Genetics Society of America
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Peer-Reviewed Education Portal

Laboratory Protocol: Recombination Calculations by Branch Diagram

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Accepted for publication June 20, 2013

Citation:

Gilliland, William D. and Rosenbaum, Michael G. (2013). Recombination Calculations by Branch Diagram. *Genetics Society of America Peer-Reviewed Education Portal (GSA PREP)*. Retrieved from http://genetics-gsa.org/education/education_resource_Recombination_Calculations_by_Branch_Diagram_6_20_2013.shtml

Supplemental Material

To provide sample data sets for use with this method, we reproduce some of the two and three marker crosses from Table 8 of A.H. Sturtevant's original 1913 publication of the first genetic maps in any organism. We have translated the genotypes into modern nomenclature, and present the progeny in the same order used by the branch diagram method. In Sturtevant's crosses, only male progeny were informative for these *X*-linked traits, as recombining females were not mated to males that carried all recessive markers. Therefore, we have omitted the male parents from these crosses. Note that most of these data show a slight viability effect that reduces the number of mutant alleles. This tends to be more pronounced when a genotype carries a larger number of mutant alleles.

Known map positions, from http://flybase.org (Marygold *et al* 2013):

yellow (y)	***0***
white (w)	***1.5***
crossveinless (cv)	***13.7***
vermillion (v)	***33.0***
miniature (m)	***36.2***
forked (f)	***56.7***

Cross 1: *yellow* and *white (white-eosin allele[1], w^e)*

Recombining Parent: ♀ $\frac{y^+\ w^e}{y^-\ w^+}$

Progeny:	NR	$y^+\ w^e$	*176*
	SR	$y^+\ w^+$	*0*
	SR	$y^-\ w^e$	*2*
	NR	$y^-\ w^+$	*195*

Cross 2: *yellow* and *vermillion* (*cis* configuration)

Recombining Parent: ♀ $\frac{y^+\ v^+}{y^-\ v^-}$

Progeny:	NR	$y^+\ v^+$	*59*
	SR	$y^+\ v^-$	*16*
	SR	$y^-\ v^+$	*24*
	NR	$y^-\ v^-$	*33*

[1] When the original work was published, it was thought that *white* and *eosin* were different genes.

Cross 3: *yellow* and *vermillion* (*trans* configuration)

Recombining Parent: ♀ $\frac{y^+\ v^-}{y^-\ v^+}$

Progeny:			
	NR	$y^+\ v^-$	*149*
	SR	$y^+\ v^+$	*54*
	SR	$y^-\ v^-$	*41*
	NR	$y^-\ v^+$	*119*

Cross 4: *yellow* and *miniature*

Recombining Parent: ♀ $\frac{y^-\ m^+}{y^+\ m^-}$

Progeny:			
	NR	$y^-\ m^+$	*82*
	SR	$y^-\ m^-$	*48*
	SR	$y^+\ m^+$	*51*
	NR	$y^+\ m^-$	*89*

Cross 5: *white-eosin, vermillion* and *miniature*

Recombining Parent: ♀ $\frac{w^+\ v^-\ m^+}{w^e\ v^+\ m^-}$

Progeny:			
	NR	$w^+\ v^-\ m^{+-}$	*109*
	SR2	$w^+\ v^-\ m^-$	*3*
	DR	$w^+\ v^+\ m^+$	*1*
	SR1	$w^+\ v^+\ m^-$	*49*
	SR1	$w^e\ v^-\ m^+$	*53*
	DR	$w^e\ v^-\ m^-$	*0*
	SR2	$w^e\ v^+\ m^{+-}$	*8*
	NR	$w^e\ v^+\ m^-$	*85*

Cross 6: *yellow, crossveinless, vermillion,* and *forked*

The final cross was conducted by crossing mutant females (a stock with an *X* chromosome marked with *y cv v f)* to wildtype males (Oregon-R), then allowing the F1 males and females to mate in bottles for 5 days. A large sample was collected to attempt to get triple recombinants, a single one of which was observed. Adults were then discarded, and progeny were counted until day 18. F2 males and females were both scored, but not recorded separately.

Parents: $\female \frac{y^+\ cv^+\ v^+\ f^+}{y^-\ cv^-\ v^-\ f^-} \times \frac{y^-\ cv^-\ v^-\ f^-}{Y} \male$

Progeny:

NR	+ + + +	*1174*
SR3	+ + + *f*	*343*
DR23	+ + *v* +	*56*
SR2	+ + *v f*	*317*
DR12	+ *cv* + +	*12*
TR	+ *cv* + *f*	*0*
DR13	+ *cv v* +	*32*
SR1	+ *cv v f*	*120*
SR1	*y* + + +	*187*
DR13	*y* + + *f*	*28*
TR	*y* + *v* +	*1*
DR12	*y* + *v f*	*13*
SR2	*y cv* + +	*270*
DR23	*y cv* + *f*	*19*
SR3	*y cv v* +	*240*
NR	*y cv v f*	*540*

(For clarity, superscripts have been omitted. Instead, + denotes wildtype phenotype for that trait, while the gene symbol denotes a mutant phenotype.)