Heed, W.B. University of Arizona, Tucson, Arizona. Distribution extensions and gene arrangements for D. parthenogenetica and D. montana.

Three specimens of D. parthenogenetica were collected July 27 and 28, 1971, by banana traps near highway 15, 4 miles south of the state line of Sonora - Sinaloa, Mexico, in tropical thorn forest along with 456 D. arizonensis, 34 D. mojavensis, 6 D. simulans, and 2 D. aldrichi. The morning collection was better. At 7 A.M. the rel. humidity was 80% and the temp. was 90°F. This represents a northern range extension of almost 900 miles for D. parthenogenetica (from Atlixco, Pueblo). Chromosome 2L, the only polymorphic arm, was fixed for inversion A' which is the more common sequence north of Panama. (Heed and Russell, 1971, Univ. Texas Publ. 7103).

One fertile D. montana female was collected at dusk (7:45 P.M.) under hot windy conditions July 10, 1971, by banana traps at the Radar Collecting Station (9000') on the north slope of the Santa Catalina Mts., Tucson, Arizona, in a Douglas Fir community among 2,429 specimens representing 7 other species and among 15,700 specimens for the 2 week period. This represents a western range extension of approximately 120 miles from Glenwood, N.M. The strain was homozygous and was checked for specific inversions by hybridizing with strain 1218.8d from Cottonwood Canyon, Utah, with which it was also homozygous. Therefore, the montana female was fixed for inversions 4g and 4h, the typical arrangements in Utah, Colorado, and New Mexico (Moorhead, 1954, Univ. Texas Publ. 5422). This record is probably the result of long distance dispersal from the north or west. Only 1 other montana has ever been captured in the Santa Catalina Mts. over a more than 10 year collecting period. (Thanks to M.R. Wheeler for providing the Utah strain.)

Heed, W.B. and S.R. Heed. University of Arizona, Tucson, Arizona. Ecology, weather, and dispersal of Drosophila on an island mountain.

The breeding sites of 75% of the 36 described species of Drosophila inhabiting southern Arizona and the Gulf Coast of Sonora, Mexico, are now known. Fermenting cactus accounts for 37%, rotting fungus for 26%, and slime flux from trees and fermenting bark for 22% of the 27 species. The remaining few were bred from flowers and fruits. The only substrates of any importance in the mountains are the fungi (Hirtodrosophila, macroptera gp., rubrifrons gp., quinaria gp.) and tree fluxes (obscura gp., melanica gp.). However, the second most abundant species in the Santa Catalina Mts., Tucson, is D. hamatofila, which breeds in Opuntia pads on the desert floor, where it is the most abundant form (Heed et al., 1962, DIS). The Basin and Range Province in S. Arizona permits the treatment of its mountains as islands for distribution studies since they are surrounded by deserts and grasslands.

It is proposed that the vast majority of D. hamatofila (and D. longicornis) in the Catalina Mts. are transients transported by air currents from the desert below at 2500 ft. elevation. Table 1 illustrates the sensitivity of these flies to daily weather conditions. Collections were made by banana bait in 5 gallon containers in Douglas Fir communities at elevations of 8500 ft. (Mt. Bigelow) and 9000 ft. (Radar Station). All collections were in the late afternoon until dark. There is an age effect by the bait but it was strongly outweighed by weather. Intense observations were made of moving flies silouetted against the sky over the traps from above on a hill slope with binoculars in the evening of July 10. Flies disturbed from the traps rose 30 to 40 ft. in the air before dispersing (actively or passively ?) in the wind. The "cross-traffic" between the tree tops was noticeable.

1971	pseudoobscura & lowei	hamatofila & longicornis	total flies	location	weather
June 22	26%	73%	4365	Mt. Bigelow	clear, dry
June 24	9%	90%	2919	Radar Station	clear, strong wind from below
July 5	76%	22%	1783	" "	cloudy
July 8	84%	14%	1995	" "	light rain
July 10	28%	70%	2430	" "	clear, warm strong wind from below

The importance of these observations lies in the fact that D. hamatofila and D. longicor-

nis are consistently abundant in early summer mountain collections but they are not part of the permanent breeding populations there. In early July, 10 specimens of the two species were collected from slime fluxes of Douglas Fir where they were actively feeding. The males had active sperm but the females were reproductively very immature. The large majority of the two species in the traps were young individuals. D. longicornis was about 10% of the total of the two species in all collections.

Moravec, J. J.E. Purkyně University, Brno, Czechoslovakia. Variability of the frequency of recombination between cn and vg in different second chromosome subpopulations of D.m. originating from nature.

Twenty different chromosome subpopulations originating from natural population samples, H. B and M, which were normal in viability were tested for recombination frequency by means of crossing with the cn vg/Oregon K strain approximately in the 50th generation. In subpopulations H7, M2 and M8, the recombination frequency was found to be significantly higher, in subpopulations B10 and M3 significantly lower than the standard value (Table 1).

Table 1

Subpopulations	H1	H5	H7	H8	B1	B4	B8	B10
Recombination frequency	9.19	7.28	11.79	7.85	9.61	8.95	8.86	5.73
$\chi^2_{(1)}$	0.52	3.81	15.27	1.29	1.69	.10	.12	17.02
Subpopulations	M2	M3	M4	M8		(standard value)		
Recombination frequency	12.36	6.79	8.37	12.12		8.66		
$\chi^2_{(1)}$	19.08	6.88	.17	15.06				

Approximately in the 70th generation, the recombination tests were repeated with the "high" subpopulation M2 and with the "low" one B10. Thirty different males were studied in each subpopulation. The crosses with cn vg/Oregon K and subsequent measurements of recombination frequency were repeated three times so that the proportion of the genetic background originating from Oregon K rose from 50 per cent in the first cross to 75 and 87.5 per cent in the second and third crosses, respectively. Other $\bar{p}$ values were found than in the 50th generation (Table 2). In the M2 subpopulation, the original high recombination frequency was preserved; it did not substantially change during the three successive crosses. On the other hand, in the B10 subpopulation, higher recombination frequencies were found than in the 50th generation, and the recombination frequencies decreased during the increase of the proportion of Oregon K genome. At the same time, this subpopulation was found to be desintegrated into two groups: in the "low" group comprising 13 original males, the recombination frequency was constant, while in the "high" one (17 original males), the recombination frequency decreased with increasing proportion of the Oregon K genome.

Table 2

Subpopulation	1st cross		2nd cross		3rd cross	
	$\bar{p}$	c.v.	$\bar{p}$	c.v.	$\bar{p}$	c.v.
M2	11.35	19.8	10.68	18.8	11.39	21.1
B10	11.27	35.7	10.38	35.0	10.01	26.9
B10 "low" group	7.29	21.6	6.83	23.2	7.57	18.0
B10 "high" group	14.32	15.0	13.08	15.5	11.86	19.3

These results suggest that (1) genetic factors modifying the recombination frequency can be present in the natural material, (2) these factors can mutate spontaneously during the long-termed cultivation, and (3) additional variability of recombination frequency can be introduced by changing the genetic background.