) Genotypic value equal to the average of the homozygotes.

**(c) Higher genotypic value than both homozygotes.**

(d) Genotypic value that depends solely on the environment.

1. The degree of dominance (d/a) provides information about:

(a) The number of genes affecting the trait.

(b) The contribution of environmental factors.

**(c) The relative effect of the A1 and A2 alleles.**

(d) The rate of genetic drift in the population.

1. What is the equation that represents the relationship between phenotypic value, genotypic value, and environmental deviation?
2. **P = G + E**
3. P = G – E
4. P = 2G + E
5. P = G / E
6. What happens to the mean environmental deviation in a population?
7. It increases over time
8. It is always positive
9. **It is taken to be zero**
10. It varies with genetic makeup
11. In a randomly breeding population with two alleles (A1 and A2) at a single locus, what is the formula for the population mean (M)?

(a) pq + ad

**(b) a(p + q) + 2dpq**

(c) a(p - q) + 2dpq

(d) 2a(p - q) + dpq

1. In animal breeding, the concept of population mean is important for:

(a) Predicting the genotypic value of individual animals.

(b) Determining the heritability of a trait and evaluating the effectiveness of inbreeding.

(c) Designing selection programs to improve desired traits.

(d) **All of the above.**

1. Which of the following factors does NOT directly influence the population mean for a single-locus trait?

(a) Gene frequencies

(b) Degree of dominance

**(c) Environmental variance**

(d) Overdominance

1. In a population where A1 is fixed (p = 1), the population mean will be:

(a) Equal to the value (-a) of A2

**(b) Equal to the value(+a) of A1**

(c) Intermediate between the values of A1 and A2

(d) Cannot be determined without knowing the genotypic values

1. If there is no dominance (d = 0), what is the equation for the mean with respect to the gene frequency?
2. M = a(1 + 2q)
3. M = a(1 - q)
4. M = a(1 + q)
5. **M = a(1 - 2q)**
6. Under what condition are all definitions of average effects equivalent?

a) Under selective breeding

**b) Under random mating**

c) In a controlled environment

d) When there is genetic mutation

1. How is the average effect of a particular gene (allele) defined?
2. As the total contribution of that gene to the population
3. **As the mean deviation from the population mean of individuals receiving that gene**
4. As the difference in genotypic values between parents and offspring
5. As the sum of all genotypic values in the population
6. What is the average effect of the gene substitution?
7. a - d
8. p(a - d) + q(d + a)
9. **a + d(q - p)**
10. d + a
11. What is the average effect of a gene substitution?
12. The sum of the average effects of two alleles
13. **The difference between the average effects of two alleles**
14. The product of the average effects of two alleles
15. The ratio of the average effects of two alleles
16. The breeding value of an individual is determined by:

(a) Its own genotype alone.

**(b) The average effects of the genes it carries and the population mating context.**

(c) The difference between its own phenotype and the population mean.

(d) The dominance relationships between alleles at different loci.

1. The statement "One cannot speak of an individual's breeding value without specifying the population" emphasizes:

(a) The influence of environmental factors on breeding value.

**(b) The dependence of breeding value on the gene frequencies of the chosen mates.**

(c) The need to consider dominance relationships within the population.

(d) The limitations of breeding value as a predictor of individual offspring phenotypes.

1. The relationship between breeding value and average effects:

(a) Allows prediction of offspring phenotypes with high accuracy.

(b) Simplifies breeding program design by ignoring individual genotypes.

**(c) Provides insights into the genetic contribution to trait variation in populations.**

(d) Explains dominance relationships between different alleles at a locus.

1. What is the breeding value of an individual when mated to a number of individuals taken at random from the population?
2. Half the mean deviation of the progeny from the population mean
3. The average effect of the individual's genes
4. **Twice the mean deviation of the progeny from the population mean**
5. The sum of the genotypic values of the progeny
6. How is the breeding value of an individual defined in terms of average effects?
7. As the difference of the average effects of the genes it carries
8. **As the sum of the average effects of the genes it carries**
9. As the product of the average effects of the genes it carries
10. As the ratio of the average effects of the genes it carries
11. In a population in Hardy-Weinberg equilibrium, what is the mean breeding value?
12. The mean breeding value must be equal to the mean phenotypic value
13. **The mean breeding value must be zero**
14. The mean breeding value must be equal to the mean genotypic and phenotypic values
15. The mean breeding value must be equal to the mean genotypic value
16. Non-additive gene interactions can cause a discrepancy between:

(a) Breeding value and average effect calculations.

(b) Phenotypic and genotypic values within a population.

(c) Genotype frequencies and Hardy-Weinberg equilibrium.

**(d) Breeding value predictions and actual offspring phenotypes.**

1. The term "additive genotype" is sometimes used synonymously with:

(a) Genotype directly contributing to the observed phenotype.

(**b) Breeding value of an individual based on average gene effects.**

(c) Dominant allele effects contributing to trait variation.

(d) Non-additive interactions between genes at different loci.

1. In the context of quantitative genetics, "additive variation" refers to:

**(a) The portion of trait variation explained by individual gene effects.**

(b) The combined effects of all genes influencing the trait.

(c) The deviation of breeding values from the population mean.

