

Popular Article

Quantitative Genetics: A better tool to understand animal population

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Abstract

Quantitative genetics or population genetics is a subfield of genetics that deals with genetic differences within and between populations, and is a part of evolutionary biology. Studies in this branch of biology examine such phenomena as adaptation, speciation, and population structure. The average effect and average excess of a gene substitution are formulated in terms of gene frequencies and inbreeding coefficient. The role of population mean, average gene effect and variances plays an important role in population study.

Introduction

Genetics can no longer be regarded as a very young science. To be sure, no part of the genetic theory is established firmly enough and elaborated completely enough to be respectfully embalmed for all time to come in textbooks and manuals. (Meglitsch, 1954). Nevertheless, some basic rules of the transmission of heredity from parents to offspring are so well known that the ignorance of a Lysenko is needed to deny them. Chromosomes and their parts can be, in well studied organisms, juggled almost at will. The genetic consequences of this juggling are predictable with sufficient accuracy to be used as safe problems for doctoral dissertations. In contrast to the rules of the transmission of heredity, population genetics is quite young. Quantitative genetics deals with phenotypes that vary continuously (in characters such as height or mass)—as opposed to discreetly identifiable phenotypes and gene-products (such as eye-color etc.) Due to the continuous distribution of phenotypic values, quantitative genetics must employ many other statistical methods (such as the effect size, the mean and the variance) to link phenotypes (attributes) to genotypes. (Álvarez-Castro and Carlborg, 2007)

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What is the Gene Effect?

Sir Ronald Fischer (1930) defined the gene effects as deviations from a central value—enabling the use of statistical concepts such as mean and variance, which use this idea. The central value he chose for the gene was the midpoint between the two opposing homozygotes at the one locus. The deviation from there to the "greater" homozygous genotype can be named "+a"; and therefore, it is "-a" from that same midpoint to the "lesser" homozygous genotype.

This is the "allele" effect mentioned above. The heterozygote deviation from the same midpoint can be named "d", this being the "dominance" effect referred to above. The diagram depicts the idea. However, in reality we measure phenotypes, and the figure also shows how observed phenotypes relate to the gene effects. (Zeng et al., 2005)

Suppose take the value of locus A, with alleles **A** and **a**.

So, the Individuals with genotype will be **AA, Aa and aa**.

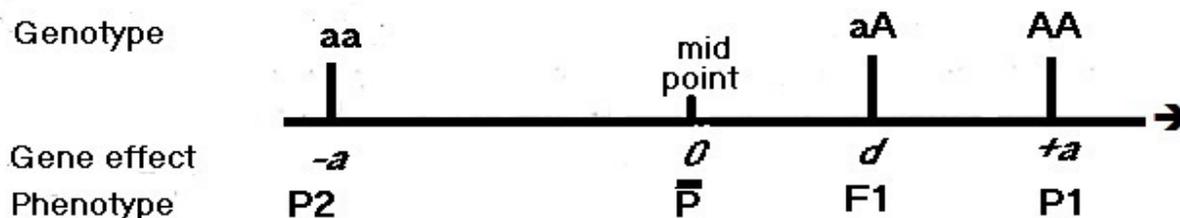


fig.1: Genotypic and gene value of Phenotype (source: Wikipedia)

Here, **A** allele is increasing the value and **a** is decreasing and **d** is the degree of dominance.

- $d=0$, when there is no dominance.
- If **A** is dominant than **a**, then d is positive and *vis a versa*. (Partial dominance).
- If **A** is completely dominant, then **Aa** will be same as **AA**. and $d= a$
- If **a** is completely dominant, then **Aa** will be same as **aa**, and $d= -a$.
- In case of over dominance, then $d>a$ or $d<-a$.

Population mean:

Let the Frequency of A gene= p, i.e., f(A) = p and f(a) =q

Genotypes	Frequency	Value	f x v
AA	p ²	+a	ap ²
Aa	2pq	d	2pqd
aa	q ²	-a	-aq ²

$$\begin{aligned} \text{Total} &= ap^2+2pqd-aq^2 \\ &= a(p^2 - q^2) + 2pqd \\ &= a(p-q) + 2pqd \quad \text{----- (1)} \end{aligned}$$

So, Mean phenotypic value in a population= Mean genotypic value in a population=
M=a (p-q) +2pqd

In a random breeding population, where f x v and sum of it gives the mean value of the whole population.

Here, **a (p-q) is attributed to homozygous.**

2pqd is attributed to heterozygous.

