

PublisherInfo		
PublisherName	:	BioMed Central
PublisherLocation	:	London
PublisherImprintName	:	BioMed Central

Fly SNPs

ArticleInfo		
ArticleID	:	4257
ArticleDOI	:	10.1186/gb-spotlight-20011121-01
ArticleCitationID	:	spotlight-20011121-01
ArticleSequenceNumber	:	328
ArticleCategory	:	Research news
ArticleFirstPage	:	1
ArticleLastPage	:	2
ArticleHistory	:	RegistrationDate : 2001-11-21 OnlineDate : 2001-11-21
ArticleCopyright	:	BioMed Central Ltd2001
ArticleGrants	:	
ArticleContext	:	130592211

Jonathan B Weitzman

Email: jonathanweitzman@hotmail.com

The availability of a dense map of sequence polymorphisms is invaluable to speeding-up the mapping of mutations linked to phenotypes or disease. In the Advanced Online Publication issue of *Nature Genetics*, Jurg Berger and colleagues from *Research Institute of Molecular Pathology* in Vienna report the identification of 7,223 single nucleotide polymorphisms (SNPs) and 1,392 insertions/deletions (indels) in laboratory strains of *Drosophila* (DOI:10.1038/ng773). They used a directed strategy involving the amplification and sequencing of short sequences from two strains, and found a sequence polymorphism every 150-200 bp and many constitute restriction site polymorphisms (RFLP-SNPs). The SNP map of the *Drosophila* genome generated by Berger *et al.* will allow rapid and accurate mapping of many fly mutations.

References

1. A rapid method to map mutations in *Drosophila*.
2. *Nature Genetics*, [<http://genetics.nature.com>]
3. *Research Institute of Molecular Pathology* , [<http://www.imp.univie.ac.at>]