(d) The contribution of non-additive gene interactions to the phenotype.

1. The expression "Po = Ao = 1/2 (As + Ad)" refers to: where the subscripts o, s, and d refer to offspring, sire, and dam respectively.

(a) The relationship between average effects of alleles and breeding values.

**(b) The expected breeding value of an offspring based on parental values.**

(c) The contribution of dominance relationships to breeding value calculations.

(d) The deviation of offspring breeding value from the mean under random mating.

1. How is the transmission of value from parents to offspring expressed in terms of breeding value? where the subscripts o, s, and d refer to offspring, sire, and dam respectively.
2. **Po = 1/2 (As + Ad)**
3. Po = Po + 1/2 (As + Ad)
4. Po = 1/2 (As + Ad)
5. Po = (As + Ad)
6. What is the relationship between the genotypic value (G) and the breeding value (A)?
7. G = A - D
8. G = A / D
9. G = A \* D
10. **G = A + D**
11. In quantitative genetics, the "dominance deviation (D)" of a genotype refers to:

(a) The average effect of an allele on the trait, independent of dominance relationships.

**(b) The difference between the breeding value and the genotypic value of the same genotype.**

(c) The deviation of a heterozygous genotype from the midpoint of the two homozygotes.

(d) The combined effect of all genes influencing the trait, including non-additive interactions.

1. The concept of dominance deviation arises due to:

(a) The presence of multiple alleles at a single locus.

**(b) The interaction between alleles within a specific genotype.**

(c) The difference in frequencies of dominant and recessive alleles in the population.

(d) The limitations of using average effects to explain all genotypic effects.

1. In the absence of dominance relationships at a locus, the dominance deviation:

**(a) Becomes zero for all genotypes.**

(b) Remains constant but independent of genotype.

(c) Cannot be distinguished from the breeding value.

(d) Depends on the specific gene frequencies in the population.

1. From a statistical perspective, dominance deviations are considered:

(a) Additive gene effects contributing to the overall trait variation.

**(b) Non-additive interactions between alleles within a single locus.**

(c) The combined effect of all genes across different loci.

(d) Statistical errors associated with measuring genotypic values.

1. Compared to breeding values, dominance deviations:

(a) Are directly measurable through individual phenotypic values.

(b) Do not depend on the specific gene frequencies in the population.

**(c) Explain the portion of trait variation not accounted for by average effects.**

(d) Provide information about the location and function of specific genes.

1. What is the difference between the genotypic value (G) and the breeding value (A) of a genotype known as?
2. Additive deviation
3. **Dominance deviation**
4. Genotypic discrepancy
5. Breeding discrepancy
6. Under what condition do breeding values and genotypic values coincide?
7. In the presence of dominance
8. **In the absence of dominance**
9. When the gene frequency is high
10. When the gene frequency is low
11. How can dominance deviation be best described in the context of allele interaction?
12. As the sum of the effects of alleles
13. **As the within-locus interactions of alleles**
14. As the between locus interactions of alleles
15. As the environmental influence on allele expression
16. In the absence of dominance (d = 0), the dominance deviation for all genotypes:

**(a) Becomes zero, making breeding and genotypic values equal.**

(b) Remains constant but independent of genotype and population frequencies.

(c) Cannot be distinguished from the breeding value, regardless of allele effects.

(d) Depends on the specific average effects of the alleles at the same locus.

1. The statement "genes that show no dominance are called additive" implies that:

**(a) Their effects on the trait simply add up linearly, regardless of interactions.**

(b) They contribute equally to the trait variation irrespective of gene frequencies.

(c) Their dominance deviations are always zero, but non-additive interactions might exist.

(d) They have no significant impact on quantitative trait inheritance in populations.

1. Which of the following terms is NOT synonymous with "additive genes"?

(a) Genes with no dominance (d = 0).

**(b) Genes showing complete dominance relationships.**

(c) Genes exhibiting average effects that contribute linearly to the trait.

(d) Genes whose breeding values coincide with their genotypic values in the absence of dominance.

1. When genes at different loci exhibit 'epistasis', what does it imply?
2. There is a lack of interaction between the genes
3. **The genes interact or affect each other's expression**
4. The genes act independently
5. The genes are expressed additively
6. If the interaction deviation is zero, how are the genes said to act?
7. **Additively between loci**
8. Independently between loci
9. In a dominant manner
10. In an epistatic manner
11. The symbol "VA" (additive variance) represents the variance of:

(a) The combined effects of all genes influencing the trait, including dominance and interactions.

**(b) The average contribution of individual alleles to the genotypic value, independent of dominance.**

(c) The deviations of individual phenotypes from their expected values based on genotypic values alone.

(d) The non-additive interactions between two or more genes affecting the trait expression.

1. What does the additive variance (VA) measure?
2. The variance of phenotypic values
3. The variance of environmental deviations
4. **The variance of breeding values**
5. The variance of interaction deviations
6. "Heritability in the broad sense" (VG/Vp) estimates:

**(a) The proportion of phenotypic variance directly determined by individual genotypes.**

(b) The extent to which phenotypes are influenced by genes transmitted from parents to offspring.

(c) The degree of resemblance between related individuals due to shared genes.

(d) The practical importance of genetic factors in shaping phenotypic variation.

