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Influence of maternal effects on heritability of wing length in *Drosophila melanogaster*.

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Heritability in wider sense is a useful parameter if we are interested in the genotype and environmental influences in formation of phenotypic differences between individuals of a population. In the paper of Stani_ and Marinkovi_ (1999), it has been shown that heritability of wing length in wider sense is 0.26 in the female sex and 0.83 in the male sex of *Drosophila melanogaster* individuals. If we try to answer the question which part of phenotypic differences between parents could be expected in descendants, or among relatives (additive, dominant or epistatic), we need to count heritability in narrower sense. Geneticists who are occupied by quantitative genetic analysis have developed different methods for counting heritability coefficients, and each of them requires a specific experimental design. One of them is the regression method.

Previous investigations the show that body size is positively correlated with mating success (Taylor, 1987; Partridge *et al.*, 1987; Stamenkovi_-Radak, 1992; Stani_ and Marinkovi_, 1998). It has been established that acoustic stimuli play a very important role in reproductive behavior of *Drosophila* (Spieth, 1952; Von Schilcher, 1976). Bastoc (1956), performing comparison of sex behavior of male of *yellow* mutant and wild type, has found that reproductive stimulation of females to a remarkable level attains the count of vibrations of wings of males. In courtship time, *yellow* males vibrate by wings with lower intensity and through greater intervals than males of wild type. That leads to significant decrease of reproductive ability of mutants. Ewing (1977) reveals analogue facts on a line characterizing the level of reduction of the wing plate.

In numerous papers, morphometric analysis of *Drosophila melanogaster* individuals has been performed to understand sexual and reproductive selection better. This form of selection occurs when one phenotypic aspect of the organism varies, influencing mating success and inducing competition within the same sex (Wilkinson, 1987). In natural habitats the wing size was larger in mated *D. melanogaster* males in comparison with those that did not mate with females (Taylor and Keki_, 1988). Also, body size dependent assortative mating was demonstrated in laboratory lines. This success in mating of males with longer wings could be explained by stronger acoustic stimulation, greater competition ability, and the fact that larger males live longer. Taking into consideration all of this, we decided to perform quantitative analysis of wing length in *Drosophila melanogaster* using regression method for a determination of the heritability coefficient of this character.

The experiment was performed with individuals of Canton-S wild type and *sepia (se)* individuals of a mutant line of *Drosophila melanogaster* purchased from the Umea Stock Center. The flies have been maintained on standard nutritious medium for Drosophilidae (cornmeal, sugar, agar, yeast) in thermostat, under optimal conditions, at 25°C and humidity of 60%. Since development has been conducted under optimal conditions, new individuals of wild type were hatched from eggs 12-15 day after laying eggs, while mutant line individuals were not hatched until the 20th day.

Initially, we have formed groups of close relatives (parents - descendants) in both lines, and after that proceeded with morphometric analysis of all individuals (P and F₁ generation) according to the method of Partridge (1987). The wing of each individual was taken and placed on a microscopic glass slide in a drop of 70% ethanol, and using the ocular with a measuring scale, the distance from the cross of the frontal transversal and longitudinal vein, to the spot where longitudinal vein joins the distal edge of the wing was determined. The wing length was expressed in measurement units on an ocular scale, where 38 units = 1mm. On the basis of covariances of individuals, the values of h_n^2 were determined separately for individuals of the male and female sex in both lines ($h_n^2 = S_a^2/S_f^2$). On the basis of comparisons of obtained results our conclusions are presented in the text to follow.

By calculating the regression coefficient of one or both parents on descendants of male or female sex, similarity between close relatives was determined; in that way heritability in narrower sense for wing length in individuals of wild type, as well as in the mutant sepia line, was determined. The method of controlled crossing to obtain the data on which h^2 was determined has allowed us to have information about maternal effect in *Drosophila*.

The results we obtained show (Tables 1a and 1b) that the additive genetic component contributes to a greater similarity between parents and female progeny in mutant *sepia* line, while in individuals of wild type that component of genetic variability is more expressed between parents and male progeny. On the basis of this, we assume that rather nonadditive effects could explain phenotypic variance among individuals of wild type *Drosophila*, i.e. by mechanisms marked as epistasis and dominance (dom-rec. interactions). As can be seen, the mutation process clearly influences the components of phenotypic variability of quantitative traits, which is in agreement with the original hypothesis of Sewal Wright (Wright, 1932).

