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LACK OF RECOMBINATION BETWEEN X CHROMOSOMES IN INTERSPECIFIC HYBRIDS OF THE *ANOPHELES GAMBIAE* GROUP OF SPECIES

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CURTIS AND CHALKLEY (1979) suggest that asynapsis in polytene chromosomes, particularly in the sex chromosomes, in F_1 interspecific hybrids between *Anopheles gambiae*, *A. arabiensis*, and *A. quadriannulatus*, might be indicative of asynapsis during meiosis in these same hybrids. If this is true, they argue, then crossing over would most likely not occur in hybrids during meiosis. They then present data which they consider tests " these expectations with regard to the X chromosome ".

The data consist of breeding experiments between a strain of *A. gambiae* carrying a sex-linked mutant, and strains of *A. arabiensis* and *A. quadriannulatus* which are wild-type with respect to the mutant marker. Each species has a distinct X chromosome. In numerous back-cross progeny from the F_1 hybrids $\times$ *A. gambiae* males, no recombinants were recovered, *i.e.*, the sex-linked mutant only and always occurred when the *gambiae* type X chromosome was homozygous (the mutant is recessive). The authors conclude from these results that it is likely that there is no pairing or crossing over between the X chromosomes at meiosis in female hybrids. However, it is probable that neither of these conclusions is valid from the data.

Curtis and Chalkley (1979) point out that these species differences in the X chromosomes " can be largely explained by postulating a series of inversions ". Figure 1 shows a diagram of the X chromosome of *A. quadriannulatus* with the break-points of these inversions, and the specific inversion formulae for this arm for each species.

A. gambiae Xag, *A. arabiensis* Xbcd

FIG. 1.—A diagram of the X chromosome of *A. quadriannulatus* showing the association of interspecific, fixed inversions between it and *A. gambiae* and *A. arabiensis* (after Coluzzi and Sabatini, 1968; Coluzzi *et al.*, 1979). The arrow indicates the centromeric end of the arm.

F_1 interspecific hybrids between *A. gambiae* and *A. arabiensis* will be heterozygous for Xagbcd which involves about 85 per cent of the arm, and, between *gambiae* and *quadriannulatus*, heterozygous for Xag involving about 75 per cent of the arm. We do not know where the mutant locus is located

along the X. Most of the back-cross individuals of Curtis and Chalkley (1979) were between *gambiae* and *arabiensis* (n = 134), and very few between *gambiae* and *quadriannulatus* (n = 17). It is highly unlikely that any cross-overs in the heterozygotes for Xagbcd would result in viable gametes within the inversion complex, and those outside it would not be detected unless the mutant locus lay in this 15 per cent of the arm. In fact the actual portion available for recoverable recombinants would probably be less, due to the well known effect of paracentric inversions on chromosome segments lying immediately outside inversion loops. It might be argued that recombination in the terminal, centromeric segment would have been detectable, as synapsis might be expected where a terminal piece of a *gambiae* X had been recombined with an *arabiensis* X, but it is a tenuous expectation at present.

It seems reasonable to suggest that the questions posed by Curtis and Chalkley (1979) concerning asynapsis and no crossing over in F_1 hybrids can only be answered in the absence of other variables which are known to have a powerful effect on the phenomenon under test. Their projected work on the homosequential autosomes of these species would seem to meet this requirement.

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