1. "Heritability in the narrow sense" (VA/Vp) specifically measures:

(a) The overall genetic determination of phenotypes across a population.

**(b) The proportion of phenotypic variance due to the average effects of individual genes (breeding values).**

(c) The contribution of non-additive gene interactions to the observed trait variation.

(d) The practical application of heritability estimates in breeding programs for selection.

1. In the context of breeding programs, the term "heritability" typically refers to:

(a) The degree of genetic determination (VG/VP) reflecting overall genetic influence.

**(b) The heritability in the narrow sense (VA/VP) determining resemblance between relatives.**

(c) The specific genes and their individual effects contributing to the trait.

(d) The statistical methods used to estimate the various components of variance.

1. Techniques for estimating VG and VE experimentally often involve:

**(a) Analyzing phenotypic variation in populations with identical genotypes (e.g., clones).**

(b) Directly measuring and quantifying the specific environmental factors influencing the trait.

(c) Isolating individual genes and their effects through genetic engineering and manipulation.

(d) Conducting breeding experiments across multiple generations with controlled environments.

1. Identical twins, despite their identical genotypes, are not ideal for partitioning variance due to:

**(a) Their shared environmental experiences throughout life.**

(b) The potential presence of epigenetic differences influencing gene expression.

(c) Their limited availability for research studies compared to other populations.

(d) The difficulty in accurately measuring their phenotypic values for the trait of interest.

1. Which of the following statements about estimation of variance components is NOT true?

(a) Different experimental designs and statistical methods can be used depending on the research question and organism.

(b) Assumptions about the underlying genetic architecture and environmental influences can affect the accuracy of estimates.

(c) Precise estimations may not always be achievable, but relative comparisons between components can be valuable.

**(d) Estimates can be influenced by factors like sample size, population structure, and environmental heterogeneity.**

1. What does the heritability in the narrow sense (VA/VP) determine?
2. The degree of environmental influence on phenotypes
3. **The degree of resemblance between relatives**
4. The variability of phenotypes within a population
5. The impact of genetic mutations
6. What does VG/VP represent in genetic studies?
7. Environmental influence on phenotypes
8. **Genetic determination of phenotypes**
9. Variability of breeding values
10. Impact of genotype on environment
11. Compared to crossbred heterozygous individuals, the inbred homozygous individuals:

(a) Always show lower environmental variance due to their genetic uniformity.

**(b) Can be more sensitive to environmental differences and exhibit higher VE.**

(c) Are not suitable for estimating **VE** because their genotypes are not representative of the population.

(d) Do not experience any interaction between their genotype and the environment.

1. Clonally propagated individuals offer an advantage in estimating VG because:

(a) They represent a wider range of genotypes compared to inbred lines or crosses.

**(b) They provide multiple replicates for each genotype, reducing the impact of environmental fluctuations.**

(c) Their environmental variance is always negligible and does not influence the genotypic estimate.

(d) They allow for direct measurement of individual gene effects and their contribution to VG.

1. The term "clonal repeatability" refers to:

**(a) The proportion of phenotypic variance explained by genotypic differences between clones.**

(b) The consistency of phenotypic expression across different environments for each clone.

(c) The degree of resemblance between phenotypes of individuals produced from the same clone.

(d) The accuracy of VG estimation using clonal replicates compared to other methods.

1. The "clonal repeatability" estimate of VG:

(a) Is always an accurate reflection of the true genotypic variance in the population.

**(b) Can be an overestimate of VG due to potential environmental effects transmitted to clones.**

(c) Does not require any assumptions about the environmental variance or its uniformity across genotypes.

(d) Provides a direct measure of the interaction deviation (Vi) between clones and their environments.