1. If d=0 (Where there is no dominance)

$$\Rightarrow M = a(p-q) \quad \text{----- (2)}$$

population mean \propto gene frequency

2. If d = +a (complete dominance,

Then, M = a(p-q)+ 2pqa

$$= a(p-q+ 2pq)$$

$$=a [1-q-q+2q-2q^2]$$

$$M = a(1-2q^2) \quad \text{----- (3)}$$

3. If A is fixed, p=1 and q=0 (a won't occur at all)

$$\Rightarrow M =a \quad \text{----- (4)}$$

And if a is fixed then M= -a ----- (5)

4. If a character contains several allele then the equation will be

$$M= \sum a(p - q) + 2 \sum pqd \quad \text{----- (6)}$$

Average Effect

- Parents pass on their genes but not the genotype as it is formed freshly within. Therefore a new value is required referring to Genes.

- So breeding value is associated with the value of genes that are transmitted to The Offspring. This is the average effect in crude or rough sense.
- By definition, **the average effect of a gene is the mean deviation from population. Mean of individuals which receives that Gene from one parent. The other gene from other parents comes at random from the population.** Another way of explaining the average effect is, if we could change A2 Gene into A1 at random in the population, the resulting change of the value is the average effect of the gene substituted. ([Falconer and MacKay, 1996](#)).

Average Effect of Gene Substitution

- If we could change say, A2 gene <----->A1 gene at random in the population and could note the resulting change of value. Then this is called the average effect of the gene's substitution. It is equal to the difference between the average effect of A1 and A2.

Average Effect w.r.t. a and da and d:

- Let the Average Effect of A1 gene = α_1
- If gametes carrying A1 unite at random with other gametes from the population, now the genotype produced from A1A1 will be **p** proportion of **f(A1A1)** of previous population and **q** proportion of **f(A1A2)**. [As, A2 is converted to A1 so, A2A2 is A1A2]
i.e. A1A1 individuals produced are of p proportion and A1A2 in q proportion.
So the mean value of gene A1 = $pa + qd$, resulting change i.e.,

$$\alpha_1 = [pa + qd] - [a(p-q) + 2pqd]$$

$$= pa + qd - pa + qa - 2pqd$$

$$= q(d+a) - 2pqd$$

$$\therefore \alpha_1 = q [a + d(q-p)]$$

Similarly, Average effect of A2 gene (α_2) = $-p[a + d(q-p)]$

Dominance Deviation

- We know that,

$$G = A + D$$

$$\Rightarrow D = G - A$$

Genotypic Value of A1A1 = +a

Population Mean = $a(p-q) + 2pqd$

\therefore Genotypic value as a deviation from population mean (As Breeding value are always expressed as deviation from population)

Genotypic value = $a - [a(p-q) + 2pqd]$

$$= [a - ap + aq - 2pqd]$$

$$= [a - a(1-q) + aq - 2pqd]$$

$$= [a - a + aq + aq - 2pqd]$$

$$= 2q [a - dp]$$

$$\therefore A1A1 = 2q(a-dp)$$

$$A2A2 = -2p(a+qd)$$

$$A1A2 = d-a + 2q(a-dp)$$

Interactive Deviation

$$P = G + E$$

$$= A + D + I + E$$

Inter allelic Interaction or epistasis is due to interaction among more than one locus i.e., when more than 1 locus is involved then there is epistasis (I).

$$G = G_A + G_B + I_{AB}$$

G_A is genotypic value at locus A

G_B is genotypic value at locus B.

Variance

In probability theory and statistics, variance is the expectation of the squared deviation of a random variable from its population mean or sample mean. Variance is a measure of dispersion, meaning it is a measure of how far a set of numbers is spread out from their average value. Variance has a central role in statistics, where some ideas that use it include descriptive statistics, statistical inference, hypothesis testing, goodness of fit, and Monte Carlo sampling. Variance is an important tool in the sciences, where statistical analysis of data is common. The variance is the square of the standard deviation, the second central moment of a distribution, and the covariance of the random variable with itself, and it is often represented by V_A or σ_A^2 .

Variance components:

Components	Symbol	Value
Phenotypic	V_P	Phenotypic Value
Genotypic	V_G	Genotypic Value
Additive	V_A	Breeding Value
Dominance	V_D	Dominant Deviation
Interaction	V_I	Interaction deviation
Environmental	V_E	Environment Deviation

Conclusion

Fisher's concepts of average effects and average excesses are at the core of the quantitative genetics' theory. Their meaning and relationship have regularly been discussed and clarified. Here we develop a generalized set of one locus two-allele orthogonal contrasts for average excesses and average effects, based on the concept of the effective gene content of alleles. The article helps understand the average excesses of alleles for the biallelic case. It has been discussed how average excesses relate to the average effects and to the decomposition of the genetic variance.

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