Doane, W. W. Yale University, New Haven, Connecticut. The Amylase locus in Drosophila hydei.

Recombination experiments were performed to determine to which linkage group the Amy locus belongs in D. hydei. Berendes (1963, Chromosoma 14: 195) showed that linkage group V (referred to as III by Spencer, 1949) belongs to chromosome 5 in hydei. This is homologous to 2R in melanogaster, wherein lies the Amy locus of the latter species (e.g., Kikkawa & Abe, 1960).

Females from a Chile wild strain, homozygous for the electrophoretic variant Amy^8 (Doane, DIS 41: 74), were crossed to males from a strain homozygous for Amy^7 and which contained the recessive markers bb, p and vg in linkage groups I, II and V, respectively. The reciprocal cross was made and F_1 females of both crosses were testcrossed to males of the marker strain. Progeny were aged one week and each recombinant class homogenized en masse in an equivalency of 1 fly/5µl of water. Cell debris was spun down and 10 µl samples of supernatants were analyzed quantitatively by disc electrophoresis (method of Doane, 1967, J. Exp. Zool., 164: 363). In those cases where both bands #7 and #8 were separated from a given class, determination of the relative activity in each band provided estimates of the frequency of the two Amy alleles. Results showed that Amy is linked with vg, i.e., in linkage group V. Similar experiments using st, sca and jv (groups II, V and III, resp.) confirmed this finding.

A 3-point crossover analysis was next made using sca and cn as markers linked with Amy^7 on the fifth chromosome. Flies from the following cross were aged one week and tested electrophoretically: sca cn Amy^7/+ + Amy^8♀ x sca cn Amy^7♂. Recombinants between markers were tested individually; parental types were tested from mass homogenates of 20 flies or less, as above. In a subsequent 4-point analysis of a parallel nature, vg was included among the markers and a reciprocal cross also made. Testcross results are summarized in the table with the maternal genotype for each listed at the left.

Maternal Genotype	No. of Progeny	Number of Crossovers Between Markers					
		sca-cn	sca-Amy	sca-vg	cn-Amy	cn-vg	Amy-vg
sca cn Amy^7	927	186	210		42		
+ + Amy^8		(20.1%)	(22.6%)		(4.5%)		
sca cn Amy^7 vg	715	122	166	182	52	112	76
+ + Amy^8 +		(17.1%)	(23.2%)	(25.4%)	(7.3%)	(15.7%)	(10.6%)
+ + Amy^8 + *	877	150	190	222	48	100	72
sca cn Amy^7 vg		(17.1%)	(21.7%)	(25.3%)	(5.5%)	(11.4%)	(8.2%)

*From reciprocal mating.

The linear sequence of markers with reference to Amy is: sca cn Amy vg, with no stipulation as to the direction it is read. This is in contrast to the sequence in melanogaster which reads cn sca vg Amy. The % c.o. between each marker, when averaged from the data of all three experiments, is: sca-cn, 18.1%; cn-Amy, 5.8%; and Amy-vg, 9.4%. When the data is corrected for the lowered viability shown by the parental type with the multiple markers, the values become: 17.2%, 5.5% and 8.9%, respectively. (Supported by N.S.F. grant GB 1718. The marker strains were gratefully received from Dr. H. D. Berendes.)

Holm, D. G. University of Connecticut, Storrs, Connecticut. Construction of a dor^+Yy^+ chromosome.

X-rayed y^2 su-w^a w^a $Y^{S \cdot}Y^L$ y^+ (no free Y) males were mated to yf:= females. The viable y^+ female progeny each carry a Y chromosome obtained by a gross deletion of the paternal X. Subsequent mating to dor males permitted the recovery of a newly synthesized Y carrying a dor^+ duplication. Additional analysis revealed that this duplication covered the distal tip of the X including y^2 su-w^a dor^+ and covers 1(1)7. The proximal portion of the duplication includes the region from l114 to su-f (see Schalet and Finnerty, this issue). The presence of the dor^+ Y y^+ chromosome in males gives rise to reduced body size and a pronounced Hairy-wing effect; in compound-X females the body size is apparently normal and the Hairy-wing effect is poorly and infrequently expressed.