1. Which variance component is crucial for understanding resemblance between relatives?
2. **Additive variance**
3. Dominance variance
4. Interaction variance
5. Environmental variance
6. In the context of a single locus with two alleles, what is temporarily excluded?
7. Additive variance
8. Dominance variance
9. **Interaction variance**
10. Environmental variance
11. In populations derived from a cross of two highly inbred lines, how do the expressions for VA and VD simplify?
12. VA = 2pqa2, VD = (2pqd)2
13. **VA = 1/2 a2, VD = 1/4d2**
14. VA = 0, VD = 1/4d2
15. VA = 1/2 a2, VD = 0
16. If inbred lines are available, what can be estimated more accurately?
17. Genotypic variance
18. Phenotypic variance
19. Environmental variance
20. **Additive variance**
21. How is the additive variance from multiple loci calculated in a random mating population in equilibrium?
22. As the product of the variances of each locus
23. **As the sum of the additive variances of each locus**
24. By averaging the variances of each locus
25. By subtracting the non-additive variances from the total variance
26. What is interaction variance (VI) a result of?
27. **The interaction of genotypes at different loci showing epistatic interaction**
28. The interaction of environmental factors
29. The sum of additive variances
30. The sum of dominance variances
31. What kinds of two-factor interactions contribute to interaction variance?
32. **Additive X additive, additive X dominance, dominance X dominance**
33. Additive X environmental, dominance X environmental
34. Environmental X environmental
35. Additive X additive, additive X environmental
36. In simple experiments, with which component is most of the interaction variance included?
37. Additive genetic variance
38. **Non-additive genetic variance**
39. Environmental variance
40. Phenotypic variance
41. What additional source of genetic variance arises when a population is not in equilibrium under random mating?
42. **Disequilibrium variance**
43. Environmental variance
44. Additive variance
45. Dominance variance
46. What happens to the genetic variance due to gametic phase disequilibrium in unlinked loci over generations?
47. It increases exponentially
48. It remains the same
49. **It is reduced by half in each generation**
50. It is increased by double in each generation
51. Which example demonstrates a correlation between phenotypic value and environmental deviation?
52. **Milk yield in dairy cattle**
53. Plant growth in different soil types
54. Fish size in various water temperatures
55. Insect behavior in different habitats
56. What happens to the phenotypic variance (VP) when there is a correlation between genotypic values and environmental deviations?
57. It remains constant
58. It is reduced
59. **It is increased**
60. It becomes unpredictable
61. What is genotype-environment interaction?
62. The independence of genotypic values from environmental factors
63. The effect of environment on genotype without any variation
64. **The variation in genotype response to different environmental conditions**
65. The constant effect of environment across all genotypes
66. How is the phenotypic value of an individual expressed when considering genotype-environment interaction?
67. P = G + E
68. **P = G + E + IGE**
69. P = VG + VE+ IGE
70. P = G – E
71. What happens to the phenotypic variance when there is genotype-environment interaction?
72. It remains the same as without interaction
73. It is reduced significantly
74. **It increases due to an additional source of variation**
75. It can only be determined with environmental sensitivity
76. What does the “environmental sensitivity” of a genotype refer to?
77. Its response to genetic changes
78. Its ability to adapt to different environments
79. **The effect of a given environmental difference on the genotype**
80. Its resistance to environmental stressors
81. What is the 'reaction norm' in genetics?
82. The standard response of a genotype to environmental changes
83. The average genetic makeup of a population
84. **The environmental sensitivity of a genotype**
85. The normative distribution of genotypes in an environment
86. What is a consequence of significant genotype-environment interaction?
87. Uniform performance across different environments
88. **Specific genotypes need to be chosen for specific environments**
89. Reduced need for environmental control in experiments
90. Decreased genetic diversity in populations
91. If there is no interaction between genotypes and environments, what can be inferred?
92. **The best genotype in one environment will be the best in all**
93. Environmental factors do not affect genotypic expression
94. All genotypes will perform poorly in all environments
95. The environment has a greater influence than the genotype
96. What is a critical factor to consider when rearing individuals of a particular population under different conditions?
97. The constant genetic makeup of the population
98. **The genotype-environment interaction**
99. The uniformity of the environment
100. The phenotypic variance alone
101. What is the aim of experimenters or breeders regarding environmental variance?
102. To increase it for better genetic studies
103. **To reduce it for more precision in genetic studies**
