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A burst of spontaneous mutations in isofemale lines of Drosophila melanogaster from Senegal.

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Introduction

With more than a century of use Drosophila melanogaster has proven to be a good model for genetic studies (Green, 2010). In addition to the ease of handling the species in laboratory, it is particularly interesting because of its ability to produce spontaneous mutants (Lindsley and Zimm, 1992). These mutants have played a fundamental role in understanding genetic mechanisms and most of them are now characterized at the molecular level and the function of the affected genes is known. Therefore, recovering classical mutant phenotypes is today of little value as they are not going to improve our knowledge much. However, recovering these phenotypes might be relevant for indicating genetic instability in natural populations. Indeed a large proportion of natural mutations is due to mobile element activity, and this mutagenic activity is associated with stress (Capy et al., 2000) or possibly with the admixture of divergent populations as in the P-M system (Kidwell et al., 1977).

From the biogeographical distribution of species closely related to it, D. melanogaster probably...
originated in Africa and then invaded the world as a human commensal (Lachaise et al., 1988). Genetic divergence is now observed between the cosmopolitan populations outside of Africa and their African counterparts (Begun and Aquadro, 1993; Kauer et al., 2002; Baudry et al., 2004). Genetic conflicts are thus possible when secondary contacts occur between African and cosmopolitan populations. In this context it is particularly interesting to observe the presence of several mutants in isofemale lines from Senegal in Africa. Several phenotypes affecting wings or eyes have been observed in these lines. Two of them we isolated and characterize here.

Materials and Methods

Isofemale lines were established from flies collected at Salemata (SM) in Senegal in 2008. Since then some lines have gone extinct, but 17 SM lines are still in culture. Two other stocks have been used for outcrossing: \( vg^{null}/CyO \) (from Institut Jacques Monod, Paris) and \( y\ cn\ bw\ sp \) (from Kyoto Drosophila Genetic Resource Center). The \( vg^{null} \) allele is a full deletion of the coding sequence of the \( vestigial \) gene generated by excision of the P element of the \( vg^{21} \) allele (Bernard et al., 2003). Crosses were made in vials at room temperature with usual fly medium. 5-10 virgin females were outcrossed to males of the appropriate other stock.

Results

Wingless mutants were isolated from the line SM15. The phenotype was typical of \( vestigial \) (\( vg \)) and apparently similar to \( vg^{1} \). Virgin females were crossed to males of \( vg^{null}/CyO \). Two phenotypes were observed in the progeny: \( [vg] \) and \( [Cy] \) indicating that the mutation found in SM15 line affects the \( vestigial \) gene and is recessive. The new allele is denoted \( vg^{SM15} \).

Mutants with bright red eyes were isolated from the line SM23. The mutant was crossed to wildtype flies from another SM line. The progeny were completely wildtype, indicating that the mutant was recessive. The mutant was also crossed with a \( y\ cn\ bw\ sp \) stock that was available at the laboratory. The progeny all had the \( [cn] \) phenotype indicating that the mutation found in the line SM23 affected the \( cinnabar \) gene. We denoted the new allele \( cn^{SM23} \).

Discussion

We isolated two mutants and identified the affected genes as \( vestigial \) and \( cinnabar \) through crossing. These mutants have very obvious phenotype and are viable and fertile. They are then easily detected and consequently many similar alleles are already known. Indeed, FlyBase lists 390 classical alleles for \( vestigial \) and 225 for \( cinnabar \). Other phenotypes, mostly involving position of wings, were observed and are currently under isolation. More careful observation of these lines is necessary to reveal more discrete phenotypes.

These mutations with large phenotypic effect are expected to be at very low frequency in natural populations due to strong selection against them. It is therefore unlikely that so many mutations were sampled by chance in isofemale lines. Thus, the presence of large numbers of mutants in the Salemata lines suggests a genetic basis at the origin of the mutational process. This genetic basis is probably the insertion of mobile elements at different loci. Mutagenic activity by mobile elements can increase under environmental stress (Capy et al., 2000) or when a genomic conflict arises by the admixture of two diverging populations. Senegal is at the north-western edge of the Afrotropical realm and is an important step on the commercial route with Europe. It is consequently very likely that this area is a contact zone between native African populations and cosmopolitan ones that differ in their mobile element composition. Under these conditions, numerous insertional mutations would be present in the field and so be collected. However, it is also possible that the mutation process has also been exacerbated in the laboratory by increasing homozygosity in the isofemale lines.

The identification of mutated genes is the first step necessary before characterization of the mutations at the molecular level. Further studies are thus necessary to identify the true nature of these mutations and to validate a possible genomic conflict following population admixture.
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Phenology or resources limit Drosophila local biodiversity in a southern Asian continental subtropical forest.

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Introduction

Biodiversity is typically greater in the tropics and semitropics than in temperate areas. The question then is, how is this greater biodiversity achieved? High diversity would result if there were more resources in low latitudes than in high with a small number of species using each resource. High diversity would also result from greater spatial or temporal (i.e., phenological) variability in species identities. This mechanism also suggests that local species numbers will be small. The proportional sampling model, however, predicts high local diversity (Cornell and Lawton, 1992). This is because the proportional model holds that interspecific competition is relatively unimportant. The number of species coexisting locally is then a simple proportion of the number of species in the regional pool.

As an initial step towards examining this question in Drosophila, we sampled flies in a species rich semitropical forest in continental southern China. This genus is species rich with 2874 species world-wide (Wheeler, 1981, 1986) and provides a very diverse but phylogenetically restricted fauna. The genus is better known, particularly in the tropics, than most dipteran taxa. We looked at continental eastern Asia because there are no major barriers to north-south movement of faunas at this longitude. The existing faunas are, therefore, unlikely to be affected by restricted post-glacial colonization. Major barriers do exist at other longitudes. The Himalayas and Caucuses, together with deserts, limit exchange in western Asia. The subtropical African faunas are separated from Europe by the double barrier of the Sahara desert and the Mediterranean sea. And in the Americas the relatively recent rise of the Isthmus of Panama is a similar complicating factor. Diverse drosophilid faunas are, however, found in tropical mainland Asia. In an area of only 1130 ha, our main study site in southern China has over 115 drosophilid species. Of these, 63 are currently in the genus Drosophila (Toda and Peng, 1989; Peng et al., 1990a, 1990b). This contrasts markedly with 54 Drosophila species recorded for the entire British Isles. We, therefore, concentrated our study on the Drosophila faunas of two locations near Guangzhou, Guangdong Province, China. Local biodiversity was remarkably low. This completely contradicts the proportional sampling model. We are now investigating the contribution of spatial, temporal, and resource variability in species richness to the high biodiversity of continental southern Asia.