Steiner, W.W.M., W.E. Johnson and H.L. Carson. University of Hawaii, Honolulu and Western Michigan University, Kalamazoo, Michigan. Molecular differentiation in D. grimshawi.

Drosophila grimshawi is currently known from all major islands of the Hawaiian chain with the exception of the island of Hawaii. Here, it's homosequential relative D. pullipes replaces it. In the Maui complex of islands (West and East Maui connected by a narrow, low-elevation land bridge; Molokai and Lanai) D. grimshawi occurs generally above 300 meters altitude.

Carson and Sato (1969) found populations of Drosophila grimshawi differentiated on the Maui complex with respect to the 4th chromosome. Although Molokai and Lanai populations were similar, subpopulations of D. grimshawi on East and West Maui appeared genetically distinct. As a result of these findings a preliminary electrophoretic survey was undertaken to determine the extent of genic differentiation (techniques to be published elsewhere). The results are presented in Table 1, which also includes data for the Hawaii representative D. pullipes. The abbreviation N designates the number of flies examined for each locus.

The expectation of gene pool differentiation with regard to different gene frequencies is met at the Esterase-2 (ES-2), Leucine Aminopeptidase-2 (LAP-2), Octanol dehydrogenase (ODH),

Table 1. Allelic frequencies in Drosophila grimshawi and D. pullipes.

Species:		D. grimshawi								D. pullipes	
Collection No.:		R11,S15,Q80		R8		S16		Q20			
Locus	Allele	W. Maui	N	E. Maui	N	Molokai	N	Lanai	N	Hawaii	N
ES-2	.97		19	0.050	20		72		6		3
	.98			0.050							
	.99	0.210		0.025		0.028					
	1.00	0.158		0.775		0.375		0.750		1.000	
	1.01	0.026		0.050		0.069					
	1.02	0.553				0.361					
	1.03	0.053		0.050		0.132		0.250			
	1.04					0.028					
	1.05					0.007					
LAP-2	.96	0.021	24	0.025	20	0.019	77		6	0.166	3
	.98					0.006					
	1.00	0.458		0.950		0.442		1.000		0.333	
	1.02	0.521				0.526					
	1.04			0.025		0.006				0.500	
ODH	.90	0.368	19				65		6		3
	1.00	0.632				0.885		1.000		1.000	
	1.10					0.115					
MDH-1	.94		23	0.350	20	0.006	83		6		3
	1.00	0.328		0.625		0.982		1.000		1.000	
	1.06	0.652		0.025		0.012					
PGM	1.00	0.800	20			0.972	72	0.500	6		
	1.04	0.200				0.028		0.500			
GOT-1	96		16		13	0.012	83				3
	1.00	0.969		1.000		0.982				1.000	
	1.04	0.031				0.006					
GOT-2	.96	0.028	18		13		81				3
	1.00	0.916		1.000		0.988				1.000	
	1.04	0.056				0.012					

(Table continues)

Locus	Allele	W. Maui	N	E. Maui	N	Molokai	N	Lanai	N	Hawaii	N
IDH	.96		15		20	0.012	81		3		3
	1.00	0.967		1.000		0.988		1.000		1.000	
	1.04	0.033									
HK-1	1.00	1.000	8	1.000	2	0.971	52			1.000	3
	1.02					0.029					
ME	.98		21		20	0.008	59		6		3
	.99					0.008					
	1.00	0.952		1.000		0.949		1.000		0.833	
	1.01	0.048				0.034				0.166	
ADH	1.00	0.969	16	0.975	20	0.973	75			1.000	3
	1.04	0.031		0.025		0.027					
α-GPDH	.90		24	0.050	20		81		6		3
	1.00	0.979		0.950		1.000		1.000		1.000	
	1.10	0.021									

and Malate dehydrogenase-1 (MDH-1) loci. These loci plus Glutamate Oxaloacetate Transaminase-1 (GOT-1), Glutamate Oxaloacetate Transaminase-2 (GOT-2), Isocitrate dehydrogenase (IDH), Hexokinase-1 (HK-1), Malic Enzyme (ME), and alpha-Glycerophosphate dehydrogenase (α-GPDH) display different low frequency alleles between the islands.

Fractionation of the gene pool of D. grimshawi as found by Carson and Sato (1969) is bourne out by these molecular data. In both ES-2 and MDH-1, populations from Molokai, West Maui and East Maui are different from one another. ODH and LAP-2 provide further examples of differences between Molokai and West Maui and East Maui respectfully. It is interesting to note that the Molokai sample displays more alleles per locus than any other population and the extent this reflects sample size should be investigated.

Despite the small sample sizes, the genic similarity between D. pullipes and D. grimshawi is remarkable. The occurrence of the 1.04 allele at the LAP-2 locus suggests a relationship To east Maui or Molokai populations. Deeper invesitigation of the extent of inter- and intra-island differentiation appears warranted and should yield an exemplar of Hawaiian Drosophilid evolution.

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References: Carson, H.L. and J.E. Sato 1969, Evolution 23:493-501.

Fountatou-Vergini, J. Agricultural College of Athens, Greece. Is Drosophila subobscura monogamic?

It is generally considered that adult females of Drosophila subobscura (Col.) mate only once during their lifetime. We have recently collected data indicating that this is not true. As a by-product of another research work we have electrophoretically determined Est-5 genotype of six F_1 progeny separately from each female captured in the wild. These females originated from two different natural populations, from Mt. Parnes in Attica, and from Alikianon village in Crete. Est-5 located near the centromere end of chromosome O (an autosome), is polymorphic (at least six electrophoretically detectable alleles). At least fourteen out of 474 females (= 0.03 ± 0.008) studied from Mt. Parnes were found on qualitative grounds to be digamic (or polygamic), one on the grounds of the number of alleles found in her progeny (exceeding 4) and 13 on their genotypes. In the Cretan population 8 out of 199 females (= 0.04 ± 0.014) studied were found to be digamic (or polygamic), all on the qualitative grounds of the genotypes of their progeny. Since we have studied only one gene and only six individuals from each female progeny the estimate of the frequency of digamic females is the most conservative one. Furthermore, allele frequencies in the populations, sperm stratification, or a nearly complete sperm utilization before the second mating would tend also to underestimate greatly this frequency.