

Revision problems (Tutorials 1-3)

- Test whether the following observed distributions of genotypes vary significantly from an expected distribution of 9:3:3:1

(a)

Genotype	A	B	C	D
Observed frequency	160	120	80	40

(b)

Genotype	A	B	C	D
Observed frequency	120	40	30	10

(c)

Genotype	A	B	C	D
Observed frequency	56	18	8	5

- Calculate the frequencies of the different alleles in the following cases

(a)

Genotype	AA	AB	BB
Frequency	56	78	22

(b)

Genotype	AA	AB	AC	BB	BC	CC
Frequency	120	40	30	10	30	10

(c)

Genotype	AA	AB	AC	BB	BC	CC
Frequency	56	18	8	15	18	5

- Test whether the above distributions vary significantly from Hardy-Weinberg expectations
- Calculate observed heterozygosity (H_{obs}), expected heterozygosity (H_{exp}), and the effective number of alleles (n_e) for each case in Question 2.
- Estimate the frequencies of as many alleles as you can in the following case of complete dominance:

Phenotype	Green	Blue
Genotype	AA and AB	BB
Frequency	56	8

6. Calculate polymorphism (P), average allelic diversity (A), and average n_e for each of the following cases:

(a)

Locus	allele1	allele2	allele3	allele4	allele5
1	0.40	0.30	0.10	0.10	0.10
2	0.65	0.25	0.05	0.05	
3	0.70	0.30			
4	0.80	0.20			
5	1.0				

(b)

Locus	allele1	allele2	allele3	allele4
1	0.55	0.35	0.05	0.05
2	0.50	0.30	0.10	0.10
3	0.60	0.30	0.10	
4	1.0			
5	1.0			

7. Calculate linkage disequilibrium (D) in a population with the following gametic frequencies.

(a)

Genotype	A_1B_1	A_1B_2	A_2B_1	A_2B_2
Frequency	0.130	0.260	0.150	0.460

(b)

Genotype	A_1B_1	A_1B_2	A_2B_1	A_2B_2
Frequency	0.375	0.050	0.150	0.425

(c)

Genotype	A_1B_1	A_1B_2	A_2B_1	A_2B_2
Frequency	0.3	0.3	0.2	0.2

8. You have a laboratory population of plants that mature at a mean height of 1.2m. If you knew that the heritability (h^2) of height in your population was 0.56, how tall would you predict plants in the F1 generation to be (on average) if you bred from a selection of F0 parents with an average height of 1.8m?

9. You then choose individuals from your F1 generation that again averaged 1.8m, and bred from them to generate an F2 generation. How tall would then you predict your F2s to be (on average)?

10. Draw a (not-to-scale) circle diagram that illustrates the variances of a quantitative trait in each of the following cases. You will need to calculate the missing values and indicate them in your diagrams:

(a) $V_G = 105$, $V_E = 35$, $V_P = ???$

(b) $V_P = 150$, $V_G = 20$, $V_E = ???$

(c) $V_G = 32$, $V_A = 16$, $V_{D+I} = ???$

(d) $V_A = 25$, $V_E = 120$, $V_P = 160$, $V_{D+I} = ???$

11. We measure a trait for the full-siblings across multiple families. By looking at the similarity between the offspring within each family, we calculate genetic variance as 0.68. We then subtract this value from the total phenotypic variance to estimate V_E as 1.24. What type of heritability could you estimate using these data? Actually calculate the estimate for heritability.

12. Estimate heritability from the measurements of parents and their offspring as given below.

(a)

Family	Sire	Dam	Son	Daughter
A	8	12	11	9
B	14	14	10	14
C	17	19	20	8
D	26	18	18	14
E	32	20	22	14

