



Quantitative Genetics and Evolution

KRUNOSLAV BRČIĆ-KOŠTIĆ

Laboratory for Evolutionary Genetics
Department of Molecular Biology
Ruđer Bošković Institute, Zagreb, Croatia
E-mail: brcic@irb.hr

Abstract

Today, evolution is a unifying concept in biology. A century and half ago, Darwin developed the theory of natural selection, and proposed it as the main mechanism of evolution. A quantitative approach to the study of evolution required new theoretical developments in population and quantitative genetics. Here, I review the basic concepts of quantitative genetics necessary to understand microevolutionary change. Natural selection is a consequence of differences in fitness (reproductive success) between individuals in a population. But natural selection is not equal to evolution. In order to achieve evolutionary change, variation in fitness must be heritable, i. e. it must be transmitted by genes from parents to offspring. Besides fitness differences, individuals within a population often differ in many other characters (morphological, physiological and behavioural) which are also genetically transmitted from generation to generation. It is crucial to distinguish the process of selection which operates in an existing generation from the evolutionary change which is visible in the next generation. Most concepts of quantitative genetics centre around variances and covariances, and include the evolutionary potential of a population or heritability (ratio of additive genetic variance and phenotypic variance), the strength of selection on a particular trait (covariance of particular trait and fitness), the total strength of selection (phenotypic variance in fitness) and evolutionary response (phenotypic change in the next generation) which can be predicted by breeder's equation.

HISTORICAL BACKGROUND

On the 24th of November 1859, Charles Darwin published his famous and most influential book *The Origin of Species (1)*. From that point on biology was not the same. In *The Origin of Species* he thoroughly developed the theory of natural selection providing numerous empirical and experimental examples which support natural selection as the mechanism of evolution. Natural selection is a consequence of variation in fitness (reproductive success) between individuals in a population. The existence of variation in fitness is a prerequisite but not sufficient for evolution to occur. Another essential requirement leading to evolutionary change is that fitness as a trait is inherited through genes from parents to offspring. Evolution can be viewed as the change of allele frequencies (classical population genetics), as the change of the mean phenotype and variance in a population (quantitative genetics), and as the rate of allele substitutions in a population (molecular population genetics). The first two aspects concern short-term evolution (microevolution), whereas the latter concerns long-term evolution (macroevolution). In this review I will describe the basic concepts of quantitative genetics required to understand microevolutionary change.

Quantitative genetics was developed as a solution to the debate between two opposing views on evolution and the mechanism of inheritance (2). According to saltationism evolution was viewed as very fast and an abrupt process visible through the change of Mendelian (simple) traits. Mendelian traits are determined by a single gene with large allelic effects on phenotype, and almost no environmental influence. Such phenotypes are qualitative in nature (they are verbally described), and are suitable to standard genetic analysis. In contrast, gradualism assumed that evolutionary change is gradual, and that it is a consequence of selection on quantitative traits. Such traits (body size, antipredator behaviour, fitness components etc.) are expressed as quantities in particular units. At that time, both saltationists and gradualists believed that Mendel's particulate theory of inheritance can be applied only to simple traits. The inheritance of quantitative traits on the other hand, are believed to follow different laws connected with the action of fluids (blending inheritance). In his seminal work Fisher showed that inheritance and variation in quantitative traits can be explained by simultaneous segregation of many Mendelian factors (genes) (3). Consistent with this, quantitative (complex) traits are determined by many genes with very small allelic effects, but with substantial environmental influence on phenotype. Since inheritance and variation in quantitative traits are based on the aggregate action of many loci, they are described by statistical terms (means and variances) without information about the individual effect of any given locus. Phenotypic values for most quantitative traits are normally distributed around a mean, and in theoretical quantitative genetics normality is always assumed. Besides its origin in the field of evolution, the important application of quantitative genetics is primarily in the field of animal and plant breeding which greatly stimulated its development.

Darwin introduced the verbal concepts of evolution, and he noticed that two visible manifestations of evolution are genetic variation and evolutionary change. To describe evolution quantitatively, we must introduce the basic theoretical concepts of quantitative genetics (4, 5, 6) which are incorporated in quantitative genetic equations. From these equations we will understand the relationships between evolutionary change, genetic variation and the process of selection.

