

for *D. suzukii* and *D. nasuta*, are fundamental to understanding the dynamics of biological invasions.

Acknowledgments: We thank *Reserva Ecológica do IBGE, Instituto Federal de Brasília (Campus Planaltina)* and *Universidade de Brasília* for logistical support. This research was funded by the Conselho Federal de Desenvolvimento Científico e Tecnológico (CNPq) and Coordenação para Aperfeiçoamento de Pessoal de Ensino Superior (CAPES/PROEX/PPG-Ecologia).

References: Asplen, M.K., G. Anfora, A. Biondi, D.S. Choi, D. Chu, K.M. Daane, P. Gilbert, A.P. Gutierrez, K.A. Hoelmer, W.D. Hutchison, R. Isaacs, Z.L. Jiang, Z. Kárpáti, M.T. Kimura, M. Pascual, C.R. Philips, C. Plantamps, L. Ponti, G. Véték, H. Vogt, V.M. Walton, Y. Yu, L. Zappalà, and N. Desneux 2015, *J. Pest Sci.* 88: 469–494; Benito, N.P., M.L. Silva, and R.S.S. Santos 2016, *Pesqui. Agropecu Bras.* 51: 571–578; Brake, I., and G. Bächli 2008, *World catalogue of insects 9: drosophilidae (Diptera)*. Stenstrup, Appolo Books; David, J.R., and L. Tsacas 1981, *C.R. Soc. Biogéog.* 57: 11–26; Deprá, M., J.L. Poppe, H.J. Schmitz, D.C. De Toni, and V.L. Valente 2014, *J. Pest Sci.* 87: 379–383; Döge, J.S., H.O. Valadão, and R. Tidon 2015, *Biol. Invasions* 8: 2461–2474; Eiten, G., 1972, *Bot. Rev.* 38: 205–341; Gilbert, P., M. Hill, M. Pascual, C. Plantamp, J.S. Terblanche, A. Yassin, and C.M. Sgrò 2016, *Biol. Invasions* 18: 1089–1103; Kitagawa, O., K. Wakahama, Y. Fuyama, Y. Shimada, E. Takanashi, M. Hatsumi, M. Uwabo, and Y. Mita 1982, *JPN. J. Genet.* 57: 113–141; McKinney, M.L., and J.L. Lockwood 1999, *Trends Ecol. Evol.* 14: 450–453; Oliveira, O.S., and R.J. Marquis 2002, *The cerrados of Brazil: ecology and natural history of a neotropical savanna*. New York, Columbia University Press; Paula, M.A., P.H.S. Lopes, and R. Tidon 2014, *Dros. Inf. Serv.* 97: 113–115; Roque, F., R.A. Mata, and R. Tidon 2013, *Biodivers. Conserv.* 22: 657–672; Roque, F., L. Mencarini, B.F.D. Leão, M.D. Delgado, and R. Tidon 2016, *Dros. Inf. Serv.* 99: 48–49; Roque, F., S.C.F. Oliveira, and R. Tidon 2011, *Dros. Inf. Serv.* 94: 140–141; Tidon, R., 2006, *Biol. J. Linn. Soc.* 87: 233–247; Tidon, R., M.S. Gottschalk, H.J. Schmitz, M.B. Martins 2016, *Drosophilidae in Catálogo Taxonômico da Fauna do Brasil. PNUD*. Available: <http://fauna.jbrj.gov.br/fauna/faunadobrasil/183241> (Accessed 02 November 2016); Tidon, R., D.F. Leite, and B.F.D. Leão 2003, *Biol. Conserv.* 112: 299–305; Tochen, S., J.M. Woltz, D.T. Dalton, J.C. Lee, N.G. Wiman, and V.M. Walton 2016, *J. App. Entomol.* 140: 47–57; Vilela, C.R., 1999, *Dros. Inf. Serv.* 82: 37–39; Vilela, C.R., and B. Goñi 2015, *Rev. Bras. Entomol.* 59: 346–350; Walsh, D.B., M.P. Bolda, R.E. Goodhue, A.J. Dreves, J. Lee, D.J. Bruck, V.M. Walton, S.D. O’Neal, and F.G. Zalom 2011, *J. Integ. Pest Man.* 106: 289–295.



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

Cossard, Raynald^a, and Stéphane R. Prigent^b. ^aInstitut de Biologie Intégrative de la Cellule (I2BC) UMR 9198 CEA/CNRS/UPSUD, Gif-sur-Yvette, France; ^bInstitut

Systématique Evolution Biodiversité (ISYEB) UMR 7205 CNRS-MNHN-UPMC-EPHE, PSL University, Paris, France. E-mail: stephane.prigent@mnhn.fr

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.

Acknowledgments: We would like to thank Michel Veuille (ISYEB), Alexis Lalouette (Institut Jacques Monod), and the *Drosophila* Genetic Resource Center (Kyoto) for providing the stocks used in this study, and Andrew Davis (Max Planck Institute of Chemical Ecology, Jena) for improving the English.

References: Baudry, E., B. Viginier, and M. Veuille 2004, *Molecular Biology and Evolution* 21: 1482–1491; Begun, D.J., and C.F. Aquadro 1993, *Nature* 365: 548–550; Bernard, F., A. Lalouette, M. Gullaud, A.Y. Jeantet, R. Cossard, A. Zider, J.F. Ferveur, and J. Silber 2003, *Developmental Biology* 260: 391–403; Capy, P., G. Gasperi, C. Biéumont, and C. Bazin 2000, *Heredity* 85: 101–106; Green, M.M., 2010, *Genetics* 184: 3–7; Kauer, M., B. Zangerl, D. Dieringer, and C. Schlötterer 2002, *Genetics* 160: 247–256; Kidwell, M.G., J.F. Kidwell, and J.A. Sved 1977, *Genetics* 86: 813–833; Lachaise, D., M.L. Cariou, J.R. David, and F. Lemeunier 1988, *Evolutionary Biology* 22: 159–222; Lindsley, D.L., and G.G. Zimm 1992, *The Genome of Drosophila melanogaster*. Academic Press, San Diego. 133pp.



Phenology or resources limit *Drosophila* local biodiversity in a southern Asian continental subtropical forest.

Davis, A.J.^a, T-X. Peng^b, and X. Li^b. ^aBiological Sciences, University of Leeds, Leeds

LS2 9JT UK (current address: Max Planck Institute for Chemical Ecology, Hans-Knoell-Strasse 8, 07745 Jena, Germany); ^bGuangdong Institute of Entomology, Guangzhou 510260, Guangdong, PR China.

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 Caucasus, 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.