

- 1.a) Plate strains on lawn of Mata and Mat α on $-Ura$ or $-Lys-Ura$ or $-Leu$ or $-Leu-Lys$. If yeast colonies grow on Mata, then the strain must be Mat α (and vice versa).

Therefore, strains 1-10 are Mat α and strains 11-20 are Mata

- b) Plate strains 1-10 with MAT α wt (wild type) and strains 11-20 with MAT α wt on YPD 37 $^{\circ}$ medium. Thus, only strain 8 is dominant, as there is no growth of yeast colonies when mated with wt. The rest of the strains (1-7, 9-20) are recessive.

- c) Plate strains 1-10 and MAT α wt with strains 11-20 and MAT α wt on YPD 37 $^{\circ}$ medium. The following results appear with "+" indicating growth and "-" indicating no growth of colonies. Can also plate on minimal at 37 degrees. Both ways will get you the same answer.

MAT α strains

	11	12	13	14	15	16	17	18	19	20	wt
1	+	+	+	+	+	+	+	+	+	+	+
2	+	+	+	+	-	+	+	-	+	-	+
3	+	+	+	+	+	+	-	+	+	+	+
4	+	+	+	+	-	+	+	-	+	-	+
5	+	+	+	+	+	+	-	+	+	+	+
6	-	+	-	+	+	+	+	+	+	+	+
7	+	+	+	+	+	-	+	+	-	+	+
8	-	-	-	-	-	-	-	-	-	-	-
9	-	+	-	+	+	-	+	+	-	+	+
10	-	+	-	+	+	+	+	+	+	+	+
wt	+	+	+	+	+	+	+	+	+	+	+

"+" means complementation (different genes) and "-" means no complementation (same genes). Thus, the groups are as follows:

Group I: 1

Group II: 2, 4, 15, 18, 20

Group III: 3, 5, 17

Group IV: 6, 10, 11, 13, (9)

Group V: 7, 16, 19, (9)

9 is a double mutant since it can be placed in 2 complementation groups. 8 cannot be placed in a group since it is dominant. 12 and 14 could define either one or two additional groups (same mating type, so we cannot mate to test complementation).

1 d) The minimum number of genes is 6: (1, 8[?]), (2, 4, 15, 18, 20, 8[?]), (3, 5, 17, 8[?]), (6, 10, 11, 13, 9, 8[?]), (7, 16, 19, 9, 8[?]), (12, 14, 8[?]).

The maximum number of genes is 8: (1), (2, 4, 15, 18, 20), (3, 5, 17), (6, 10, 11, 13, 9), (7, 16, 19, 9), (8), (12), (14)

2 a) Mate strains 1-6 with MAT α wt on min + FOA media. No growth results for strains 1, 2, 4-6, but growth with strain 3. Thus, strains 1, 2, 4-6 are recessive and strain 3 is dominant.

Mate strains 7-12 with MAT α wt on min + FOA media. No growth is seen for strains 7-11, but growth is seen for 12. Thus, strains 7-11 are recessive and strain 12 is dominant.

b) Mate strains 1-6 and MAT α wt with strains 7-12 and MAT α wt on Min + FOA media. "+" = no complementation (same gene). "-" means complementation (different genes). REMEMBER, we are dealing with a "resistance" phenotype.

MAT α strains

MAT α strains

	7	8	9	10	11	12	wt
1	-	+	-	+	-	+	-
2	+	-	-	-	+	+	-
3	+	+	+	+	+	+	+
4	-	-	+	-	-	+	-
5	+	-	-	-	+	+	-
6	-	-	+	-	-	+	-
wt	-	-	-	-	-	+	-

Group I: 1, 8, 10

Group II: 2, 5, 7, 11

Group III: 4, 6, 9

3 and 12 cannot be placed since they're dominant alleles.

c) Min. number of genes is 3: (1, 8, 10, 3[?], 12[?]), (2, 5, 7, 11, 3[?], 12[?]), (4, 6, 9, 3[?], 12[?])
Max number of genes is 5: (1, 8, 10), (2, 5, 7, 11), (4, 6, 9), (3), (12)

3 a) Cross #1 to analyze mutant 1

mutant 1
wingless
 $\sigma^7 \frac{mut1}{?}$

x

wild type
winged
 $\phi \frac{+}{+}$

? = mut1 or y
or +



all winged progeny (F1) \Rightarrow recessive

Crossing F1 progeny:

winged (from F1) x winged (from F1)

$\sigma^7 \frac{mut1}{+} \text{ or } \frac{+}{y}$

$\phi \frac{mut1}{+}$



no wingless females

$\sigma^7 \frac{mut1}{y}$ (wingless); $\sigma^7 \frac{+}{y}$ (winged); $\phi \frac{mut1}{+}$ (winged)
offspring generated