CONCEPTS

Genetic basis of quantitative trait

If a quantitative trait is transmitted by genes from parents to offspring, then we expect that parents with higher trait value will give offspring with higher trait value, and vice versa. In contrast, if a trait is not genetically transmitted, then the offspring of the parents with any trait value will have similar (population mean) trait value. The equation which connects the average trait value of particular offspring with the average trait value of their parents (midparent value) is the regression equation

$$Y = (1-h^2)M + h^2X \quad (1)$$

Y is the average phenotypic value of offspring from particular parent pair, X is the average phenotypic value of a parent pair (midparent value), M is the average phenotypic value of parental population (population mean), and h^2 is heritability of a trait (slope of regression line). Heritability is the ratio of additive genetic variance and total phenotypic variance, and its meaning will be fully described later. Phenotypic variances and covariances are essential in quantitative genetics, and before further consideration it is useful to define them. From elementary statistics we know that

$$V_x = \frac{1}{n} \sum_{i=1}^n (x_i - \bar{x})^2 = \bar{x}^2 - (\bar{x})^2$$

$$\text{cov}_{xy} = \frac{1}{n} \sum_{i=1}^n (x_i - \bar{x})(y_i - \bar{y}) = \bar{xy} - (\bar{x})(\bar{y}) \quad (2)$$

where x_i and y_i are the phenotypic values of i -th individual, \bar{x} and \bar{y} are the mean population values for traits x and y , and n is the number of individuals in a population. The variance of a trait x , V_x is a measure of variation in a population, and represents the mean square deviation, or mean square minus square of the mean. The covariance between traits x and y , cov_{xy} is a measure of the linear relationship between two traits, and represents the mean product deviation, or mean product minus product of the means. If variance and covariance are estimated from a population sample, then in the upper formulas instead of $1/n$ we use $1/(n-1)$.

Decomposition of the phenotype

Each individual in a population has its own phenotypic value which can be measured. Phenotypic value can be decomposed into casual components (5, 6). First, the phenotypic value P is the sum of the effects of a genotype and environment. In the simplest case, when there is no covariance between genotype and environment, $P = G + E$, where G is a genotypic value and E is an environmental deviation. Since environmental deviation is random, the mean environmental deviation in a large population is equal to zero, and the mean phenotypic value is equal to the mean genotypic value. Second, the genotypic value of a particular individual (or genotype) G is the sum of different genetic effects. One is transmission of genes between generations, and the other are allele interactions (dominance and epistasis). According to this, we have that $G = A + D + I$, where A is a breeding value (genic value or additive phenotype), D is a dominance deviation, and I is an interaction (epistatic) deviation. Among the components of genotypic value, only the breeding value is essential for evolution since it measures the potential of a particular individual (or genotype) to change the population mean in the next generation.

In order to understand the meaning of breeding value, we will consider a simple genetic model introduced by Fisher (3). It assumes that genotypic value is affected by a single locus with two alleles. In such a situation there is

no effect of epistasis, and contribution of a single locus to genotypic value is $G = A + D$. The genotypic values for three genotypes are A1A1 (a), A1A2 (d) and A2A2 ($-a$), whereas allele frequencies are A1 (p) and A2 (q). Let us assume that the A1 allele increases and A2 allele decreases the trait value. The genotypic value of a heterozygote d reflects the degree of dominance. To clearly distinguish breeding value from genotypic value let us assume that in this particular example the A1 allele is dominant over the A2 allele. This means that both the »good« homozygote (A1A1) and the heterozygote (A1A2) have the same genotypic value equal to a . Before defining the breeding value, we should introduce the concept of the average effect of an allele (Figure 1). Let us assume we perform two crosses. In the first, the male of A1A1 homozygote mates with a random sample of females from a population, whereas in the second, the A1A2 heterozygote mates with a random sample of females from a population. The mean genotypic value in a population before the cross is M , after the homozygotic cross M' , and after the heterozygotic cross M'' . The change of the population mean in the next generation $\Delta M' = M' - M$ is larger than $\Delta M'' = M'' - M$. The reason is obvious because the homozygote always gives a »good« allele (A1) to its progeny, whereas the heterozygote gives a »good« allele (A1) only to half of its progeny. The change in the population mean as a consequence of transmission of an allele from a particular individual (or genotype) is called the average effect of that allele. From the homozygotic cross the average effect of allele A1 is $\alpha_1 = \Delta M'$, whereas the mean average effect of alleles from the heterozygotic cross is $\alpha_{12} = \Delta M''$. The breeding value of the individual (or genotype) A1A1 is $A_{11} = 2\Delta M'$, whereas the breeding value of the individual (or genotype) A1A2 is $A_{12} = 2\Delta M''$. It is twice the average effect of an allele since each individual (or genotype) has two alleles, but gives only one to its progeny.

