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Spectrum of visible mutations isolated out of wild populations of *Drosophila melanogaster* in 2000.

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One of the tasks of experimental genetics of populations is estimation of genetic diversity in natural populations. Within the frames of continuing traditional studies on monitoring of wild populations (Golubovsky *et al.*, 1974; Weisman *et al.*, 1995; Weisman and Zakharov, 1997), the present work is devoted to analysis of representative samples of flies from geographically remote populations of *Drosophila melanogaster*, as well as to analysis and identification of visible mutations.

Drosophila melanogaster from nature were collected in two regions of Russia: from Altai, populations Askat and Belokurikha; and from Republic of Udmurtia, populations Izhevsk, Karambai, and Pyuchas. The samples consisted of 160-941 individuals. For isolation of iso-female strains and their subsequent analysis of families, 50 fertilized in nature females were randomly selected.

Mutations with similar phenotypes from a single population and from different populations were tested for allelism. Linkage groups for each of the isolated mutations were determined by means of marked chromosomes 1, 2, and 3 laboratory strains, *C(1)DX,ywf; B w^a/Y*, and *Cy/L;D/Sb*, respectively. Identification of mutations was performed by using the strains of *Drosophila melanogaster* with the known genotype from the foundation of Laboratory of Genetics of Populations of the Institute of Cytology and Genetics SB RAS. Each of the isolated mutations is maintained in culture as a homozygous strain or as a strain with the balanced chromosome.

Males and females of *Drosophila melanogaster* caught from nature were mostly of wild type phenotype. However, in Izhevsk population, we have observed high concentration of flies with slight disruptions of abdomen segmentation (14% females, 2% males). The females with the similar phenotype were found within the limits of 1% in two other populations from Republic of Udmurtia. With the frequency of 1%, the males were found with brown eyes in populations from Askat and Karambai.

In addition to aberrations found in flies that were caught directly from nature, by familial analysis of F₁ and F₂ in 5 populations, we have determined some other inherited modifications of a phenotype (see Table 1). In all populations studied, the share of females, which offspring carry visible recessive mutations, is rather high, up to 20-40%. Studying of the offspring of relatively small samples of flies enabled us to isolate from 6 to 10 different types of visible mutations, some of them multiply occurring in the population. The great majority of isolated mutations were recessive, except the single dominant mutation, *i.e.*, brown eyes from Karambai. The population from Izhevsk is characterized not only by the highest concentration of visible mutations, but also by their most broad spectrum.

Note that geographically remote populations, as a rule, possess by sets of mutations of different genes. Only a single mutation of the chromosome 3, with eye color alteration (dark-red eyes), was found both in Izhevsk and Pyuchas. Some aberrations were found with particularly high frequency, namely, disruption of abdomen segmentation in Askat and Karambai; as well as mutations of the chromosome 3, reduction of bristles and rough eyes in Izhevsk and mutation *ebony* in Belokurikha.

In some families, several mutations were isolated. For example, in the family _35 from Askat population, *forked*- and *white*- chromosomes were found simultaneously; whereas in Belokurikha - *ebony* and *brown* (family B7); and in Pyuchas population, mutation 'bright eyes' and 'rudimental wings' (family P24). In the offspring of a single female from Karambai population (family _3), mutations of two genes that determine brown and red matted colour of eyes were found. In the families from Izhevsk population, two or more inherited alterations were found simultaneously: *stabbloid* and *detached* (family I47); *strow* and 'wing cuttings' (family I50); 'rough eyes', 'reduction of bristles', and 'wing cuttings' (family I40). Mutations 'rough eyes' and 'reduction of bristles' from Izhevsk population, in all 9 cases were found in the same chromosome 3.

Note, in all five populations studied, the most frequently occurring mutations were those modifying the eye colour. It is necessary to note distribution in all populations of inherited disruptions, with different extent of penetration, of abdomen segmentation. However, genetic analysis of this

Table 1. Visible mutations isolated in iso-female strains.

Chromosome	Mutation	Mutation phenotype	Number of strains	Population, region
1	<i>white</i>	ruby eyes	2	Askat, Altai
	<i>forked</i>	forked bristles	1	
	<i>yellow'</i>	yellow body	1	Belokurikha, Altai
	<i>singed</i>	singed bristles	1	
	<i>prune</i>	red matted eyes	1	Izhevsk, Republic of Udmurtia
	not identified	wing cuttings	3	
	<i>visiculated</i>	crumpled wings	2	Karambai, Republic of Udmurtia
2	<i>brown</i>	brown eyes	4	Belokurikha, Altai
	<i>net</i>	additional vein	1	
	<i>straw (?)</i>	golden hairs	3	Izhevsk, Republic of Udmurtia
	<i>lightoid</i>	yellow-pink eyes	2	
	<i>black</i>	black body	1	Karambai, Republic of Udmurtia
	not identified	red matted eyes	1	
	not identified	rough eyes	2	Pyuchas, Republic of Udmurtia
	not identified	short bristles	2	
3	<i>ebony</i>	dark body	1	Askat, Altai
	not identified	bright eyes	1	
	<i>ebony</i>	dark body	5	Belokurikha, Altai
	not identified	reduction of bristles	9	
	not identified	rough eyes	9	Izhevsk, Republic of Udmurtia
	<i>stabbloid</i>	short bristles	3	
	<i>detached (?)</i>	incomplete posterior crossvein	2	
	not identified	dark-red eyes	2	
	not identified	ruby eyes	3	Pyuchas, Republic of Udmurtia
	not identified	dark-red eyes	1	
	not identified	bright eyes	3	
	not identified	spread rudimental wings	3	
4	<i>cubitus interruptus</i>	disturbed vein L ₄	1	Askat, Altai
Not localized	not identified	disruption of abdomen segmentation	8	Askat, Altai
	not identified	disruption of abdomen segmentation	6	Belokurikha, Altai
	not identified	disruption of abdomen segmentation	2	Izhevsk, Republic of Udmurtia
	not identified	disruption of abdomen segmentation	13	Karambai, Republic of Udmurtia
	not identified	brown eyes	2	
	not identified	short bristles	1	
	not identified	disruption of abdomen segmentation	4	

aberration is not performed yet. It could be supposed that relationship between our results and observations made by R.L. Berg, who has noticed since 1968 sharp increase in concentration of abnormalities similar to mutation *abnormal abdomen* (Berg, 1972a,b; Golubovsky *et al.*, 1974).

Alleles of some known genes isolated from nature were shown to have some peculiarities of penetration. For instance, the mutants *ebony* from Belokurikha and Askat have more dark colored body than that of flies of laboratory strain *ebony*. In addition to this observation, in *ebony* homozygotes from Askat, the stigma in larvae were uncolored. The mutants *black* from Karambai were also more light by color than that of “homonyms” from the strain maintained in fund collection.

The novel recessive allele of the gene *net* (*net-B27*) from population Belokurikha has a homozygous penetration in a form of additional vein fragment at the 3rd dorsal wing compartment near by middle of the anal longitudinal vein. This allele has incomplete penetration and varying expression. In heterozygote with the standard *net* allele (Lindsley and Zimm, 1992), the allele *net-27B* is dominant.

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