104. To manipulate it for specific genetic outcomes
105. To ignore it as it is negligible
106. Which are common external causes of environmental variation?
107. Genetic mutations and breeding choices
108. **Nutritional and climatic factors**
109. The age and gender of the organism
110. The geographical location of the study
111. What is a source of environmental variation that is less susceptible to control, particularly in mammals?
112. Genetic diversity
113. **Maternal effects**
114. Laboratory conditions
115. Breeding methods
116. What type of characters are more susceptible to influences of the external environment?
117. Characters connected with anatomical structure
118. **Characters connected with metabolic processes**
119. Genetically determined characters
120. Characters with low developmental variation
121. What does the within-individual component of variance represent?
122. Genetic variance
123. **Environmental variance**
124. Developmental variance
125. Measurement error
126. What are examples of characters repeated in time?
127. Plant height and leaf size
128. **Milk-yield and litter size**
129. Fruit shape and seed content
130. Number of bristles on Drosophila
131. What is 'special environmental variance' (VES) in genetics?
132. **Variance arising from temporary or localized circumstances**
133. Variance caused by permanent environmental factors
134. Genetic variance among different individuals
135. Variance due to spatial repetition
136. What is the 'general environmental variance' (VEG)?
137. **Environmental variance contributing to the between-individual component**
138. Variance due to general genetic factors
139. Variance due to overall environmental conditions
140. Variance from non-localized circumstances
141. What does the intraclass correlation (r) in repeatability studies represent?
142. Correlation between different environmental conditions
143. **Correlation between repeated measurements of the same individual**
144. Genetic correlation between individuals
145. Correlation between different characters
146. How does the repeatability of a character affect the estimation of genetic determination (VG/VP)?
147. **It sets an upper limit to the degree of genetic determination**
148. It directly determines genetic determination
149. It reduces the degree of genetic determination
150. It has no impact on genetic determination
151. Why is repeatability important in breeding programs?
152. It indicates the environmental stability
153. **It helps predict future performance from past records**
154. It determines the genetic makeup of offspring
155. It measures the rate of genetic mutations
156. What do the terms ‘special environmental variance’ and ‘general environmental variance’ refer to in the context of repeatability?
157. VES refers to genetic variance, and VEG refers to environmental variance
158. **VES refers to variance from temporary circumstances, and VEG refers to variance from permanent circumstances**
159. VES refers to variance within individuals, and VEG refers to variance between individuals
160. VES and VEG both refer to different types of environmental variance
161. How does repeatability contribute to understanding the nature of environmental variance?
162. By distinguishing between genetic and environmental sources of variance
163. **By separating environmental variance into temporary and permanent components**
164. By identifying the genetic factors responsible for environmental variance
165. By eliminating environmental variance from genetic studies
166. Which among the following is a deviation from the idealized breeding structure?
167. Migration
168. Mutation
169. Selection
170. **All of the above**
171. If the breeding structure doesn’t conform to that specified for the idealized population, it is possible to evaluate the dispersive process in terms of
172. Variance of gene frequencies
173. Rate of inbreeding
174. **Either a or b**
175. Neither a nor b
176. In the idealized population, the rate of inbreeding (ΔF) is related to the population size (N) by equation
177. ΔF = N
178. ΔF = 2N
179. **ΔF = 1/2N**
180. ΔF = 1/4N
181. For different numbers of males and females, the effective population size \_\_\_\_\_\_the harmonic mean of the numbers in two sexes.
182. Half
183. **Twice**
184. Thrice
185. None of the above
186. For unequal number of animals in successive generations, the effective number is the \_\_\_\_\_\_ of the numbers in each generation.
187. Arithmetic mean
188. Geometric mean
189. **Harmonic mean**
190. Least squares mean
191. Which among the following is not a cause of genetic correlation?
192. Pleiotropy
193. Linkage
194. Heterozygosity
195. **Homozygosity**
196. Correlation between the traits caused by dominance effects and epistatic effects comes under
197. Genetic correlation
198. **Environmental correlation**
199. Both a & b
200. None of the above
201. Genotypic correlation is analogous to
202. **Heritability in broad sense**
203. Heritability in narrow sense
204. Total heritability
205. None of the above
206. Genotypic correlation depends upon
207. Average effect of genes at each locus
208. Dominance effect
209. Epistatic effect
210. **All of the above**
211. Mark the most appropriate option concerning the following statements.