If we know the average effects of both alleles in the genotype, then the breeding value of this genotype is simply the sum of the average effects of its alleles (5). It is important to note that genotypic value is a constant quantity (for particular environment), whereas the average effect of allele and the breeding value are relative quantities which are dependent on the referent population, i. e. on

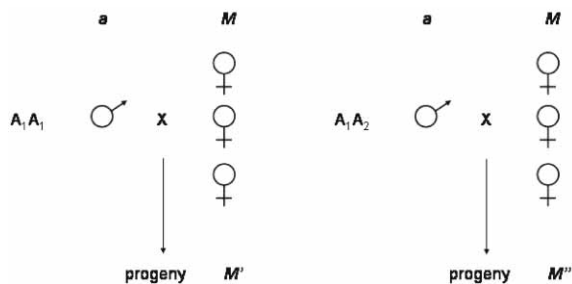


Figure 1. Average effect of allele – Two individuals (genotypes A1A1 and A1A2) with the same genotypic value (a) have different potential to change population mean genotypic value (M). The mean progeny genotypic value of the homozygotic cross is M' and of heterozygotic cross is M'' . For details see the text.

its allele frequency. This means that a particular individual (or genotype) always has the same genotypic value, but has different breeding values in different populations. Also, from the above example it is obvious that in the case of complete dominance, the dominant homozygote and heterozygote have the same genotypic values, but different breeding values. It can be shown that the average effects of alleles A1 and A2 expressed as deviations from the population mean are

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

$$\alpha_2 = -p[a + d(q - p)] \tag{3}$$

The corresponding breeding values of the three genotypes A1A1, A1A2 and A2A2 are

$$A_{11} = 2\alpha_1 = 2q[a + d(q - p)]$$

$$A_{12} = \alpha_1 + \alpha_2 = (q - p)[a + d(q - p)]$$

$$A_{22} = 2\alpha_2 = -2p[a + d(q - p)] \tag{4}$$

In all of the above formulas, there is a common factor (in square brackets) which is called the average effect of allele substitution α . Its meaning is $\alpha = \alpha_1 - \alpha_2 = a + d(q - p)$. After defining the breeding value, we can understand the meaning of the dominance deviation. It is the difference between genotypic value and breeding value $D = G - A$. According to the above model, the dominance deviations of the three genotypes are

$$D_{11} = -2q^2d$$

$$D_{12} = 2pqd$$

$$D_{22} = -2p^2d \tag{5}$$

It is important to note that breeding value and dominance deviation are statistical descriptions, and that both are dependent on allele frequencies. In addition, the breeding value depends on the genotypic values a (homozygote) and d (heterozygote), whereas dominance deviation depends only on d (heterozygote). If there is no interaction (dominance) between alleles, then genotypic value is equal to breeding value.

Partitioning the variance

After decomposition of the phenotype, we can proceed with the study of phenotypic variation and the variation in its components. If we know the phenotypic values of individuals in a population, we can estimate the phenotypic variance V_P . Phenotypic variance is the total variance in a population, and as with phenotypic value, it can be partitioned into casual components (5, 6). A particular theorem of random variables states that variance of the sum is equal to the sum of variances. Since phenotypic value is the sum of its components, it follows that $V_P = V_G + V_E$, where V_G is genotypic variance (total genetic variance) and V_E is environmental variance. Similarly, genotypic variance can be further partitioned, and we have $V_G = V_A + V_D + V_I$. These components are the variance of breeding value V_A , the variance of dominance deviation V_D and the variance of epistatic deviation V_I .

Evolutionary significance lies with the variance of breeding value V_A , and it is called the additive genetic variance. Additive genetic variance is part of the phenotypic variance caused by transmission of genes to the next generation. According to the above model, in the absence of epistasis, we have $V_G = V_A + V_D$. It can be shown that additive genetic variance and dominance variance are equal to

$$V_A = 2pq[a + d(q-p)]^2 = 2pq\alpha^2$$

$$V_D = (2pqd)^2 \quad (6)$$

Both variances are dependent on $2pq$ which represents the equilibrium heterozygosity, and is a measure of genetic variation in classical population genetics. Additive variance depends on both genotypic values (homozygotes and heterozygotes), whereas dominance variance depends only on the genotypic value of heterozygotes.

Additive genetic variance is often expressed as heritability, or the ratio of additive genetic variance and total phenotypic variance

$$h^2 = \frac{V_A}{V_P} \quad (7)$$

Heritability represents a proportion of total phenotypic variance attributable to the transmission of genes from parents to offspring. It is a measure of the evolutionary potential of a population. The reason for this lies in the fact that genes are inherited between generations, whereas gene interactions are not. Gene interactions are properties of genotypes which are *de novo* formed in each generation. Heritability is sometimes called narrow sense heritability to distinguish it from the so called broad sense heritability (degree of genetic determination of a trait) which is the ratio of genotypic variance and phenotypic variance, $H^2 = V_G/V_P$

Breeder's equation

As we mentioned earlier, two essential requirements for evolutionary change to occur are the presence of genetic variation in a population and the action of evolutionary force, i. e. natural selection or genetic drift. We will here consider Darwinian evolution by natural selection. More precisely, we will deal with a particular type of natural selection called directional selection (Figure 2). Directional selection operates on fitness itself and its components (life history traits), as well as on other quantitative traits which are (in a particular environment) positively correlated with fitness. Under the term fitness