In regard to the importance of genetic variance components, the results indicate the following:

1. In wild type *Drosophila* - additive between parents and descendants of male sex; dominance and epistasis between parents and descendants of female sex;
2. In individuals of the *se* line - additive between parents and descendants of female sex;

dominance and epistasis between parents and descendants of male sex with maternal effect.

Regression coefficients, and in agreement with them the heritability coefficient in narrower sense, are completely different in individuals of the mutant line, in relation to wild type of *Drosophila*. Variability of wing length in individuals of male sex of wild type *Drosophila* is conditioned by additive action of genes ($f - 0.13$; $m - 0.29$). Opposite to these data, in individuals of the analyzed mutant line, part of the additive action of genes

Table 1a. Regression coefficients (b) and heritability for wing length in "*sepia*" line

b	I	II	b	h^2	Heritabilnost
MD	-0.2344	-0.2742	-0.2543	0.5086	MD = 50.86%
MS	-0.0195	-0.0666	-0.0431	0.0862	MS = 8.62%
FD	-0.0170	-0.1092	-0.0631	0.1262	FD = 12.62%
FS	-0.0908	-0.0923	-0.0007	0.0014	FS = 0.14%
PD	-0.1349	-0.3275	-0.2312	0.2312	PD = 23.12%
PS	0.0687	-0.1396	-0.0709	0.0709	PS = 7.09%

Table 1b. Regression coefficients (b) and heritability for wing length in Canton-S *Drosophila melanogaster*

B	I	II	b	h^2	Heritabilnost
MD	0.1596	-0.0893	0.0351	0.0703	MD = 7.03%
MS	0.0104	0.0125	0.0114	0.0229	MS = 2.29%
FD	0.0706	0.1992	0.1349	0.2698	FD = 26.98%
FS	0.0943	0.2020	0.1481	0.2963	FS = 29.63%
PD	0.1757	0.0011	0.0884	0.0884	PD = 8.84%
PS	0.0912	0.1781	0.1346	0.1346	PS = 13.46%

MD: mother-daughters; MS: mother-sons; FD: father-daughters; FS: father-sons; PD: parents-daughters ; PS: parents-sons

is remarkably higher in female sex (0.23; 0.50) than in male sex (0.07; 0.08). For variability of wing length of *se* line males, interactions between allelic and nonallelic genes are more important than cumulative action of those genes.

These differences in heredity of wing length we may be explained by cytoplasmic-genetic form of maternal effect. The highest heredity was established in pairs of mothers-female progeny of the *se* line; that could be explained by influence of additive action of nuclear genes, additive action of cytoplasmic (mitochondrial) genes, and interactions between nuclear and cytoplasmic genes.

It means in the analyzed mutant line that the maternal effect is especially expressed between "mothers" and female progeny, while in the wild type of *Drosophila* the influence of maternal extra chromosomal effects is more expressed in female progeny. Based on that fact we generally conclude that:

- mutations of genes determining qualitative traits influence also variability of quite different quantitative traits;
- mutations appear as a factor that causes a conversion of epistatic interaction in additive genetic variance, that is in accordance with the assertion of some former findings (Wade and Goodnight, 1998).

This mechanism exists in relatively small populations, and it accelerates the process of genetic differentiation, which is one of the first steps in the process of speciation. Our results suggest the presentation of total genetic variance in the form of the next equation: $V_G = V_A + V_D + V_C + V_{AC} + V_{DC}$, where the V_A and V_D are additive and dominant components of genetic variance of genes from nucleus, V_C is variance of additive effects of cytoplasmic genes, and V_{AC} and V_{DC} are variances of interactions between genes of nucleus and cytoplasm (Lynch and Walsh, 1998). Also, the regression coefficient between fathers and their progeny is modified because of genetic covariance between direct and maternal effects, since the similarity between "father" and his descendants is influenced by genes from the nucleus, as well as by genes that have origin from his mother and such maternal effects. Cited facts should be taken into account when differences in heritability between laboratory and field estimations are considered (Weigensberg and Roff, 1996), as well as the influence of additive genetic variance on adaptive evolution of natural populations.

KEY WORDS: *D. melanogaster*, *sepia*, heritability, wing length, regression, maternal effects.

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