

of the ring, from the ring synthesis are usually sterile or virtually so; moreover, those animals which are virtually sterile--at most 2 progeny--have sterile or nearly sterile progeny. R(3)S1, Df(3R)P47+ progeny from R(3)S1/Df(3R)P47 mothers also show this pattern of sterility. The few crossovers which are completely fertile show no indication of sterility in subsequent generations.

Because of this sterility problem and because of the lowered viability of R(3)S1+ due to hyperploidy, it is desirable to selectively recover ring-bearing progeny when inserting markers into the ring from a standard sequence chromosome. This can be accomplished by crossing R(3)S1, Df(3R)P47/marker females to Df(3R)P47/Dp(3;3)MRS, Sb--+ males to recover recombinant R(3)S1 chromosomes (with or without the marker) over Df(3R)P47 and later test for presence of the marker. To transfer markers from the ring to In(3R)C, it is convenient to recover an In(3LR)Ubx^{ULP88R}+(3R)C, sbd² chromosome with the marker from R(3)S1, marker/In(3LR)Ubx^U+(3R)C, sbd² ss Ubx^U mothers: sbd² provides a marker for the inversion, and absence of the Ubx^U phenotype identifies a crossover.

Stocks of (1) R(3)S1, Df(3R)P47, ca/In(3R)C, Sb cd Tb ca,
(2) Df(3R)P47/Dp(3;3)MRS, Sb--+,
and (3) In(3LR)Ubx^U+(3R)C, sbd² ss Ubx^U cd/T(2;3)ap^{Xa} are available from the Pasadena stockcenter.

Craymer, L. California Institute of Technology, Pasadena, California USNA.

Transferring markers to or from autosomal inversions.

Markers can be transferred from a standard sequence chromosome into a large pericentric inversion by double crossing over. For inversions of moderate length--on the order of 10 numbered divisions--such double crossovers can be exceedingly rare and are prohibitively rare

for small inversions. It is, however, possible to transfer markers from one inversion to another through a sequence of selected single crossovers. InA/InB females are crossed to InB^{AR}/InA^{LB} males to selectively recover recombinant InA^{LB} and InB^{AR} chromosomes (it is assumed that InA^{LB}/++ and InB^{AR}/++ are lethally aneuploid genotypes). InA and InB are then reconstituted by crossing InA^{LB}/InB^{AR} females to structurally normal males. The reconstituted InA and InB chromosomes are frequently double crossover chromosomes, so that markers may be transferred from one inversion to the other via this sequence of crosses.

Transferring markers from a structurally normal chromosome to moderate length or smaller inversions is accomplished by first transferring the markers into a large inversion, then transferring the markers from the large inversion to the smaller one. As an example, the following sequence of crosses was used to insert se, h², rs², and th into In(3L)P:

P₁ C(1)M4, y²; In(3L)C90/se h² rs² th st cp in ri p^P females were crossed to se h² rs² th st cp in ri p^P males.

C(1)M4 is present in this cross to increase crossing over. In(3L)C90 is a large pericentric inversion with 62B and 80 breaks. In(3L)C90, se h² rs² th st was recovered in the P₂. A balanced stock of C(1)M4, y²; In(3L)C90, se h² rs² th st/In(3L)P, Me h D³ was then constructed.

P₄ C(1)M4, y²; In(3L)C90, se h² rs² th st/In(3L)P, Me h D³ females were crossed to In(3L)C90^{LPR}+(3R)P18, Ubx e⁴/In(3L)P^LC90^R males, to recover In(3L)C90^{LPR}, se h² rs² th st/In(3L)P^LC90^R (recognizable as being Me⁺ and Ubx⁺) and In(3L)P^LC90^R, se h² D³/In(3L)C90^{LPR}+(3R)P18, Ubx e⁴. These two genotypes were crossed to each other to produce a

C(1)M4, y²; In(3L)C90^{LPR}, se h² rs² th st/In(3L)P^LC90^R, se h² D³ stock.

P₆ C(1)M4, y²; In(3L)C90^{LPR}, se h² rs² th st/In(3L)P^LC90^R females were crossed to th st cp in ri p^P males.

A few th₂st⁺ offspring (In(3L)P, se h² rs² th) offspring were produced and a stock of In(3L)P, se h² rs² th was then established.

The $\text{In}(3\text{L})\text{P}, \text{D}^3$ combination used in the above synthesis was derived in a somewhat similar manner; h was inserted into $\text{In}(3\text{L})\text{P}$ by a rare double crossover, and $\text{In}(3\text{L})\text{P}, \text{Me } h \text{ D}^3$ was constructed from these chromosomes and $\text{In}(3\text{L})\text{P}, \text{Me}$.