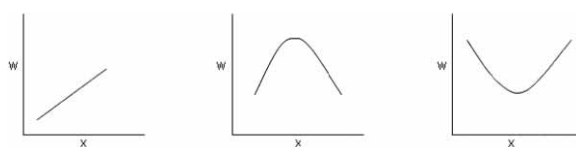


Figure 2. Relationship between trait and fitness reflects the type of natural selection – On the left, there is a linear relationship between trait and fitness (directional selection), in the middle (stabilizing selection) and on the right (disruptive selection) the relationship between trait and fitness is nonlinear (quadratic).

we assume standardized fitness which is called relative fitness. One type of directional selection is artificial selection where the breeder wants to increase (or decrease) the population mean of a particular quantitative trait. To achieve this, the breeder in each generation selects individuals with high (or low) trait value as parents for the next generation. The final consequence of directional selection is fixation of the »best« allele of the locus, and the stable equilibrium allele frequency is $p = 1$ and $q = 0$ (or $p = 0$ and $q = 1$) (7). At the level of change of allele frequency the general selection equation is

$$\Delta p = \frac{pq[p(w_{11} - w_{12}) + q(w_{12} - w_{22})]}{\bar{w}} \quad (8)$$

This equation describes the unit change of allele frequency Δp (between two successive generations) due to selection. The w_{11} , w_{12} and w_{22} are the fitnesses of A1A1, A1A2 and A2A2 genotypes respectively, whereas \bar{w} is the mean fitness of a population. Two important inferences can be drawn from this equation. First, it is visible that selection is based on fitness differences between individuals (genotypes), and second, that evolutionary change is faster when genetic variation in a population is larger, i. e. when p and q tend to have intermediate values.

To derive an analogous equation which shows the unit change of mean phenotype (between two successive generations) in a population due to selection, we must go back to the regression equation. In its original sense, it relates the mean phenotype of particular offspring with the mean phenotype of their parents (midparent value). It can also relate the mean phenotype of all individuals in the offspring generation (all offspring of all parents) and the mean phenotype of all parents (8, 9). Now we have

$$\bar{Y}_{t+1} = (1 - h^2)\bar{Y}_t + h^2\bar{X}_t \quad (9)$$

where \bar{Y}_{t+1} is the mean phenotype of offspring generation, \bar{Y}_t is the mean phenotype of parent generation (all individuals) and \bar{X}_t is the mean phenotype of the individuals selected as parents. To obtain the breeder's equation in its recognizable form, the upper equation must be rearranged

$$\bar{Y}_{t+1} - \bar{Y}_t = h^2(\bar{X}_t - \bar{Y}_t)$$

$$\bar{Y}_{t+1} - \bar{Y}_t = h^2(\bar{X}_t - \bar{Y}_t) \quad (10)$$

$$R = h^2S$$

In the breeder's equation, S is the strength of selection called selection differential which is the difference between the mean phenotype of selected individuals (parents) and the mean phenotype of the population before selection (all individuals) (5, 6). Heritability h^2 is the genetic variation attributable to the additive effects of genes. Finally, R is the evolutionary change called the response of the population to selection, or evolutionary response. It represents the difference between the mean phenotype of offspring of the selected parents and the mean phenotype of the population before selection (5, 6). The above description gives us one meaning of the selec-

tion differential. It does not tell us anything about the relation of a particular trait and fitness. It is intuitive for artificial selection (truncation selection) when individuals are selected if their phenotypic value is equal or higher than the determined value (truncation point). It is also intuitive for strong natural selection which acts at the level of viability, i. e. when the population experiences a high mortality rate due to environmental factors. In this scenario, the selection differential can be estimated as the difference between the mean phenotype of survivors and the mean phenotype of all individuals (before selection). In most real situations natural selection is not so strong, and is manifested through the action of both viability and fertility. When differences in fertility are more important for fitness, the above meaning of selection differential is not so intuitive although it is correct. For such a scenario, we will apply a different definition for selection differential, and will arrive at a simple and intuitive expression which relates a particular trait with fitness.

