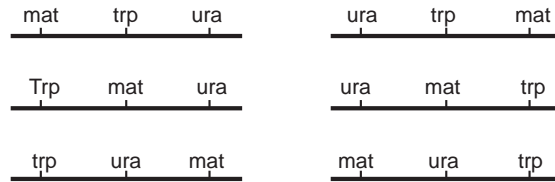


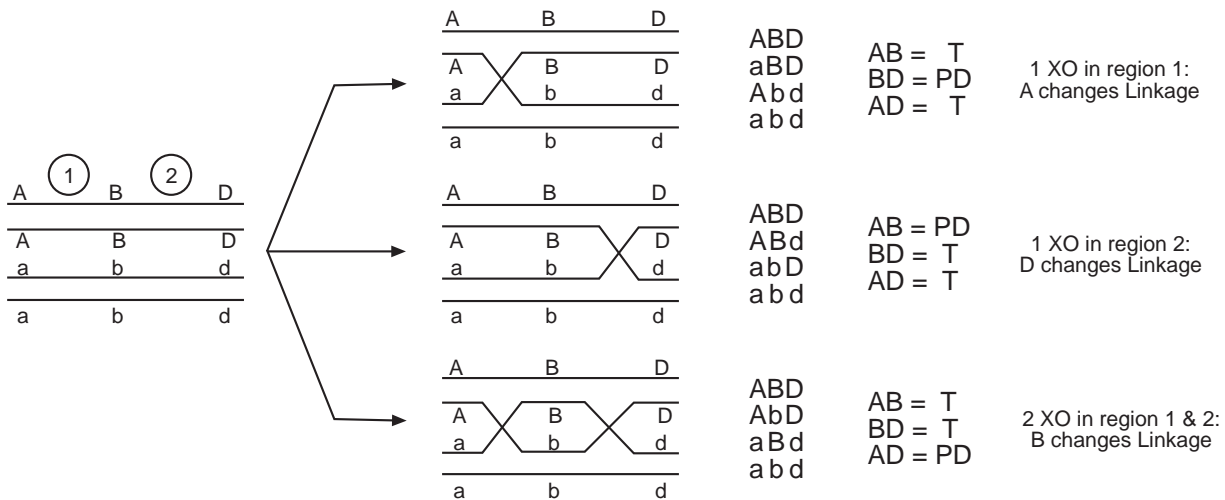
# Cross: a trp1 x α ura3

|             |             |             |             |
|-------------|-------------|-------------|-------------|
| I           | II          | III         | IV          |
| a ura+ trp1 | a ura+ trp1 | a ura+ trp1 | a ura+ trp1 |
| a ura+ trp1 | α ura+ trp1 | a ura3 trp1 | a ura+ trp+ |
| α ura3 trp+ | a ura3 trp+ | α ura+ trp+ | α ura3 trp1 |
| α ura3 trp+ | α ura3 trp+ | α ura3 trp+ | α ura3 trp+ |
| 274         | 140         | 73          | 13          |

3 Possible Orders:



- In the absence of an outside marker, there is no difference between left to right and right to left
- What is most important is the identification of the middle gene



- In a double recombinant, the middle marker changes linkage
- A double recombinant will always be the lowest tetrad

Tetrad IV is the lowest tetrad → trp is the gene that switched linkage

Therefore, the sequence is: mat trp ura      ura trp mat

Tetrad II is an XO between mat & trp:  $\text{mat} / \text{trp} = \frac{1}{2} \frac{(\text{II} + \text{IV})}{500} \times 100 = \frac{1}{2} \frac{(140 + 13)}{500} \times 100 = 15.3 \text{ cM}$

Tetrad III is an XO between trp & ura:  $\text{trp} / \text{ura} = \frac{1}{2} \frac{(\text{III} + \text{IV})}{500} \times 100 = \frac{1}{2} \frac{(73 + 13)}{500} \times 100 = 8.6 \text{ cM}$