\therefore Mutant 1 is X-linked recessive with genotype $\frac{Mut1}{y}$

Cross #2 to analyze Mutant 2

mutant 2
wingless
 $\sigma^7 \frac{mut2}{?}$

x

wildtype
winged
 $\phi \frac{+}{+}$

? = mut2, y, or +

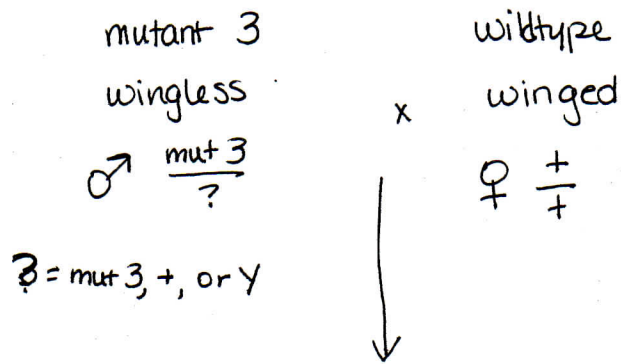


$\sim 50\%$ winged (mix of sexes)

$\sim 50\%$ wingless

\therefore Mutant 2 is autosomal dominant and the genotype is heterozygous $\frac{mut2}{+}$

Cross #3 to analyze mutant 3

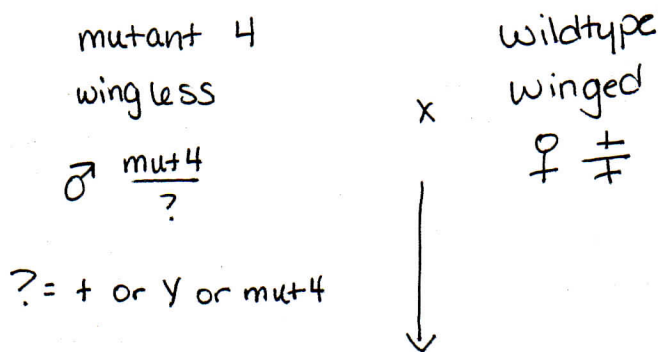


no wingless σ 's or winged ϕ 's.

only wingless $\phi \frac{mut3}{+}$ and winged $\sigma \frac{+}{Y}$ offspring generated.

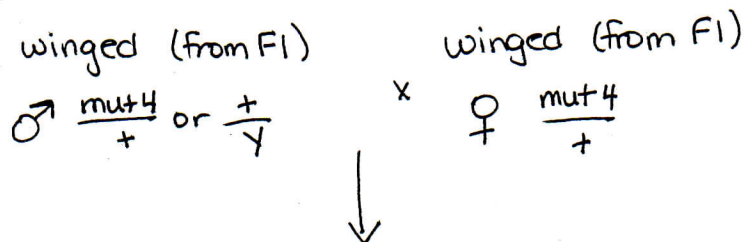
\therefore mutant 3 is X-linked dominant with genotype $\frac{mut3}{Y}$

Cross 4 to analyze mutant 4



all winged progeny \Rightarrow recessive

Crossing F1 progeny:



$\sim 75\%$ winged
 $\sim 25\%$ wingless

\therefore mutant 4 is autosomal recessive with genotype $\frac{mut4}{mut4}$

mutant 4 could have come from a true-breeding line (all flies homozygous for the mut4 allele. Additionally, mut1 and mut 3 could come from true-breeding lines where females are homozygous $\frac{x^{mut}}{x^{mut}}$ and males are $\frac{x^{mut}}{y}$.

Mutant 2, however, must come from a cross.

4 a) Mechanism a

Wild type x wingless

AA

aa



Aa (F1 = normal wings)

Aa x Aa



1 AA : 2 Aa : 1 aa

Phenotypically: 3 wt : 1 wingless
(25% F2 wingless)

Mechanism b

Wild type
AABB

wingless
aabb

x



AaBb (F1 = normal wings)

AaBb x AaBb



	AB	Ab	aB	ab
AB	ABAB	AABb	AaBB	AaBb
Ab	AABb	AAbb	AaBb	Aabb
aB	AaBB	AaBb	aaBB	aaBb
ab	AaBb	Aabb	aaBb	aabb

∴ phenotypically: 15 winged : 1 wingless (6.25% of F2 wingless).

Mechanism C

Wildtype wingless
AABB x aabb, aaB-, A-bb

Since "-" means blank, it can be either allele (use table from mechanism b)

Phenotypically: 9 winged : 7 wingless (43.75% F2 wingless)

Mechanism D

Wildtype x wingless
AABB aaB^D-

Again, look @ mechanism b table. However, since wingless mut is produced from recessive allele of 1 gene ("aa") but dominant allele of the other (BB or Bb), phenotypic ratio is 13 wt : 3 wingless (18.75% of F2 is wingless).

With Star Genetics

Cross mut ♂ to wt ♀, then cross any F1 ♂ to cross to any F1 ♀. Note F2 ratios to determine mechanism (make sure to generate enough F2 progeny for a significant result). Below is a REAL star genetic trial.