Fundamental theorem of natural selection

Let us assume that selection on a trait x operates due to differences in fertility. Since the contribution to the next generation will vary among individuals, the difference between the phenotypic value of a particular individual and the population mean must be weighted by the fitness of this individual. Then, the selection differential is defined as

$$S_x = \frac{\sum_{i=1}^n w_i (x_i - \bar{x})}{n} \tag{11}$$

where w_i is the fitness of i -th individual, x_i is the phenotypic value of i -th individual, \bar{x} is the mean phenotypic value of a population, and n is the number of individuals in a population (5). The upper expression can be rearranged in the following way

$$S_x = \frac{\sum_{i=1}^n w_i x_i}{n} - \frac{\sum_{i=1}^n w_i \bar{x}}{n} = \frac{\sum_{i=1}^n w_i x_i}{n} - \bar{x} \frac{\sum_{i=1}^n w_i}{n} \tag{12}$$

$$S_x = \overline{wx} - (\bar{w})(\bar{x}) = \text{cov}_{wx}$$

It implies that selection differential operating on a trait x is equal to the phenotypic covariance between trait x and fitness (10, 11, 12). This is intuitive and logical conclusion since the primary target for natural selection are fitness differences. It is important to note that both meanings of selection differential are mathematically equivalent (13), and that they only refer to different points of view. The strength of selection is sometimes expressed as the intensity of selection which is the standardized selection differential scaled by phenotypic standard deviation (5, 7) or by phenotypic variance (9). Selection intensity is useful for comparing the strength of selection between different traits.

Since the primary target of selection is fitness, it is important to describe the selection differential for fitness it-

self, and the rate of change in population mean fitness. In order to define selection differential for fitness, we can apply the same logic. We have

$$S_w = \frac{\sum_{i=1}^n w_i (w_i - \bar{w})}{n} = \frac{\sum_{i=1}^n w_i^2}{n} - \frac{\sum_{i=1}^n w_i \bar{w}}{n}$$

$$S_w = \frac{\sum_{i=1}^n w_i^2}{n} - \bar{w} \frac{\sum_{i=1}^n w_i}{n} = \overline{w^2} - (\bar{w})^2 \tag{13}$$

$$S_w = V_{Pw}$$

The selection differential for fitness is equal to the phenotypic variance of fitness in a population. It is also known as the opportunity for selection (14). To express the change of mean fitness between two successive generations as a result of natural selection, we will apply the breeder's equation to fitness as a trait (5). We have therefore that

$$R_w = h_w^2 S_w = h_w^2 V_{Pw}$$

$$R_w = V_{Aw} \tag{14}$$

This expression is called the fundamental theorem of natural selection, and was discovered by Fisher (4). The change of mean fitness in a population due to natural selection between two successive generations is equal to the additive genetic variance of fitness in previous generation. Fisher's original statement was slightly different and somewhat obscure (4).

Multivariate evolution

The breeder's equation concerns selection of a single trait. In reality there are many traits which are under natural selection. Some of these traits are correlated. One can distinguish genetic correlation (correlation between breeding values) from phenotypic correlation (correlation between phenotypic values). There are two causes of genetic correlations. The first and most common cause is pleiotropy which means that the same locus determines two (or more) traits. The second is linkage disequilibrium which is a consequence of selection for particular allelic combinations of two (or more) loci which affect different traits. If two traits (x and y) are genetically correlated and natural selection acts on trait x , we expect two consequences. One is a direct evolutionary response on a trait x , and the second is an indirect (correlated) evolutionary response on trait y . The selection differential of a particular trait measures the net effect of selection caused by different factors (direct and indirect). An important question is how to distinguish the direct strength of selection on a particular trait from indirect (correlated) strength of selection on the same trait. Based on Pearson's regression theory, Lande and Arnold showed that the partial regression coefficient of fitness on any trait value is a measure of the strength of direct selection on this trait. This measure is called the selection gradient, and is designated as β (15). Avoiding details, we will just summarize the most important equations concerning multivariate evolution, and their meanings (6, 7, 8, 15).

First, we will write the breeder's equation on a single trait emphasizing that heritability is the ratio of additive variance and phenotypic variance

$$R = V_A V_P^{-1} S \quad (15)$$

The multivariate analogue of the breeder's equation can be written in matrix algebra as

$$\begin{bmatrix} R_x \\ R_y \end{bmatrix} = \begin{bmatrix} V_{Ax} & \text{cov}_{Axy} \\ \text{cov}_{Axy} & V_{Ay} \end{bmatrix} \begin{bmatrix} V_{Px} & \text{cov}_{Pxy} \\ \text{cov}_{Pxy} & V_{Py} \end{bmatrix}^{-1} \begin{bmatrix} S_x \\ S_y \end{bmatrix} \quad (16)$$

The left side term is called the vector of selection responses, and is designated as **R**. On the right side, the first term is the matrix of genetic variances and covariances, or **G** matrix; the second is the inverse of the matrix of phenotypic variances and covariances, or **P**⁻¹ matrix; and third is the vector of selection differentials, or **S**. Equation (16) can be written as

$$\mathbf{R} = \mathbf{G} \mathbf{P}^{-1} \mathbf{S} \quad (17)$$

Conveniently the product of the inverse of the **P** matrix (**P**⁻¹) and **S** is called the vector of selection gradients, and is designated as **β**. According to this, the multivariate selection equation is often written as

$$\mathbf{R} = \mathbf{G} \boldsymbol{\beta} \quad (18)$$

If the covariance term in the **G** matrix is equal to zero, then the two traits evolve independently and evolution of each trait can be described by the single trait breeder's equation (Figure 3). The multivariate breeder's equation for two traits can be written by using the ordinary algebra as

$$\begin{aligned} R_x &= V_{Ax} \beta_x + \text{cov}_{Axy} \beta_y \\ R_y &= V_{Ay} \beta_y + \text{cov}_{Axy} \beta_x \end{aligned} \quad (19)$$