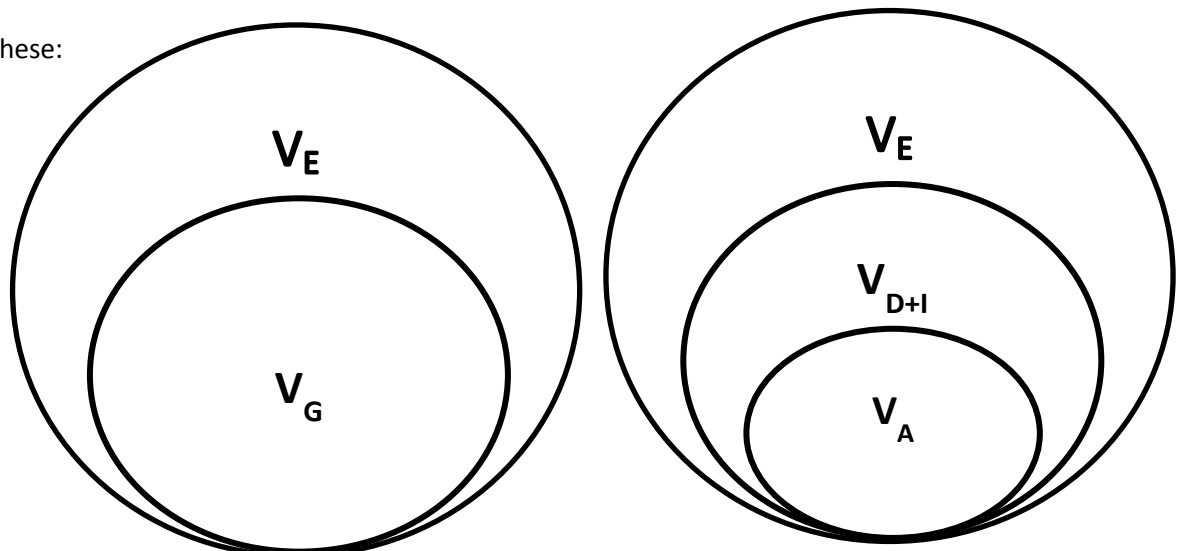
(b)

Family	Sire	Dam	Son	Daughter
A	8	12	11	9
B	15	15	11	13
C	19	21	14	14
D	26	24	18	14

Answers:

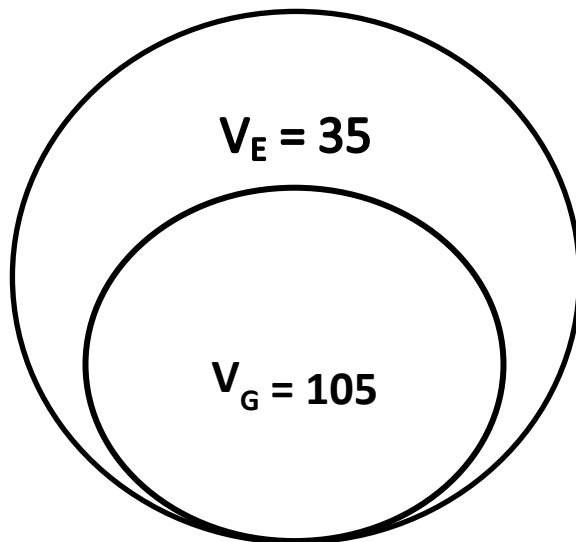
- All distributions tested against chi-squares critical value for 3 degrees of freedom (**7.81**).
 (a) Chi-square value = 55.11. Significant deviation.
 (b) Chi square value = 2.67. Not significant.
 (c) Chi square value = 5.46. Not significant.
- Use allele counting to calculate p and q (and r).
 (a) Frequency of A allele = $p = 0.609$, $q = 0.391$.
 (b) Frequency of A allele = $p = 0.6458$, $q = 0.1875$, $r = 0.1667$
 (c) Frequency of A allele = $p = 0.575$, $q = 0.275$, $r = 0.150$
- Use p,q,r to generate H-W expected frequencies then test against observed frequencies using chi-square.
 (a) Chi-square value = 0.388. Critical value for $(3-1) = 2$ d.f. is **5.99**. Hence, no deviation from H-W.
 (b) Chi-square value = 35.65. Critical value for $(6-1) = 5$ d.f. is **11.07**. Hence, significant deviation from H-W.
 (c) Chi-square value = 37.45. Critical value for $(6-1) = 5$ d.f. is **11.07**. Hence, significant deviation from H-W.
- Observed H is simply the number of heterozygotes divided by total N. Expected H is calculated using the formula for H (or could also be calculated as $2pq$ in (a) and $2pqr$ in (b). Use the formula as given for n_e .
 (a) $H_{obs} = 78/156 = 0.5$, $H_{exp} = 2pq = 0.4762$, $n_e = 1.909$
 (b) $H_{obs} = (40+30+30)/240 = 0.4167$, $H_{exp} = 2pqr = 0.5200$, $n_e = 2.083$
 (c) $H_{obs} = 0.3667$, $H_{exp} = 0.5713$, $n_e = 2.332$
- Frequency of BB = $q = 8/64 = 0.125$. At H-W equilibrium, $BB = q^2$, so $q = \sqrt{0.1429} = 0.353$.
 $p = 1 - q = 0.647$.
- (a) $P = 0.8$, $A = 2.80$, $n_e = 1.961$. (b) $P = 0.6$, $A = 2.60$, $n_e = 1.855$
- (a) $D = 0.0208$, (b) $D = 0.1519$, (c) $D = 0$
- Breeder's equation: $R = h^2S$. In this case the selection differential (S) is $1.8 - 1.2 = 0.6$. Therefore, $R = 0.56 \times 0.6 = 0.336$. The height of your F1 generation would therefore be $1.2 + 0.336 = 1.536$ m.
- In this case, the selection differential is $1.8 - 1.536 = 0.264$. Hence, $R = 0.56 \times 0.264 = 0.148$. Your F2s would therefore average $1.536 + 0.148 = 1.684$ m.
- We need $V_p = V_G [= V_A + V_{D+I}] + V_E$
 (a) $V_G = 105$, $V_E = 35$, $V_p = ?$ $V_p = V_G + V_E$...therefore $V_p = 105 + 35 = 140$
 (b) $V_p = 150$, $V_G = 20$, $V_E = ???$. $V_E = V_p - V_G$ so $V_E = 130$
 (c) $V_G = 32$, $V_A = 16$, $V_{D+I} = ???$ $V_G = V_A + V_{D+I}$ so $V_{D+I} = 16$
 (d) $V_A = 25$, $V_E = 120$, $V_p = 160$, $V_{D+I} = ???$ $V_{D+I} = V_p - (V_A + V_E) = 15$