Mut1 x wt → normal F1 → ~6% F2 wingless ⇒ Mechanism B

Mut2 x wt → normal F1 → ~28% F2 wingless ⇒ Mech. A

Mut3 x wt → normal F1 → ~17% F2 wingless ⇒ Mech. D

Mut4 x wt → normal F1 → ~40% F2 wingless ⇒ Mech. C

Chi-Square Analysis

For a given model, let's take Mutant 2 as an example (mech A).

° Freedom = # phenotypic classes - 1 = 2 - 1 = 1

level of significance = 5% ⇒ p = 0.05

From StarGenetics, we get the following observed result out of a total of 168 offspring with mechanism A. From our calculations, we get the following expected results for F2

	expected	observed	$(E-O)^2$	$(E-O)^2/E$
wt	126	120	36	0.2857
wingless	42	48	36	0.8571

$$\text{Total} = \chi^2 = 1.1428$$

Based on χ^2 table provided, P is between 10% and 50% probability (between p of 0.9 and 0.5). Since this is greater than the cutoff of 5%, a statistically significant result between the observed and expected results cannot be concluded (cannot reject null hypothesis).

Now, what if we assume mut 2 is mechanism D instead?

	E	O	$(E-O)^2$	$(E-O)^2/E$
wt	136.5	120	272.25	1.9945
wingless	31.5	48	272.25	8.643

$$\text{Total} = \chi^2 = 10.6$$

$\therefore P$ is < 0.005 . This is less than the cutoff of 0.05, so we reject the null hypothesis that mutant 2 exhibits mechanism D.

5. a) The trait is recessive. Neither the parents of individuals 3 or 2 exhibit the mutant phenotype.

$$\text{b) Bayes Theorem: } P(X|Y) = \frac{p(Y|X) * p(X)}{[p(Y|X) * p(X)] + [p(Y|\bar{X}) * p(\bar{X})]}$$

$$p(1 \text{ is a carrier, } Aa | 5 \text{ unaffected, } Aa) = \frac{\frac{1}{2} \cdot \frac{2}{3}}{(\frac{1}{2} \cdot \frac{2}{3}) + (1 \cdot \frac{1}{3})} = \frac{\frac{1}{3}}{\frac{2}{3}} = \boxed{\frac{1}{2}}$$

$$\begin{aligned} \text{c) } p(2^{\text{nd}} \text{ child with trait}) &= p(1 \text{ is carrier}) * p(2 \text{ is carrier}) * p(\text{child will be affected}) \\ &= \left(\frac{1}{2}\right)(1)\left(\frac{1}{2}\right) = \boxed{\frac{1}{4}} \end{aligned}$$

$$d) p(\text{child has trait}) = p(5 \text{ is a carrier}) * p(6 \text{ is a carrier}) * p(\text{child will be affected}) \\ = (1)(1)\left(\frac{1}{4}\right) = \boxed{\frac{1}{4}}$$

e) Since both 5 and 6 are Aa, an "unaffected child" does not change the probability of an affected child. It remains $\boxed{\frac{1}{4}}$ as in part d.

$$f) p(X|Y) = p(1 \text{ is a carrier} | 5 \text{ is unaffected}) = \frac{\frac{1}{2}\left(\frac{1}{2}\right)}{\left(\frac{1}{2} \cdot \frac{1}{2}\right) + \left(1 \cdot \frac{1}{2}\right)} = \frac{\frac{1}{4}}{\frac{1}{4} + \frac{2}{4}} = \frac{\frac{1}{4}}{\frac{3}{4}} = \boxed{\frac{1}{3}}$$

$$g) p(X|Y) = p(4 \text{ is a carrier} | 6 \text{ is unaffected}) = \frac{\frac{1}{2}\left(\frac{1}{2}\right)}{\left(\frac{1}{2} \cdot \frac{1}{2}\right) + \left(1 \cdot \frac{1}{2}\right)} = \boxed{\frac{1}{3}}$$

$$h) p(6 \text{ is a carrier}) = \boxed{1} \quad 3 \text{ is } X^m/Y, \text{ so } 6 \text{ must be a carrier}$$

$$i) p(\text{second daughter with trait}) = p(3 \text{ is carrier}) * p(4 \text{ is carrier}) * p(\text{daughter will be affected}) \\ = 1 \left(\frac{1}{3}\right) \left(\frac{1}{2}\right) = \boxed{\frac{1}{6}}$$

$$j) p(\text{son with trait}) = p(6 \text{ is carrier}) * p(\text{son will be affected}) \\ = 1 \left(\frac{1}{2}\right) = \boxed{\frac{1}{2}}$$

k) 6 is a carrier, so the probability doesn't change due to one unaffected son. The chance of the 2nd son having the trait is still $\boxed{\frac{1}{2}}$