Entomologique Suisse] 73: 23-47; Wasserman, M., and F. Wasserman 1992, Evol. Biol. 26: 357-381; Wheeler, M.R., 1957, Taxonomic and distributional studies on Nearctic and Neotropical Drosophilidae. University of Texas Publications. Studies in Genetics: 5721: 79-114.



Olfactory response of *Drosophila* flies for different fruits.

Shivanna, N.*, N.B. Vandal, S.L. Kudupali, and S.B. Shetty. Department of Zoology, Karnatak University, Dharwad-580003, India. Email: drnshivanna@rediffmail.com.

The fruit fly, *Drosophila*, is equipped with a sophisticated olfactory sense system that permits it to recognize and discriminate hundreds of discrete odorants. The olfactory response of these odorants is essential for the animal to identify relevant good sources and suitable sites for egg laying. *Drosophila* and related genera occupy a wide variety of habitats including rotting fruit and plant parts in deserts and tropical forests, slime fluxes, fungi, flowers, ferns, and crabs. A major problem in rearing such species is inducing females to oviposit. Different species may show different distribution patterns and seasonal frequencies ranging from a tight nuclear distribution at a food source to a uniform low-density distribution (Carson *et al.*, 1970; Dobzhansky and Pavan, 1950). A variety of behavioral factors are involved in habitat choice, and it is clear that different species rely on different sensory modalities to varying degrees in deciding their direction of movement. The present study was made to study the preference of adults to different fruits.

For the present investigation *D. melanogaster*, *D. simulans*, *D. ananassae*, *D. malerkotliana*, *D. yakuba*, and *D. mauritiana* were collected from University of Mysore, Mysore. These flies were used to study the olfactory response of flies in different fruits, such as banana, sapota, apple, and papaya. The sliced fruits were placed inside the four culture bottles. They were kept in each corner of the experimental transparent glass box $(35 \times 25 \text{ cm})$. 300 flies are released to the box and closed, and then the boxes were kept without any disturbance. The flies were observed, and the numbers of flies attracted towards specific fruits were recorded carefully for an interval of one hour. Three replicates were carried out at ambient temperature of $25 \pm 2^{\circ}\text{C}$. The data were analyzed by Chi-Square test.

Table 1 shows the percentage of *Drosophila* flies attracted to various fruits. Sapota was found to be a good attractant in all the species. All the species were attracted at maximum to sapota (observation I-III), except banana, which attracted more *D. simulans* flies at the end of the third observation, whereas the minimum attraction of different species of flies varies in the remaining three fruits. *D. melanogaster* and *D. bipectinata* were attracted minimum to papaya in all the observations, except the third observation of *D. simulans* (papaya). *D. yakuba* and *D. malerkotliana* were attracted least to banana and apple, respectively. The Chi-Square test reveals that the differences of attraction of flies between different fruits are found to be highly significant at all the three observations (χ^2 - 233.75, χ^2 - 209.93, and χ^2 - 239.75, df = 20).

In the present study, the percentage of olfactory responses of various species of Drosophila varies in all the fruits analyzed. It is evident that all the species prefer maximum sapota, whereas D. melanogaster, D. simulans and D. bipectinata prefer minimum for papaya (10.1%, 5.8%, and 5.6%,

respectively), D. yakuba (8.3%) to banana, D. ananassae and D. malerkotliana to apple (9% and 6.2%) in the first observation.

Table 1. Mean ± SD of olfactory response of different species of *Drosophila* flies on various fruits (Figures in parentheses are % of preference).