Then generally use these:



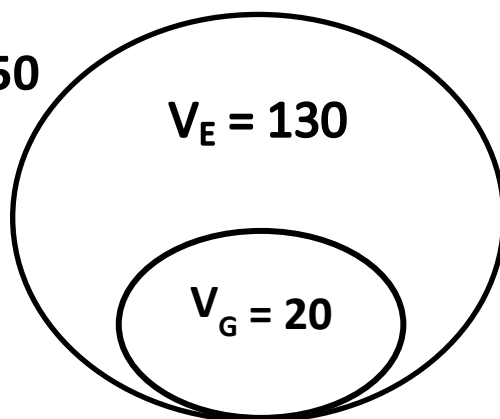
(a)

$$V_P = 140$$



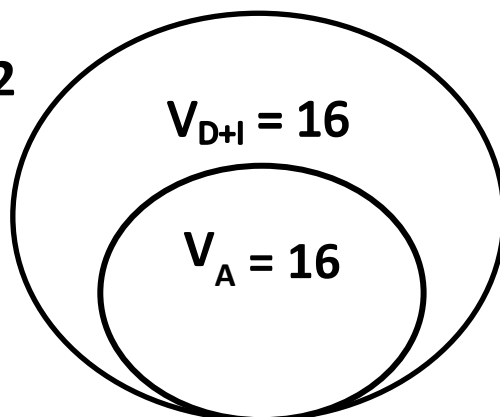
(b)

$$V_P = 150$$



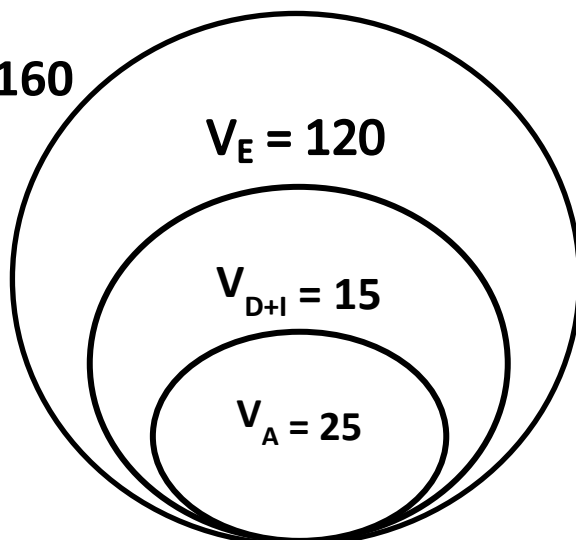
(c)

$$V_G = 32$$



(d)

