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An extraordinarily high frequency of a particular morphological aberration in *Drosophila mercatorum* in different regions of Russia. The fashion on mutation?

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In early March 2000, while examining synantropic *Drosophila* just collected in a flat in Novosibirsk city I noticed that many of the *Drosophila mercatorum* flies carried the same morphological aberration of a wing. The pattern of this aberration is as follows: the structure in the shape of a short longitudinal vein occurs in the distal part of a wing, in wing cell N4 between L3 and L4 longitudinal veins. Under maximum expression the length of that aberrant vein equals the span between the ends of L3 and L4 veins. Under minimum expression it looks like a dim spot equal in diameter to the thickness of a normal vein. The aberrant vein is not connected to natural veins of the wing (it is not a kind of their spur) and is an independent structure in the distal part of cell N4 (see Figure 1). Individual expression of that aberration ranges from perfect symmetry with maximum

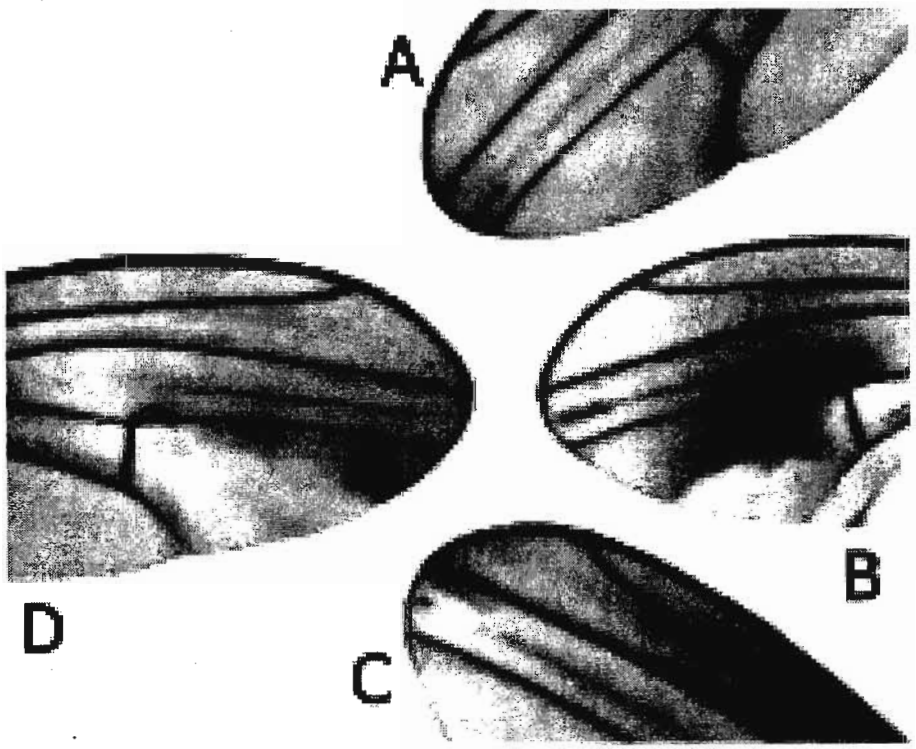

Figure 1. Pictured fenA - abnormal vein between the distal ends of L3 and L4; A, fenA strong; B, fenA moderate; C, fenA weak; D, normal.

expression (on both wings) to asymmetry with minimum expression (on one wing). Asymmetry with varying expression is often found. We labelled this aberration as fenA. In our examined collection the fraction of flies carrying fenA is extraordinarily high, about 30%.

This fact could be easily explained by the effect of inbreeding since under severe Siberian winter conditions synantropic *Drosophila* form isolated micropopulations with living space limited to the size of human dwellings, flats or houses. This explanation, however, required verification. In order to prove that hypothesis we obtained another collection of *Drosophila* in the other city district. Examination of that second collection yielded a 23% frequency of fenA in it. The hypothesis of inbreeding in micropopulation started to play out. Fortunately, summer and fall of 1999 provided us with new rich collections of *D. mercatorum* from the other regions of Russia. First was a collection of samples fixed in ethanol, which was obtained in Askat village of Altai Republic (southern part of Western Siberia, 500 km south of Novosibirsk), the other was a box population collected by undergraduate K. Gunbin in Karambai village, Udmurt Republic (the European part of Russia, 2000 km west of Novosibirsk). Examination of these materials demonstrated high frequency of fenA in both collections, 24% and 43%, respectively.

Table 1. Frequency of *fenA* in collections of *D. mercatorum* from different Russian populations (as of late March 2000).