Statement – I: Genotypic correlation can only be estimated from specialized populations.

Statement – II: Genotypic correlation can’t be used in the formulation of breeding plans.

1. Statement – I is true but Statement – II is false
2. Statement – II is true but Statement – I is false
3. **Both the statements are true**
4. Both the statements are false
5. Additive genetic correlation is analogous to
6. Heritability in broad sense
7. **Heritability in narrow sense**
8. Total heritability
9. None of the above
10. \_\_\_\_\_\_\_ is used to predict the correlated response to selection.
11. Genotypic correlation
12. **Additive genetic correlation**
13. Environmental correlation
14. None of the above
15. Genes with antagonistic effects are \_\_\_\_\_\_ affected by selection.
16. More
17. **Less**
18. Same as genes with synergistic effects
19. Either a or b, depends on gene frequency
20. The correlated response will be decreased if the genetic correlation was, to a great extent, due to
21. **Linkage**
22. Pleiotropy
23. Genetic drift
24. Homozygosity
25. Which among the following scientists have estimated the genetic correlation between wing length and thorax length in Drosophila from their famous double selection experiments.
26. Watson and Crick (1953)
27. **Reeve and Robertson (1953)**
28. Bateson and Punnett (1911)
29. Sutton and Boveri (1926)
30. Which among the following can change the genetic correlation?
31. Selection
32. Genetic drift
33. Mutation
34. **Both a & b**
35. High genetic correlation indicates
36. Linkage
37. **Pleiotropic gene action**
38. Heterozygosity
39. Crossing over
40. “A world Dictionary of Livestock Breeds, Types and Varieties” book was written by
41. Mendel
42. Bateson
43. **I. L. Mason**
44. Darwin
45. Who was the first to survey the important breeds of cattle in India?
46. I. L. Mason (1938)
47. **Olivery (1938)**
48. Camber (1938)
49. None of the above
50. MPPA was given by
51. Mason
52. **Lush**
53. Fisher
54. Sundaresan
55. The variance caused by temporary environment effects is decreased by \_\_\_\_\_ times with increase in number of observations (n).
56. n
57. **1/n**
58. 1/2n
59. 2n
60. Which among the following is/are a method of estimation of repeatability when only two records per animal are available.
61. Inter-class correlation
62. Regression
63. **Both a & b**
64. None of the above
65. A minimum of how many records per individual are required to estimate repeatability?
66. 1
67. **2**
68. 3
69. 4
70. What is the primary reason for studying the resemblance between relatives in genetics?
71. To determine the genetic diversity of a population
72. **To estimate the amount of additive genetic variance**
73. To identify genetic mutations
74. To analyze the impact of environmental factors
75. What is 'heritability' in the context of resemblance between relatives?
76. **The proportionate amount of additive variance**
77. The genetic similarity between relatives
78. The rate of genetic mutations in a family
79. The environmental influence on relatives
80. What does the intraclass correlation coefficient (t) represent in genetic studies?
81. The correlation of environmental factors
82. **The resemblance between related individuals**
83. The genetic diversity within a population
84. The rate of genetic mutations
85. What is meant by the 'covariance of members of the groups' in genetics?
86. The variation between different genetic groups
87. **The amount of variation common to members of the same group**
88. The environmental differences between groups
89. The rate of genetic mutations within a group
90. How does genetic covariance arise between relatives?
91. Through environmental influences
92. Through genetic mutations
93. **Through similarities in genetic makeup**
94. Through different breeding methods
95. What is the purpose of partitioning phenotypic variance into observational components?
96. To distinguish between genetic and environmental factors
97. **To measure the degree of resemblance between relatives**
98. To identify specific genetic mutations
99. To measure genetic and environmental variance
100. What is indicated by a high degree of resemblance between relatives in genetics?
101. A strong environmental influence
102. A high rate of genetic mutations
103. **Significant genetic similarities**
104. Uniform breeding methods
105. What assumption is made about the population when deducing genetic covariance?
106. The population is not in Hardy-Weinberg equilibrium
107. There is significant epistatic interaction
108. **The population is in Hardy-Weinberg equilibrium**
109. All mating is assortative
110. How is the covariance of offspring and one parent computed in genetics?
111. **As the covariance of an individual's genotypic value with half its breeding value**
112. By considering the environmental variance
113. Based on the phenotypic variance of the population
114. Through the dominance deviation
115. How is additive genetic variance (VA) related to the genetic covariance of offspring and one parent?
116. It is equal to the genetic covariance
117. **It is twice the genetic covariance**
118. It is half the genetic covariance
119. It is unrelated to the genetic covariance
120. How does the number of offspring used in the calculation of genetic covariance between offspring and one parent affect the result?
121. The covariance increases with more offspring
122. The covariance decreases with more offspring
123. **The covariance remains the same regardless of the number of offspring**
124. The calculation cannot be performed without knowing the exact number of offspring
125. Under what condition is the covariance of offspring with mid-parent the same as with a single parent?
126. When both parents have different variances
127. **When both parents have equal variances**
128. When the environmental influence is high
129. When there is only one offspring
130. What is the value of the covariance of offspring with mid-parent when both sexes have equal variances?
131. Equal to the additive genetic variance
132. **Half the additive genetic variance**
133. Twice the additive genetic variance
134. Unrelated to the additive genetic variance
135. How does the regression of offspring on mid-parent values compare to the regression on single parents?
136. It is the same
137. **It is twice as much**
138. It is half as much
139. It is unrelated
140. How does the covariance of full sibs differ from that of half sibs?
141. **It is more complex due to the contribution of dominance variance**
142. It is simpler and only includes the additive variance
143. It is equal to that of half sibs
144. It is unrelated to the additive variance
145. What characterizes the genetic covariance of monozygotic twins (cov(MZ))?
146. It is equal to the additive genetic variance
147. **It is equal to the entire genetic variance (VG)**
148. It is unrelated to the genetic variance
149. It is a quarter of the additive variance
150. How is the interaction variance (VI) subdivided in genetic studies?
151. **According to the number of interacting loci and type of interaction**
152. Based on the genetic diversity of the loci
153. By the rate of genetic mutations
154. According to the environmental impact on the loci
155. How do the theoretical and practical definitions of breeding value differ?
156. The theoretical includes interaction deviations; the practical excludes them
157. **The theoretical excludes interaction deviations; the practical includes them**
158. Both definitions exclude interaction deviations
159. Both definitions include interaction deviations
160. In the presence of epistatic interaction, how is full-sib and half-sib covariance affected by linkage?
161. It is decreased
162. It remains unchanged
163. **It is increased**
164. It becomes unpredictable
165. How does a common environment affect family members in genetic studies?
166. It increases differences between unrelated individuals
167. **It reduces differences between family members**
168. It has no impact on family resemblance
