

Hanks, G.D. Indiana University Northwest, Gary, Indiana. Frequency changes of marked Y chromosomes with RD background.

with Y^{bw+} . Y^{BS} increased in frequency to 1.00 when allowed to compete with Y^{bw+} . The percentage of females is 59.3 for Y^{BS} male parents, 63.4 for Y^{Y+} male parents, and 59.8 for Y^{bw+} male parents. Apparently the interaction of fitness in the diploids, meiotic drive of the Y chromosome, and selection due to the sex ratio determines which Y chromosome has the strongest competitive advantage. Probably fitness is most important in determining the frequencies of these particular Y chromosomes. The values on percentages of females given above were measured by mating each male singly to 5 females and counting progeny in 3 culture bottles. Several males of each type were tested. The relative abilities of the 3 Y chromosomes to gain in frequency are given in increasing order: $Y^{bw+} < Y^{Y+} < Y^{BS}$.

Marked Y chromosomes were tested in population cages (2Y's at a time with a frequency of 0.5 each). Y^{BS} increased to a frequency of 0.99 when placed in a cage with Y^{Y+} . Y^{Y+} increased to a frequency of 0.92 when allowed to compete

Okada, T. Tokyo Metropolitan University, Tokyo, Japan. A numerical analysis of the drosophilid fauna centering around New Guinea.

hundred species belonging to twenty-five genera, which highly surpassed the previous records, thirteen genera and about forty species. The identification of the species is still incomplete, and the faunal relationships at the genus level between New Guinea and the surrounding geographical areas, in which the drosophilid faunae have sufficiently been known and the endemic genera are relatively few, are analysed using numerical taxonomic methods, taking a geographical area as OTU and the presence and absence of a genus as states of a character, coded 1 and 0, respectively. The faunal comparison was based on several kinds of relatively simple similarity coefficients (S) and the clustering was made by WPGA and UPGA. The resulting phenograms were evaluated by means of the cophenetic correlation coefficients (r) between original and derived similarity matrices.

In 1968-9, an opportunity was given to me through courtesy of Professor M. R. Wheeler of the University of Texas, Austin, Texas, to examine a large collection of New Guinean Drosophilidae at his Genetics Foundation. The examination resulted in finding more than two

The highest cophenetic correlation coefficient, eventually the most reliable phenogram,

S	r,WPGA	r,UPGA	n_{jk} in numerator	Faunal inclusion in Europe-North American cluster
S_{J^*}	0.91	0.89	-	-
S_{RR}	0.86	0.94	-	-
S_O	0.82	0.88	±	-
MCD	0.72	0.71	+	-
S_{SM}	0.66	0.66	+	Africa
S_S	0.85	0.85	-	Africa
S_{RT}	0.64	0.64	+	Africa, Japan

* S_{J^*} , Jaccard, 1908; S_{RR} , Russel and Rao, 1940; S_O , in the present study = $(2n_{JK} + n_{jk})/n$; MCD, Cain and Harrison, 1958; S_{SM} , Sokal and Michener, 1958; S_S , Simpson, 1943; S_{RT} , Rogers and Tanimoto, 1960.

was obtained in the case of S_{RR} , UPGA ($r = +0.94$), which showed that New Guinea is nearest to South Asia including Taiwan, with them Japan, Africa, and Micronesia being combined successively, and that Europe and North America make another cluster. In the cases of the cophenetic correlation coefficients higher than +0.80, the resulting phenograms are similar as in S_{RR} , UPGA, while in the cases lower than +0.70, Africa and also Japan are tended to be included in the Europe-North American cluster. The similarity coefficients such as including negative matches (n_{jk}) at least in numerator resulted in phenograms less reliable, showing the lower cophenetic correlation coefficients, and consequently, they should better be avoided in the faunal comparison.