The selection gradient **β** for a particular trait is

$$\begin{aligned} \beta_x &= \frac{V_{Py} S_x - \text{cov}_{Pxy} S_y}{V_{Px} V_{Py} - \text{cov}_{Pxy}^2} \\ \beta_y &= \frac{V_{Px} S_y - \text{cov}_{Pxy} S_x}{V_{Px} V_{Py} - \text{cov}_{Pxy}^2} \end{aligned} \quad (20)$$

We must again emphasize that selection differential *S* measures the net effect of selection (all factors, i. e. direct and indirect), whereas the selection gradient **β** measures only the direct effect of selection on particular trait. In order to estimate **β**, we need to have estimates of selection differentials (*S*_x and *S*_y), phenotypic variances (*V*_{Px} and *V*_{Py}), and phenotypic covariance *cov*_{Pxy}. Natural selection can be visualized by individual fitness surface (selection surface) which represents the relationship between phenotypic values and corresponding individual fitness (16). Hypothetical individual fitness surface for two traits is presented in Figure 4. The empirical shape of the fitness surface, i. e. local average slopes (linear or directional selection) and local average curvatures (nonlinear selection – stabilizing or disruptive selection) can be studied by the multiple regression approach in order to estimate partial regression coefficients (selection gradients) (16).

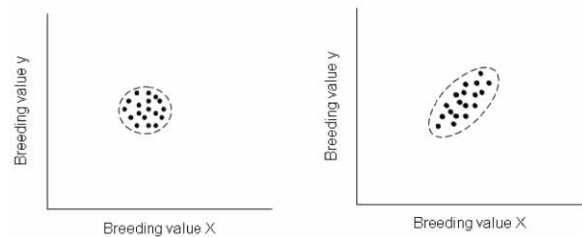


Figure 3. Relationship between breeding values of trait *x* and *y* – On the left, there is no covariance between two breeding values (each trait evolves independently); on the right, there is positive covariance between two breeding values (correlated evolution). Spots represents hypothetical individual breeding values of traits *x* and *y*.

EVOLUTION IN THE REAL WORLD

In order to predict the evolutionary response according to breeder's equation, one should have an estimate of heritability. After many generations under directional selection, heritability is no longer constant since selection erodes the additive variance and the heritability of a trait. For a certain number of generations (15–20 generations for a typical artificial selection experiment) there is no change in heritability, and the response is relatively constant (short-term response) (5). For further prediction of the response (long-term response), a new estimate of heritability is required. For the prediction of a multivariate evolutionary response it is necessary to have estimates of genetic variances and covariances, as well as selection gradients. Empirical results from selection of a single trait imply that the breeder's equation correctly predicts the response to selection. In contrast, the responses to selection on multiple traits are less consistent with the current theory. A possible explanation for this is that the multivariate model assumes multivariate normality which is often biologically inconsistent (9). Here we will briefly consider some examples of evolution in natural populations, as well as experimental evolution driven by artificial selection on quantitative traits.

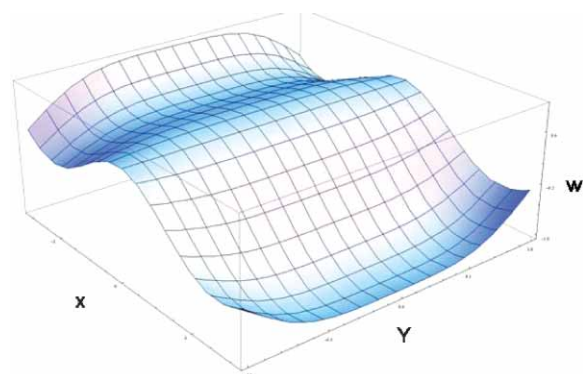


Figure 4. Hypothetical individual fitness surface – The individual fitness value in a population is a function of the phenotypic values for traits *x* and *y*.