169. It enhances genetic mutations
170. How is the environmental variance divided in genetic studies?
171. **VE = VEc + VEw**
172. VE = VG + VP
173. VE = VG + VEc
174. VE = VP + VEw
175. How does the VEc component affect the covariance of related individuals?
176. It decreases the covariance
177. It has no impact on the covariance
178. **It increases the covariance**
179. It changes the genetic basis of the covariance
180. What kind of maternal effect leads to environmental covariance between offspring and their mother?
181. **When the mother's phenotype influences the offspring's phenotype**
182. When the offspring's genotype influences the mother's phenotype
183. There is no effect of offspring’s phenotype on the mother
184. When environmental factors influence the mother's phenotype
185. What happens to the intraclass correlation when family members compete for resources?
186. It increases
187. It remains the same
188. **It decreases**
189. It becomes unpredictable
190. What is the sum of the covariances arising from genetic and environmental causes known as?
191. **Phenotypic covariance**
192. Genetic covariance
193. Environmental covariance
194. Additive covariance
195. What does the term 'common environment' refer to in genetic studies?
196. The genetic environment shared by all individuals
197. **The environmental circumstances shared by family members**
198. The cultural environment influencing a population
199. The environmental factors causing genetic mutations
200. How does the common maternal environment of full sibs affect their covariance?
201. **It increases the covariance**
202. It has no impact on the covariance
203. It decreases the covariance
204. It changes the genetic basis of the covariance
205. What is the role of the correlation between breeding values and phenotypic values in heritability?
206. **It is equal to the square root of heritability**
207. It determines the rate of genetic mutations
208. It measures the environmental impact on traits
209. It is unrelated to heritability
210. What is the impact of more variable environmental conditions on heritability?
211. It increases heritability
212. **It decreases heritability**
213. It has no impact on heritability
214. It changes the genetic basis of heritability
215. What is generally true about the heritability of traits related to reproductive fitness?
216. They tend to have high heritability due to their genetic importance
217. **They usually exhibit low heritability due to strong environmental influences**
218. Their heritability is consistently high across all species
219. They are not influenced by heritability factors
220. Which relatives typically provide the most precise heritability estimates?
221. More distant relatives
222. **Closer relatives**
223. Relatives with strong environmental influences
224. Relatives with high mutation rates
225. Which relative relationship is generally the most reliable for estimating heritability?
226. Full sibs
227. **Half sibs and offspring-parent (father)**
228. Offspring-mother
229. Distant relatives
230. What makes the full-sib correlation less reliable for estimating heritability?
231. Its independence from environmental factors
232. **The presence of a large common environmental component**
233. Its reflection of random mating patterns
234. The absence of genetic variance
235. What is the primary statistical method used for estimating variance components in classical experimental designs?
236. Chi-square tests
237. Maximum likelihood (ML)
238. **Least-squares statistical analyses**
239. Bayesian analysis
240. When both parents and a number of their offspring's phenotypes are known, how many estimates of heritability can be obtained?
241. One
242. **Two**
243. Three
244. Four
245. What does REML stand for?
246. Random Effect Maximum Likelihood
247. **Restricted Maximum Likelihood**
248. Regression Maximum Likelihood
249. Relative Estimation and ML
250. Why is REML analysis computationally intensive?
251. It uses simple algorithms
252. **It adjusts observations for the estimates of fixed effects**
253. It requires very large sample sizes
254. It is an outdated method
255. Non-additive gene action includes:
256. Dominance
257. Interaction
258. Epistasis
259. **Above all**
260. The ratio of response to selection-to-selection differential is the:
261. degree of genetic determination
262. heritability in broad sense
263. **Realized heritability**
264. heritability in narrow sense
265. In an analysis of half sib families the component of covariance between sire is:
266. 1/2 COVA
267. **1/4 COVA**
268. 3/4 COVA
269. COVAB
270. Precision of heritability estimate depends on its:
271. **standard error**
272. coefficient of variation
273. sampling variance
274. all the above
275. Highest genetic gain can be achieved by accurate estimation of breeding value by
276. sires of dams
277. dams of sires
278. **sires of sires**
279. dams of dams
280. The genetic covariance of full sib is
281. 1/2 VA
282. 1/4 VA
283. **1/2 VA + 1/4 VD**
284. 1/2 VA + 1/2 VD
285. The description of the covariance, applicable to any sort of relationship is
286. between half and full sibs
287. between offspring and mid parent
288. Between offspring and one parent
289. **all the above**
290. When repeatability is low, multiple measurements gives\_\_\_\_\_\_\_\_\_\_ gain in accuracy
291. **large**
292. little
293. both
294. none
295. The proportion of phenotypic variation expressed by repeatability is
296. permanent genetic variance
297. permanent environmental variance
298. **Both**
299. special environmental variance
300. Falconer and Latyszewski (1952) were first to plan experiment in mice to study :
301. Genetic drift
302. Genetic variability
303. **Genotype x environment interaction**
304. Genotype x environment correlation
305. A large value of within group variance in a dairy trait shows the repeatability as
306. Zero
307. **Low**
308. Medium
309. High
310. The trait is still heritable if the heritability is
311. **0**
312. <-1
313. >1
314. All the above
315. “Repeatability” term was coined by
316. Fisher
317. Johannsen
318. **Lush**
319. Henderson
320. Which among the following describes repeatability?
321. Regression of producing ability on the phenotypic value of the first record
322. Ratio of variance of producing ability to the variance of phenotypic value
323. Measure of strength of relationship between the single record and producing ability of a trait in population.
324. **All of the above**
325. The original definition of the average effect of gene substitution in terms of the linear regression of genotypic value on number of genes was given by
326. **Fisher**
327. Lush
328. Henderson
329. Johannsen
330. Population mean depends on
331. **Gene frequency**
332. Genotype frequency
333. Both a & b
334. Which of the following statements regarding breeding value is false?
335. **Can’t be expressed in absolute units**
336. Is a property of individual and its population
337. Can be expressed as deviation from the population mean
338. Twice the transmitting ability
339. Which among the following statement is false?
340. Average effect of gene substitution equals regression of phenotype on genotype.
341. **Magnitude of the average effect of gene substitution is proportional to the frequency of dominant allele**
342. Average effect of gene depends on the gene frequency and genotypic value.
343. None of the above
344. Which of the following effect can be eliminated by changing the scale of measurement?
345. Dominance effect
346. **Epistatic effect**
347. Environmental effect
348. All of the above
349. The principle that the phenotypic value is the joint product of genotype (gene effects) and environment was first given by
350. Lush
351. Fisher
352. Henderson
353. **Johannsen**
354. Which among the following is the only source of new allele at a locus?
355. Migration
356. **Mutation**
357. Selection
358. Random drift
359. Mark the most appropriate option concerning the following statements.