	I st observation				
Species	Sapota	Apple	Banana	Papaya	
D. melanogaster	112.1±15.5	36 ± 4.38	69.3 ± 22.2	30.3 ± 4.1	
	(37.3%)	(12%)	(23.1%)	(10.1%)	
D. simulans	18.6 ± 8.93 (22.5%)	32 ± 5.9 (9.7%)	53.8 ± 17.1 (14.6%)	37.3 ± 16.4 (5.8%)	
D. yakuba	52.5 ± 20.6	49.1 ± 12.1	25.1 ± 14.2	30.8 ± 42.1	
	(17.4%)	(16.3%)	(8.3%)	(10.2%)	
D. ananassae	101.3 ± 33.6	27.1 ± 4.7	36.3 ± 12.4	35 ± 8.8	
	(33.7%)	(9%)	(12.1%)	(11.6%)	
D. bipectinata	61.8 ± 14.3 (20.6%)	15 ± 2.1 (6%)	34.1 ± 5.1 (9.6%)	16.8 ± 3.3 (5.6%)	
D.malerkotliana	53.8 ± 17.1	18.6 ± 8.9	37.3 ± 16.4	32 ± 5.9	
	(17.9%)	(6.2%)	(12.4%)	(10.6%)	

	II nd observation				
Species	Sapota	Apple	Banana	Papaya	
D. melanogaster	112.5 ± 10.7	32.8 ± 6.2	62 ± 5.9	27.1±7.0	
	(37.5%)	(10.9%)	(20.6%)	(1.1%)	
D. simulans	10.8 ± 4.5	25 ± 6.2	70.5 ± 23.3	45.6 ± 21.4	
	(16.77%)	(6.8%)	(13.5%)	(11.9%)	
D. yakuba	61.5 ± 20.3	52.5 ± 13.4	25.3 ± 9.0	26.3 ± 40	
	(20.5%)	(17.5%)	(8.4%)	(8.7%)	
D. ananassae	104.6 ± 36.7	25 ± 8.6	36.3 ± 11.5	32.1 ± 4.7	
	(34.8%)	(8.3%)	(12.1%)	(10.7%)	
D. bipectinata	62.8 ± 23.6	17.5 ± 3.3	62.1 ± 18.0	13 ± 3.2	
	(20.9%)	(5.8%)	(20.7%)	(3.6%)	
D. malerkotliana	70.5 ± 23.3	10.8 ± 4.5	45.6 ± 21.4	25 ± 6.2	
	(23.5%)	(3.6%)	(15.2%)	(8.3%)	

	III rd observation				
Species	Sapota	Apple	Banana	Papaya	
D. melanogaster	116.1 ± 20.3	33 ± 3.03	60.3 ± 12.8	30.5 ±1 3.4	
	(38.7%)	(11%)	(20.1%)	(10.1%)	
D. simulans	13.8 ± 4.0	30.1 ± 9.08	63 ± 31.2	52 ± 21.9	
	(17.1%)	(12.2%)	(18.1%)	(4.6%)	
D. yakuba	68.6 ± 27.8	65.8 ± 20.9	14.5 ± 4.6	25.3 ± 45.4	
	(22.8%)	(21.9%)	(4.8%)	(8.4%)	
D. ananassae	103.3 ± 33.6	35.1 ± 2.8	35.6 ± 10.2	36 ± 11.4	
	(33.4%)	(11.7%)	(11.8%)	(12%)	
D. bipectinata	63.5 ± 30.6	18.6 ± 5.7	61.3 ± 25.6	24 ± 7.8	
	(21.1%)	(6.2%)	(20.4%)	(8%)	
D. malerkotliana	63. ± 31.2	13.8 ± 4.0	52. ± 21.9	30.1 ± 9.0	
	(21%)	(4.6%)	(17.3%)	(10%)	

Tureli *et al.* (1984) reported that D. melanogaster simulans D. showed significant, but very weak. choice than D. pseudoobscura in habitat selection in different fruit trees. In the present study, the flies of D. melanogaster and D. simulans prefer maximum for sapota in all the trials. The natural fruits, such as banana, papaya, and sapota, contain different compositions of chemicals and nutrients (Abdul Khader et al., 1985). Drosophila is sensitive to a wide variety of odorants and is odour discrimcapable of ination. It is likely that olfactory response plays an important role in the selection of food and in the identification of hazardous substances (Fuyama, 1978).