Evolution by natural selection

Lande and Arnold studied the effects of natural selection on morphological characters in the pentatomid bug *Euschistus variolarius*. They collected 94 bugs after a storm (39 survived and 55 died), and measured four morphological traits on all bugs (15). From this data they estimated phenotypic variances and covariances according to equation 2. The selection differential for a particular trait was estimated as the difference between the mean trait value of surviving bugs and the mean trait value of all bugs, whereas the selection gradient was estimated according to equation 20. They found no significant change in thorax width as indicated by selection differential. In contrast, the selection gradient indicated strong direct selection for increased thorax width. The thorax width is highly positively correlated with another trait, wing length. The selection gradient for wing length indicated strong direct selection for decreased wing length. Therefore, the absence of significant change in thorax width represents the net effect of a strong direct increase in thorax width and strong indirect (correlated) decrease in thorax width due to strong direct selection for decreased wing length. They also noticed that scutellum length decreased significantly as indicated by the selection differential while the selection gradient was not significant. From this, it can be concluded that a significant selection differential on scutellum length is a consequence of the correlated selection on scutellum length due to direct selection on other traits (thorax width and/or wing length).

Grant and Grant studied the evolution of morphological traits in Darwin's medium ground finch *Geospiza fortis* from the Galapagos islands (17, 18). Several species of Galapagos finches have been the research subject of Charles Darwin, and inspired him in the development of his ideas about evolutionary change. The normal diet of Galapagos finches includes various types of seeds, from large hard seeds to small soft seeds. The type of available seeds is determined by the amount of rainfall. The ability of a bird to handle a particular type of seed depends on the characteristics of its bill. Two periods, 1976 – 1977 and 1984 – 1986, were characterized by a severe drought, and the Grants measured the survival of *G. fortis* over these periods. During the first period only 15% of birds survived, and the survivors were larger birds. During the second period 32% of birds survived, and the surviving birds were slightly smaller. The selection differential for body weight during the first period was larger than the selection gradient, although both tended to increase body weight. The difference between them represents the strength of correlated selection since body weight is positively correlated with several other morphological traits which were directly selected to increase their phenotypic values. Interesting behaviour during the first period showed selection for bill width. The selection differential tended to increase the bill width whereas the selection gradient tended to decrease it. This can be explained by correlated selection which tended to increase bill width due to direct selection on other morphological traits (bill depth, wing length and weight). During the second period the

selection differential for bill length was weak and negative (statistically not significant) whereas the selection gradient was strong and positive. The selection differential for bill length can be explained by correlated selection on other traits which had small and weak selection gradients. The Grants also predicted the evolutionary responses for several traits (equation 16 or 19), and compared them with the observed responses (difference between the mean phenotypic value of the progeny of surviving birds and the mean phenotypic value before selection). The observed selection responses were in a good agreement with theoretical predictions, especially for the first period (1976 – 1977) when natural selection was stronger (18).

Evolution by artificial selection

Finally, I will mention two examples of experimental phenotypic evolution driven by artificial selection. One is the artificial evolution of behaviour in silver fox, a rare naturally occurring variety of red fox *Vulpes vulpes*, and the other is artificial evolution of oil content in the maize *Zea mays*. Selection experiments with silver foxes started in 1959, and were led by the Russian geneticist Dmitry K. Belyaev. In addition to its scientific purpose, the experiment was also motivated by the Russian fur industry which preferred tame animals for routine handling. Therefore the target for selection was tameness, a behavioral trait which is normally present in juvenile animals. In the original (wild) population, the vast majority of foxes showed fear and/or aggression towards humans, whereas a small fraction was more or less tolerant to humans. These tolerant animals were selected as parents of the next generation. The fox behaviour was quantified according to the degree of tameness, and in each generation animals with higher degree of tameness were further selected. The response to selection was very strong in the early generations, and after several decades of selection the end product was a unique population of domesticated foxes which are fundamentally different in many aspects from their wild counterparts. They are devoted, affectionate and capable of forming strong social bonds with people. In addition to large changes in behaviour, the domesticated foxes evolved many new characteristics, i. e. piebald coat colour, rolled tails, floppy ears and changes in reproductive cycle accompanied by changes in hormone levels. It follows that direct selection on a behavioural trait caused correlated selection responses to various morphological, physiological and life history traits (19, 20). The fur industry was not satisfied with these results since the fur of domesticated foxes was in many aspects different from the fur of wild silver foxes, and was commercially useless. Most important were the scientific implications of the results. This experiment showed that the process of domestication could be much faster than was previously thought with obvious implications to the domestication of dogs.

The last example includes the selection of a trait of agronomic importance, the oil content in maize kernels. This experiment started in 1896, and is the longest selec-

tion experiment ever performed. Geneticists from the University of Illinois continuously selected maize to change its oil content in both directions, i. e. to increase and to decrease the oil level in kernels. The base population had about 5% oil in the kernel, and after more than a century of selection the high oil-producing line has about 20% of oil in kernels, whereas the low oil-producing line has almost none (21). Subsequent analysis has shown that the number of quantitative trait loci (QTLs) which can account for half of the divergence between high and low oil producing lines is about 50 (22). All detected QTLs show a small effect, and the rest (still undetected QTLs) should have even smaller effects. This picture places the oil content in a typical quantitative trait characterized by many genes with small allelic effects. Consistent with this is the observed continuous response to artificial selection.