Large paracentrics exist for all major autosomal arms-- $\text{In}(2\text{L})\text{DTD27}$ (21B; 40), $\text{In}(2\text{R})\text{bw}^{\text{VDe1}}$ (41; 59), $\text{In}(3\text{L})\text{C90}$, and $\text{In}(3\text{R})\text{P110}$ (81F; 99). Stocks of $\text{In}(2\text{L})\text{NS}^{\text{L}}\text{DTD27}^{\text{R}}/\text{In}(2\text{L})\text{DTD27}^{\text{L}}\text{NS}^{\text{R}}$ and $\text{In}(2\text{L})\text{Cy}^{\text{L}}\text{DTD27}^{\text{R}}/\text{In}(2\text{L})\text{DTD27}^{\text{L}}\text{Cy}^{\text{R}}$ have been constructed in addition to the $\text{In}(3\text{L})\text{C90}^{\text{L}}/\text{In}(3\text{L})\text{P}^{\text{L}}\text{C90}^{\text{R}}$ complex. These stocks were derived by applying the methods which I have described for deriving crossover products of pericentric inversions (Genetics 99:75-77, 1981).

de Frutos, R., A.Latorre, and L.Pascual.
Universidad Literaria de Valencia, Espana.
Differential puffing activity in two E
chromosomal arrangements of *D.subobscura*.

A comparison of the E chromosome puffing patterns of the different gene arrangements were carried out in order to investigate the possible effect of inversions on gene expression. Two strains of *Drosophila subobscura* were used: H271 which is homozygous for E_{st} arrangement

and Ra121 which is homozygous for $\text{E}_{1+2+9+12}$ arrangement. The puffing patterns of late third instar larvae and different aged prepupae were analyzed. The prepupal samples were taken at 0, 4, 10 and 18 hrs after the eversion of the anterior spiracles. 20 individuals were analyzed per developmental stage and strain. Five nuclei were observed from each of the individuals analyzed. For the average degree of puffing activity two criteria were taken into account: (a) size of puffs, and (b) frequency of appearance of each puff at every stage analyzed. The puffs and breakpoints of $\text{E}_{1+2+9+12}$ inversion were located using the standard salivary gland chromosome map of Kunze-Mühl and Müller (1958). The breakpoints of $\text{E}_{1+2+9+12}$ arrangement are the following: E_1 58D/59A-62D/63A, E_2 58D/62D-64B/64C,

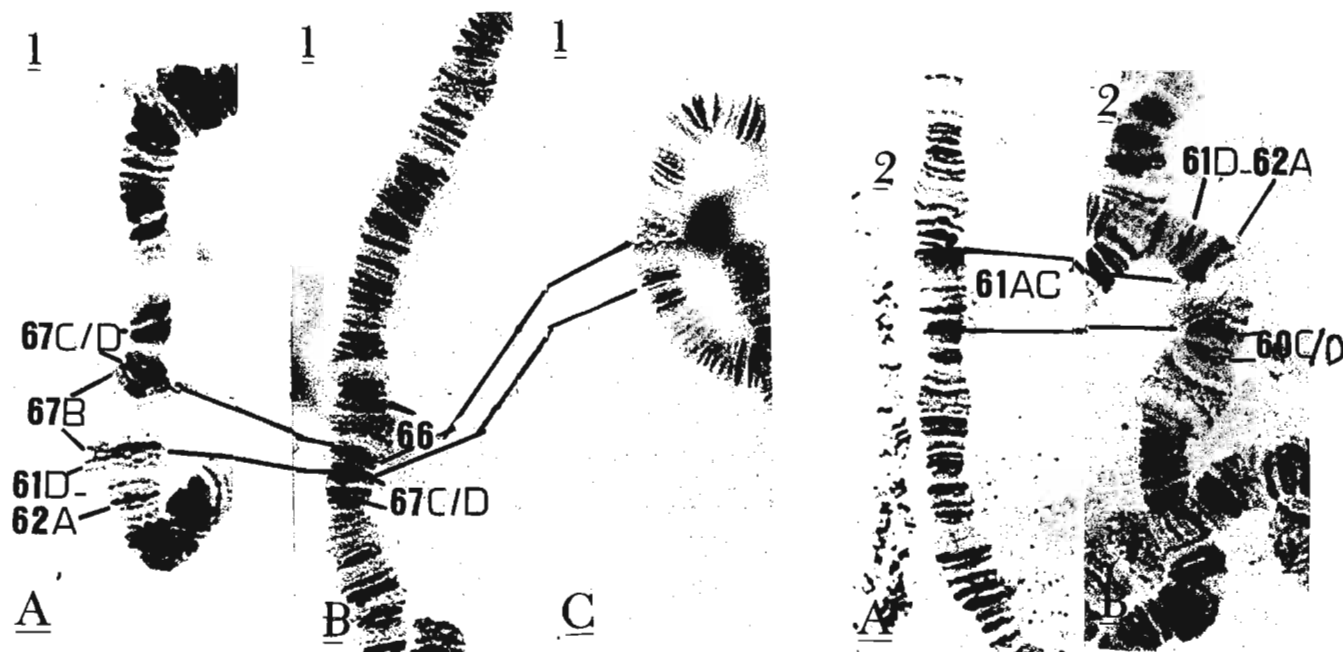


Figure. E chromosomes of *D.subobscura*: (1A) $\text{E}_{1+2+9+12}$ arrangement of Ra121 strain (18h prepupa). (1B) E_{st} arrangement of H271 strain (4h prepupa). (1C) E_{st} arrangement of H271 strain (0h prepupa). (2A) $\text{E}_{1+2+9+12}$ arrangement of Ra121 strain (0h prepupa). (2B) E_{st} arrangement of H271 strain (18h prepupa).