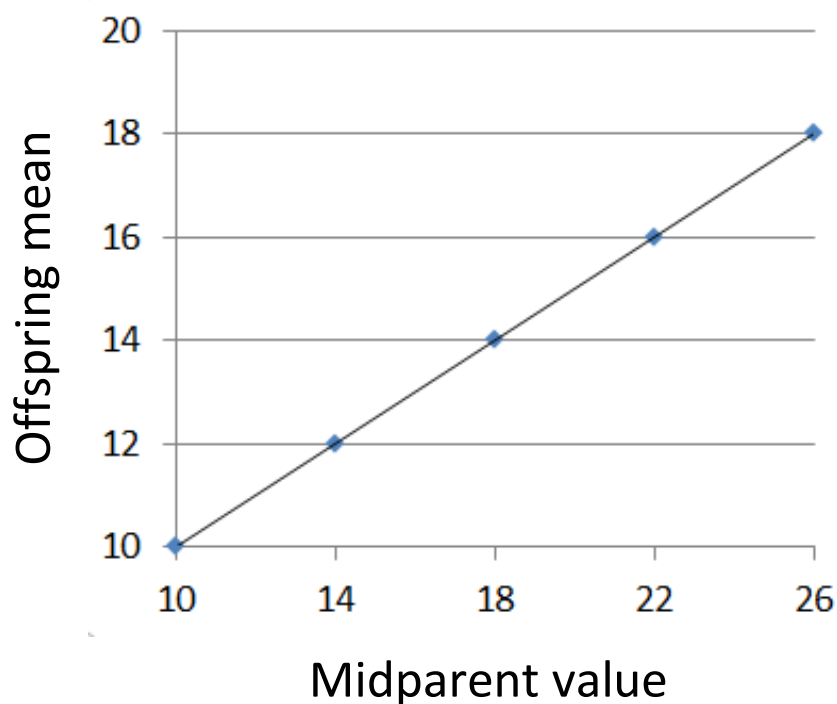
$$V_P = 160$$



11. $V_G = 0.68$ and V_E is 1.24, so the total phenotypic variance = 1.92. Heritability is broad sense heritability (H^2), calculated as $V_G/V_P = 0.68/1.92 = 0.354$.
12. First calculate the means for each set of parents and their offspring. Then plot them on a scatterplot with parents along the x-axis and offspring along the y-axis.

(a)

Family	Sire	Dam	Son	Daughter	Parent mean	Offspring mean
A	8	12	11	9	10	10
B	14	14	10	14	14	12
C	17	19	20	8	18	14
D	26	18	18	14	22	16
E	32	20	22	14	26	18

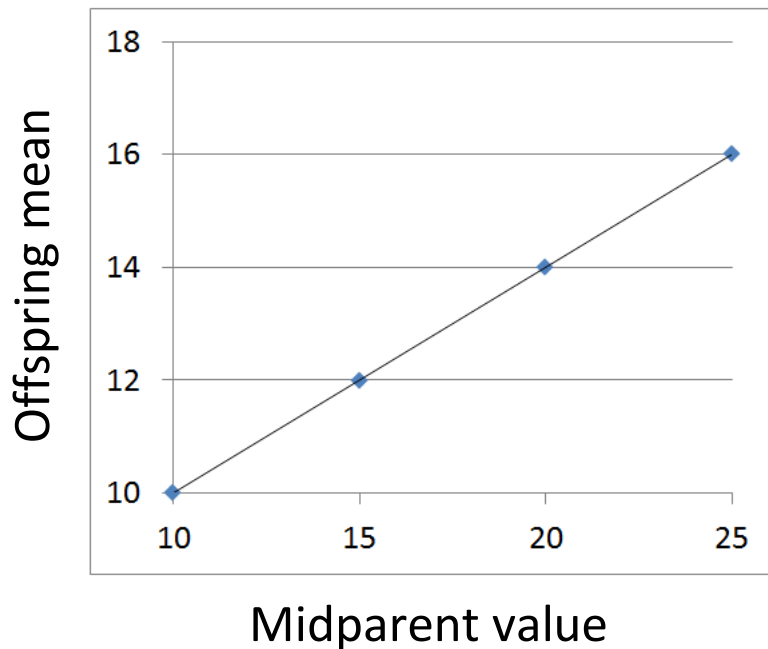


The slope of the line gives h^2 . This can be calculated by looking at how much the line rises in Y-axis units for any given change along the x-axis. So, for example, as X increases from **10 to 26 (16 units)**, Y increases from **10 to 18 (8 units)**. So the slope is therefore $Y/X = 8/16 = 0.5$.

Therefore $h^2 = 0.5$

(b)

Family	Sire	Dam	Son	Daughter	Parent mean	Offspring mean
A	8	12	11	9	10	10
B	15	15	11	13	15	12
C	19	21	14	14	20	14
D	26	24	18	14	25	16



Again - the slope of the line gives h^2 .

Here, we can calculate that as **X increases from 10 to 26 (15 units)**, the line rises **6 units in the Y-axis**. So the slope is therefore $Y/X = 6/15 = 0.4$.

Therefore $h^2 = 0.4$