CONCLUSION

Today, more than 150 years after the release of *The Origin of Species*, evolutionary theory is a unifying force for all biology. Following Darwin, new theoretical developments led to the quantitative genetic approach in the study of evolution. Most concepts of quantitative genetics centre around variances and covariances. According to the breeder's equation, the response to selection (evolutionary change) is equal to the product of heritability (genetic variation) and selection differential (strength of selection). Heritability represents the evolutionary potential of a population. Selection differential for a particular trait is equal to the phenotypic covariance of this trait and fitness. Selection differential for fitness itself measures total opportunity for selection, and is equal to the phenotypic variance of fitness. The change of mean fitness in a population between two successive generations due to natural selection is equal to the additive genetic variance of fitness in the previous generation. This statement is called Fisher's fundamental theorem of natural selection. The multivariate breeder's equation shows that the vector of selection responses is equal to the product of the genetic variance – covariance matrix (genetic variation) and vector of selection gradients (strength of selection). From the vector of selection gradients one can distinguish direct selection on a particular trait from indirect (correlated) selection on the same trait.

The mechanisms of evolution described by quantitative genetics is just one aspect of studying evolution. Other questions in evolution are studied by different approaches (paleontology, ecology, developmental biology,

bioinformatics etc.). Simultaneous achievements in all of these approaches paint a more complete picture of reality.

Acknowledgments: I thank Ignacija Vlašić and Vedran Dunjko for the help in preparation of figures. This work is supported by the Croatian Ministry of Science, Education and Sport (grant 098-0982913-2867).

REFERENCES

1. DARWIN C 1859 On the Origin of Species by Means of Natural Selection, or the Preservation of Favoured Races in the Struggle for Life. Murray, London.
2. PROVINE WB 1971 The Origins of Theoretical Population Genetics. University of Chicago Press, Chicago.
3. FISHER RA 1918 The correlation between relatives on the supposition of mendelian inheritance. *Trans Royal Soc Edinburgh* 52: 399–433
4. FISHER R A 1930 The Genetical Theory of Natural Selection. Clarendon Press, Oxford.
5. FALCONER D S, MACKAY T F C 1996 Introduction to Quantitative Genetics. Longman, Essex.
6. LYNCH M, WALSH B 1998 Genetics and Analysis of Quantitative Traits. Sinauer Associates Inc, Sunderland, MA.
7. HALLIBURTON R 2004 Introduction to Population Genetics. Pearson Education Inc.
8. ROFF D A 1997 Evolutionary Quantitative Genetics. Chapman & Hall, New York.
9. ROFF D A 2006 Evolutionary quantitative genetics. In: Fox C W, Wolf J B (ed) Evolutionary Genetics: Concepts and Case Studies. Oxford University Press, Oxford, p 267
10. ROBERTSON A 1966 A mathematical model of the culling process in dairy cattle. *Anim Prod* 8: 95–108
11. PRICE G 1970 Selection and covariance. *Nature* 227: 520–521
12. PRICE G 1972 Extension of covariance selection mathematics. *Ann Hum Genet* 35: 485–490
13. WADE M J 2006 Natural selection In: Fox C W, Wolf J B (ed) Evolutionary Genetics: Concepts and Case Studies. Oxford University Press, Oxford, p 49
14. CROW J F 1958 Some possibilities for measuring selection intensities in man. *Hum Biol* 30: 1–13
15. LANDE R, ARNOLD S J 1983 The measurement of selection on correlated characters. *Evolution* 37: 1210–1226
16. BRODIE E D III, MOORE A J, JANZEN F J 1995 Visualizing and quantifying natural selection. *Trends Ecol Evol* 10: 313–318
17. GRANT B R, GRANT P R 1989 Evolutionary Dynamics of a Natural Population. University of Chicago Press, Chicago.
18. GRANT P R, GRANT B R 1995 Predicting microevolutionary responses to directional selection on heritable variation. *Evolution* 49: 241–251
19. BELYAEV D K 1979 Destabilizing selection as a factor in domestication. *J Hered* 70: 301–308
20. TRUT L N 1999 Early canid domestication: The farm-fox experiment. *Amer Scient* 87: 160–169
21. HILL W G 2005 A century of corn selection. *Science* 307: 683–684
22. LAURIE C C, CHASALOW SD, LEDEAUX JR, MCCAROLL R, BUSH D, HAUGE B, LAI C, CLARK D, ROCHEFORD T R, DUDLEY J W 2004 The genetic architecture of response to long-term artificial selection for oil concentration in the maize kernel. *Genetics* 168: 2141–2155