Chung, Y.J. Ewha Woman's University, Seoul, Korea. Biochemical genetic study of Drosophila populations in Korea.

Enzyme polymorphism has been extensively investigated from various places by many authors. In order to establish a biochemical genetic system in Drosophila populations in Korea, six enzyme (ADH, α-GPDH, MDH-1, MDH-2, ACPH and ME) alleles of natural populations of D.melanogaster from 10 localities (Kangreung, Seoul-Seungsudong, Seoul-Wangsibri, Seoul-Sinchon, Seoul-Seungsandong, Jeonju, Pusan, Mokpo, Jeju-Hanrim and Jeju-Moseulpo) in Korea were analyzed by means of starch gel electrophoresis.

The results obtained were as follows: (1) the natural populations of D.melanogaster from 10 localities in Korea showed polymorphism as to ADH, α-GPDH, MDH-1, ACPH and ME alleles. But MDH-2 alleles were found to be monomorphic. (2) Heterozygosity was calculated to be 48.40% for α-GPDH and 28.00% for ADH allele. The rest of enzymes showed a low heterozygosity below 10%. (3) The FF genotypes of ACPH and ADH alleles were most frequently distributed through the Korean Natural populations of D.melanogaster, whereas the SS genotypes of MDH-1, MDH-2 and ME alleles were most frequently involved in all populations, and the commonest genotype of α-GPDH alleles were found to be the FS genotype. (4) The F gene frequency was found to be higher than the S gene in ACPH, ADH and α-GPDH, whereas S gene frequency was found to be higher than the F gene in MDH-1, MDH-2 and ME alleles. (5) The predominance of the FF genotype and the F gene of ADH alleles was weakened in the second year experiment compared to first year's but the genotype and gene frequencies of α-GPDH alleles showed no difference between the first and the second year experiment. However, heterozygosity revealed still high values in average (ADH:0.3048; α-GPDH:0.4645). (6) This investigation is desired to extend the other localities in Korea so that a biochemical genetic system of Drosophila populations in Korea may be established more robustly.

References: Chung, Y.J.&K.S.Lee 1972, J.Kor.Res.Inst.Bet.Liv. 9:123-132; Chung,Y.J., Y.S.Han & Y.L.Chung 1982, Kor.J.Zool. 25:123-129.

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Burgundy (bg) is a sex-linked recessive mutant of D.mauritiana that confers a dark ruby eye color with no pseudo-pupil. The mutant, available from the Bowling Green Stock Center, is one of only two described in this species (Woodruff 1980). Because of the importance of D.mauritiana in studies of the genetics of speciation, mapping of this and other markers is essential. Burgundy females of D.mauritiana were crossed to white (w, 1-4.1) males of the sibling species D.simulans. The hybrid females are fertile and heterozygous for both markers. These were crossed to wild-type D.simulans males, and the male offpspring scored for recombination between w and bg (the two species are homosequential and the hybrid females show free recombination). Since w bg males almost certainly have white eyes, there are only three phenotypes among the backcross males; the numbers scored were 362 white, 342 burgundy, and 20 wild-type. I assumed that 20 of the white males were actually w bg. A rough estimate of recombination between the loci is thus 40/724 or 0.055±0.017. An approximate location for burgundy is thus either 1-9.6 or near 1-0, the base of the X chromosome. Crosses of burgundy females to similar eye-color mutants of D.melanogaster in this region showed that the mutant is allelic with prune (pn, 1-0.8). Burgundy should thus be regarded as identical to prune.

Reference: Woodruff, R.C. 1980, DIS 55:217.