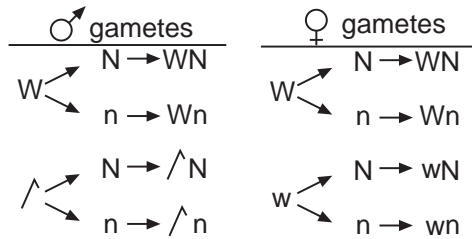


Dihybrid cross with a sex-linked gene

P1 white♂ x notched♀
 $w/\wedge NN$ x $WWnn$

F1 $W/\wedge Nn$ x $WwNn$
 normal♂ x normal♀

Calculation of F2



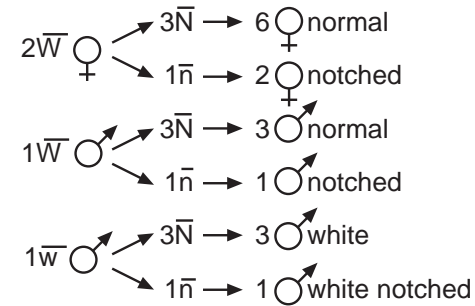
	WN	Wn	wN	wn
WN	♀ \overline{WN}	♀ \overline{Wn}	♀ \overline{wN}	♀ \overline{wn}
Wn	♀ \overline{WN}	♀ \overline{Wn}	♀ \overline{wN}	♀ \overline{wn}
$\wedge N$	♂ \overline{WN}	♂ \overline{Wn}	♂ \overline{wN}	♂ \overline{wn}
$\wedge n$	♂ \overline{WN}	♂ \overline{Wn}	♂ \overline{wN}	♂ \overline{wn}

females: 6 normal
 2 notched

males: 3 normal
 1 notched
 3 white
 1 white notched

Branching to calculate di- & trihybrid crosses involving a sex-linked gene

Monohybrid crosses involving ex-linked genes give different F2 ratios depending on whether the mutation is in the male or female in the P1. Therefore, When using branching to calculate F2 phenotypes in a cross involving a sex-linked gene, it is easiest to begin by calculating the sex-linked trait first and then adding in the standard autosomal ratios later.



the sex-linked ratios in these branching diagrams are derived from the monohybrid ratios in cross #1 on the previous page