Localities of collection in the period from summer 1999 to spring 2000 Area and site of collection	Flies examined	*fenA* Number	*fenA* %
Western Siberia, Novosibirsk, population 1	264	81	30.7
Western Siberia, Novosibirsk, population 2	52	12	23.1
South of Western Siberia, Altai Republic, Askat village	176	42	23.9
Eastern Europe, Udmurt Republic, Karambai vilage	97	42	43.3

Thus, fenA is evidently represented with extraordinarily high frequency in all four examined collections of *D. mercatorum* of 1999 and 2000 obtained in three regions of Russia rather distant from each other. The hypothesis of inbreeding therefore became absolutely unlikely. Apparently, we dealt with the phenomenon of perfectly diverse nature. The phenomenon we desrcibed very much resembles what is called in Russian-language literature "moda na mutatsiju" - fashion on mutation or mutation fashion. That population genetics phenomenon of fashion on mutation has always been an object of steadfast attention in our laboratory but its exploration was limited to a single species, *Drosophila melanogaster*.

The term "fashion on mutation" was introduced into scientific language by Raissa Berg. This term designates simultaneous rise in frequencies of particular alleles or phenotypical aberrations in geographically isolated population. Direct transfer of genetic information between such populations and in such short period of time is absolutely impossible (if only the simultaneous nature of that phenomenon does not restrain one from speaking about any "period of time" at all) (Berg, 1972, 1982; Golubovsky *et al.*, 1974). The phenomenon of "fashion on mutation" in *Drosophila melanogaster* populations was well studied in USSR. Fashions on mutations yellow body (*y*) (Golubovsky *et al.*, 1974; Zakharov and Golubovsky, 1985), singed bristles (*sn*) (Zakharov, 1984), and abnormal abdomen (Berg, 1972, 1982) were in different years detected and studied in this species. As any kind of fashion, that on mutation is transient: concentration of "fashionable" mutation gradually grows achieving its peak and then goes down to its normal value. Judging from extremely high concentrations of fenA in studied populations, the peak of above-mentioned fashion is currently in progress.

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A simultaneous appearance of an identical morphological aberration in three *Drosophila* species. A fashion for the same mutation in several species?

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"Fashion on mutation" is a term for a simultaneous rise in frequencies of particular alleles or phenotypical aberrations in different loci of a natural habitat of a species (geographically isolated populations). Fashions on mutations *singed* bristles, *abnormal abdomen* and others were described in the populations of *Drosophila melanogaster* in the former USSR (Golubovsky *et al.*, 1974; Berg, 1972, 1982). Rise in frequencies of particular alleles is often associated with spontaneous increases of mutability level in populations. Time span of fashion on mutation is usually several years. During this period a gradual elevation of the character concentration is followed by its peak and gradual decrease to its normal value. This phenomenon occurs simultaneously in all populations of the species sometimes covering vast areas. In my opinion, the phenomenon of fashions on mutations is little known due to the fact that it is absolutely beyond explanation within the paradigms of classical population genetics. However, this phenomenon is rather common for *Drosophila* populations.

Table 1. *FenA* occurrence in *Drosophila* genus flies collected in 1999 and 2000 Russia (data provided as of late March 2000).

Species	Flies studied	Flies with *fenA*
D. mercatorum	589	177
D. sp. 99-19-01 (IvAn)	10	2
D. immigrans	102	2
D. melanogaster	2690	0
D. busckii	53	0
D. histrio	193	0
D. transversa	74	0
D. funebris	94	0

Recently a wing aberration, which we designated as fenA was found to occur with incredibly high frequency (more than 20%) in collections obtained from *Drosophila mercatorum* populations from different parts of Russia in years 1999 and early 2000 (Ivannikov and Zakharov, 2000). At the same time we discovered an absolutely identical morphological aberration in another *Drosophila* species - D.sp.99-19-01(IvAn). Although specific identity or independent taxonomic status of this species has not yet been established, one can assert with perfect certainty that within the *Drosophila* subgenus it belongs to the *repleta* group and within this group to the *hydei* subgroup (Ivannikov, 2000). Two out of ten individuals of D.sp.99-19-01(IvAn) in our posession (*i.e.*, 20%) carry asymmetrically located (on left wing in both cases) and weakly expressed but anyway easily identified fenA. This unexpected coincidence encouraged us to screen all species of *Drosophila* gathered in Russia during the last and current year and represented in our collection by no less than 10 flies for the occurrence of fenA. As a result, fenA character was discovered in one more species, *D. immigrans*. Two out of 102 flies of that species collected in Askat village (Altai Republic), *i.e.*, about 2%, carried fenA. In both cases in *D. immigrans* fenA is expressed asymmetrically (both on the right wing) with strong expression in the first case and weak in the second one. It is also worth noting that although the frequency of fenA in *D. immigrans* is by an order of magnitude smaller than in two above-mentioned species of the *repleta* group, the 2% value is