microgeographic A genetic difference between habitats, which may inconsistent, has been found in D. persimilis and D. melanogaster (Taylor and Powell, 1979). Taylor and Powell (1978) and Tureli et al. (1984) studied habitat choice by mark release recapture method in D. melanogaster, D. simulans, D. pseudoobscura, and D. persimilis in canopy woods and different fruit trees. They proposed that the difference in habitat choice behaviours were

adaptive responses to patchy environment, and the habitat choice depends on the physiological conditions of the flies. Present study reveals that flies of the different species of *Drosophila* selected sapota maximum, despite all the odors of different fruits kept at each corner of the experimental box.

References: Abdul Khader, J.B.M. Md, K.P. Callappan, O. Pllai, and P.K. Chattopadhaya 1985, *Fruits, Tropical and Subtropical*. (Bose, T.K., ed.). pp. 140-161; Carson, H.L., D.E. Hardy,

H.T. Spieth, and W.S. Stone 1970, In: Essays in Evolution and Genetics in Honor of Theodosius Dobzhansky. pp. 437-543; Dobzhansky, Th., and C. Pavan 1950, J. Anim. Ecol. 19: 1-14; Fuyama, Y., 1978, Behav. Genet. 8: 399-414; Taylor, C.E., and J.R. Powell 1978, Oecologia 37: 69-75; Taylor, C.E., and J.R. Powell 1979, Genetics 85: 681-695.



Fine-scale crossover rate and interference along the XR-chromosome arm of *Drosophila pseudoobscura*.

<u>Fitzpatrick, Courtney L., Laurie S. Stevison, and Mohamed A.F. Noor.</u> Biology Department, Duke University, Durham, NC, USA; <u>NOOR@DUKE.EDU</u>.

Although broad-scale variation in recombination rates across *Drosophila* genomes is well established, recent studies have identified that fine-scale crossover rate variation also exists within the *Drosophila pseudoobscura* genome. The first study to explore such fine-scale variation focused on a 2-MB region of the XL chromosome arm and identified where crossovers fell among 370 progeny known to have had a crossover event between two phenotypic mutant markers (Cirulli *et al.*, 2007). Fine-scale recombination rates ranged from 1.4 to 52 cM/megabase. A later work examined variation across the second chromosome in crossover rate and correlated fine-scale recombination rate with patterns of nucleotide diversity within species and divergence between species (Kulathinal *et al.*, 2008). This latter study employed an illumina bead genotyping approach, but assumed that crossovers in adjacent windows likely represented an erroneous genotype (or a gene conversion event) in one of the windows.

Both of these studies assumed that crossover interference exists within *D. pseudoobscura*, an assumption that has not been tested in this species. The first study would have missed all double-crossover events within the 2-MB window because of the methods employed, while the second study would have erroneously excluded adjacent crossovers, hence underestimating overall crossover rates. One can best address this deficiency by examining many closely linked markers in a very large panel of backcross progeny.

Here, we directly measured crossover rate between markers within a 3 MB region on the XR chromosome arm of *Drosophila pseudoobscura* in a very large panel of backcross progeny. We identified fine-scale crossover rate variation in this region of the genome. We also used these results to obtain estimates of the coefficient of coincidence and interference in this species.

Materials and Methods

We crossed two strains of *Drosophila pseudoobscura*, Flagstaff 1993 and Mather 17, and backcrossed the F_1 females to males from the Flagstaff 1993 line. To achieve a sufficiently large sample size of F_2 backcross progeny, we performed two such crosses identically. We extracted DNA from and genotyped 1208 F_2 backcross individuals from the first cross and 2057 F_2 backcross individuals from the second cross, totaling 3265 F_2 backcross individuals, and we characterized crossover rate in a 3 MB region on the XR chromosome arm in these backcross progeny. Because here we examined this region exclusively, our further use of the terms "recombinant" and "non-recombinant" refers only to crossover events between XR_group8 position 5,051,027 and position 7,973,182 (Richards *et al.*, 2005).