(*9.4*) **Giddings, L. V. and W. J. Etges,** Office of Technology Assessment, Congress of the United States, Washington, D.C., and University of Arizona, Tucson. *Absence of mtDNA variation among*

karyotypically differentiated populations of Drosophila robusta.—Clines of inversion frequencies in natural populations of *D. robusta* along an elevational transect in the Great Smoky Mountains, Tennessee, are considered in the context of a selection-migration balance. Concerted changes in karyotypic frequencies over a 34-yr period (Etges, Evolution **38:** 675–688, 1984) and few or no changes over 2- to 3-yr periods in all populations suggest selection may be a dominant force in shaping these clines. Estimates of gene flow along the cline are required to measure selection intensities at varying elevations; thus, mtDNA polymorphisms, indicative of long-term dispersal of female cytoplasm, were surveyed in three populations along this transect from 1000′ (seven isolines), 2000′ (four isolines) and 4500′ (seven isolines) in elevation (total transect length = 34 km). Multiple restriction enzyme digests from single flies were assayed, and complete data for 18 restriction sites from six enzymes (BEII, BNI, *Eco*RI, *Nco*I, *Nru*I, *Xba*I) and partial data for 15 sites from seven enzymes (*Ava*II, *Bcl*I, *Cla*I, *Nde*I, *Pvu*II, *Sac*I, *Xmn*I) revealed no evidence of mtDNA restriction site variation within or between these 18 isolines and one from Forest Park, St. Louis, Missouri. This lack of variation stands in marked contrast to the results of mtDNA polymorphism studies in Hawaiian Drosophila. These results are compatible with hypotheses that invoke considerable gene flow between these populations or a remarkable dearth of mtDNA variation in *D. robusta*. The present data are insufficient to distinguish between the two. Further study is anticipated.

(*9.5*) **Hale, L. R. and R. S. Singh,** McMaster University, Hamilton, Ontario, Canada. *Mitochondrial DNA variation in natural populations of* Drosophila melanogaster *and* D. simulans.—Mitochondrial DNA (mtDNA) restriction polymorphism was studied in 18 isofemale lines of *Drosophila melanogaster* and 11 lines of *D. simulans*, representing the species' cosmopolitan distribution. Ten restriction enzymes were used, of which four (*Hae*III, *Ava*II, *Taq*I, *Mbo*I) showed substantial variation. Size variants were also found. All size variations mapped, as expected, to the A + T-rich region of the mtDNA. *D. melanogaster* showed a clear demarcation between populations from the western hemisphere (North and South America) and the eastern hemisphere (Europe, Africa and Asia). For two enzymes (*Hae*III and *Taq*I) the frequencies of two main restriction types were substantially different between the two hemispheres. The second survey involved a study of several lines from four populations (France, West Africa, Ontario, Texas) which represent two independent temperate/tropical transects. Results from *Hae*III, *Taq*I and *Mbo*I patterns confirmed the findings from the initial survey. In addition, *Mbo*I showed a fairly distinct differentiation along the North/South axis in both hemispheres. *D. simulans* showed relatively little polymorphism. Variants from the dominant patterns are few and isolated. The exception is a line from the Seychelles Islands, in which the mtDNA restriction patterns are similar to that of *D. seychellia*. On the other hand, *D. mauritiana* mtDNA restriction patterns are more similar to the dominant form found in *D. simulans*. Our results show that geographically distant populations of *D. melanogaster* are quite distinct which suggests much less gene flow between them than can be inferred from the gene enzyme data. (Supported by a grant to R.S.S. from NSERC.)

(*9.6*) **Rand, D. M. and R. G. Harrison,** Yale University, New Haven, Connecticut. *Transmission genetics of mitochondrial DNA in crickets.*—Analysis of mtDNA restriction fragment patterns in the field crickets *Gryllus pennsylvanicus* and *G. firmus* has shown that approximately 12% of field-collected individuals are heteroplasmic, *i.e.*, possess mtDNA of two or more size classes (Harrison *et al.*, Science. In press, 1985). We have identified in these species a series of discrete mtDNA size classes which differ by ~300 base pairs. To study the transmission of mtDNA we collected field-inseminated females and allowed them to lay eggs in the laboratory. Total DNA was prepared from each of the females, and heteroplasmic females were identified by the fragment pattern generated from *Eco*RI digests. We then extracted total DNA from a series of individual offspring from each heteroplasmic female. Equal quantities of mother and offspring DNA were digested separately with *Eco*RI and run on horizontal agarose gels. Southern blots were hybridized with a ^{32}P-labeled mtDNA probe. We quantified the proportions of the mtDNA size classes in the mothers and offspring by scanning autoradiographs with a laser densitometer. The heteroplasmic state is clearly maintained through one generation, although there is some drift in the relative proportions of the different mitochondrial genotypes. From the variance among offspring in proportions of mtDNA size classes we can estimate the effective size of the mtDNA population and the number of generations required to lead to fixation of one of the size classes.—Given the maternal inheritance of mtDNA, the establishment of