Statement – I: Formation of new allele is the result of amino acid substitution.

Statement – II: same results are produced by reciprocal crossing of sex-linked traits.

1. **Statement – I is true but Statement – II is false**
2. Statement – II is true but Statement – I is false
3. Both the statements are true
4. Both the statements are false
5. Extranuclear or extra-chromosomal factors are called
6. Plasmogenes
7. Cytogenes
8. Plasmids
9. **All of the above**
10. Variance is more useful than other measures of variability for its property of
11. Additivity
12. Subdivisibility
13. Multiplicity
14. **Both a & b**
15. Mark the most appropriate option concerning the following statements.

Statement – I: Special environmental effects are permanent

Statement – II: General environmental effects are temporary.

1. Statement – I is true but Statement – II is false
2. Statement – II is true but Statement – I is false
3. Both the statements are true
4. **Both the statements are false**
5. Mark the most appropriate option concerning the following statements.

Statement – I: Homozygotes are more sensitive to environment that heterozygotes.

Statement – II: Heterozygotes are more sensitive to environment that homozygotes.

1. **Statement – I is true but Statement – II is false**
2. Statement – II is true but Statement – I is false
3. Both the statements are true
4. Both the statements are false
5. VGE is regarded as part of
6. VA
7. VG
8. **VE**
9. All of the above
10. Knowledge of \_\_\_\_\_ decides the choice of environment for selective breeding and testing of sires.
11. VA
12. VG
13. **VGE**
14. VE
15. Which among the following contribute to the resemblance between relatives?
16. Genetic factors only
17. Environmental factors only
18. **Both a & b**
19. Neither a nor b
20. The c-effect between full-sib family is ­­­­\_\_\_\_\_\_ than half-sib family.
21. **More**
22. Less
23. Same
24. Depends on other factors
25. C-effect was given by
26. Hush
27. Johannsen
28. Fisher
29. **Lerner**
30. The coefficient of relationship between monozygotic twins or clones is
31. 0
32. ½
33. **1**
34. None of the above
35. The genetic covariance of offspring and parent is equal to \_\_\_\_\_ the additive genetic variance (VA).
36. Twice
37. **½**
38. ¼
39. None of the above
40. Mark the most appropriate option concerning the following statements.

Statement – I: Plasman exhibit mendelian ratios.

Statement – II: Plasmans show different results on reciprocal crossing.

1. Statement – I is true but Statement – II is false
2. **Statement – II is true but Statement – I is false**
3. Both the statements are true
4. Both the statements are false

Fill in the blanks.

1. The most convenient way of dealing with any particular deviation from the idealized breeding structure is to express the situation in terms of the **effective population size**.
2. The number of individuals that would give rise to the calculated sampling variance, or rate of inbreeding, if they bred in the manner of the idealized population is called **effective population size**.
3. The exclusion of closely related mating doesn’t affect the rate at which the inbreeding accumulates. (**T**/F)
4. Genetic properties of a population are expressible in terms of **gene frequencies** and **genotype frequencies**.
5. Magnitude of correlation due to pleiotropy depends upon **direction of their effect.**
6. The rate of decrease in correlation caused by linkage in each generation depends upon the **crossing-over distance.**
7. The effect of heterozygosity persists till **the population achieve H-W equilibrium.**
8. Correlation between the breeding values of individuals for two characters in a population is known as **additive genetic correlation.**
9. Biodiversity is the result of **evolution.**
10. Repeated records in farm animal traits are mostly **temporal** repetition.
11. Intraclass correlation among the repeated records of a trait of the same individual is called **repeatability.**
12. Performance potential of an animal for a repeated trait is known as **producing ability.**
13. Mean dominance deviation in a population is always **zero.**
14. Dominance deviations are functions of **gene frequency** and are partly property of the **population.**
15. Difference between the genotypic value (G) and breeding value (A) of a particular genotype indicates the **dominance deviation (D).**
16. Mean genotypic value of the population would be **zero.**
17. Measure of animal’s expected progeny performance relative to population mean is **breeding value.**
18. **Environmental** effects don’t contribute to the population mean.
19. The average of the two homozygotes, taken as the point of origin, is called **natural zero point.**
20. The individual can live and reproduce only within a certain limit of physical factors in its environment called as **tolerance range.**
21. Genetic equilibrium is not observed in **real population.**
22. **Wahlund effect** assumes overall population to be panmictic.
23. Environmentally induced change which is similar to the effect of a gene mutation is **phenocopy.**
24. Specific environmental change simulates the effect of a particular gene is called **phocomelia.**
25. **Variation** is the raw material for the breeder for genetic improvement.
26. Covariance between relatives is the property of **metric** characters.
27. Degree of resemblance provides the method to estimate the amount of **additive genetic variance.**
28. Regression of offspring on parent expressed as deviation from the population mean is called **resemblance between relatives.**
29. Linkage affects only the covariance between **collateral** relatives.
30. Degree of resemblance expressed as the between group component as a proportion of total variance is known as **intra class correlation.**
31. What components make up the genotypic value (G) in genetics**- A (Additive) + D (Dominance) + I (Interaction)**
32. What is the equation for phenotypic variance considering the correlation between genotype and environment= **VP = VG + VE + 2CoVGE**
33. The heritability of calving interval is **\_low\_ .**