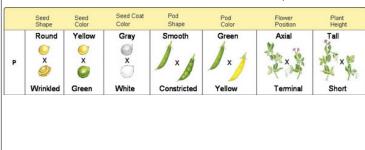
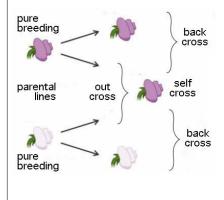


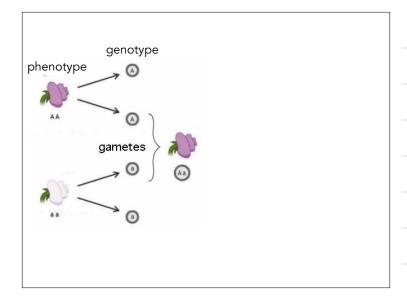
Mendel

- true breeding lines / discrete traits (independent)



Mendel's observation (1 trait, flower color)





Mendel's conclusions

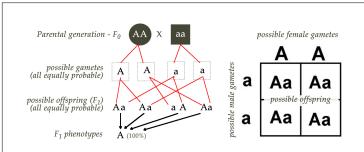
stable (trans-generational) "factors" (**genes**) influence **phenotypic** traits

Genes exist in different versions (alleles).

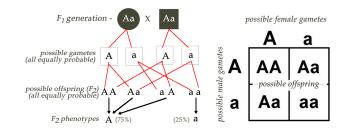
Adults have two copies of each gene (diploid)

Gametes produced by adults have one copy of each gene (haploid), a single allele for each gene

An allele can be dominant or recessive.



What percentage of phenotypes do you expect?



What percentage of phenotypes do you expect?

How can you gauge whether the number you observed are consistent with your hypothesis? the numbers not exact?

Chi square analysis

$$\chi^2 = \sum_{n=0}^{\infty} \frac{\text{(observed - expected)}^2}{\text{expected}}$$

Our hypothesis must predict what values we observe - it must be quantitative.

Chi square value enables us to conclude, tentatively, that results observed are unlikely to be due to chance (as opposed to our hypothesis being "true").

Our hypothesis is called the "null hypothesis"

Chi square analysis

Degrees of freedom (number of possible outcomes – 1)

Lowest possible "Degree of Freedom" is

"Degree of Freedom" for monohybrid cross is

Chi square analysis

Dogwood of	Chi-Square (χ^2) Distribution Area to the Right of Critical Value							
Degrees of - Freedom	0.99	0.975	0.95	0.90	0.10	0.05	0.025	0.01
1		0.001	0.004	0.016	2,706	3,841	5.024	6.635
2	0.020	0.051	0.103	0.211	4.605	5.991	7.378	9.210
3	0.115	0.216	0.352	0.584	6.251	7.815	9.348	11.345
4	0.297	0.484	0.711	1.064	7.779	9.488	11.143	13.277
5	0.554	0.831	1.145	1.610	9.236	11.071	12.833	15.086
6	0.872	1.237	1.635	2.204	10.645	12.592	14.449	16.812
7	1.239	1.690	2.167	2.833	12.017	14.067	16.013	18.475
8	1.646	2.180	2.733	3.490	13.362	15.507	17.535	20.090
9	2.088	2.700	3.325	4.168	14.684	16.919	19.023	21.666
10	2.558	3.247	3.940	4.865	15.987	18.307	20.483	23.209

Fair Die problem:

Roll die 120 times:		observed	expected
	"1"	23	20
	"2"	10	20
	"3"	35	20
	"4"	18	20
	"5"	14	20
	"6"	20	20

Degrees of freedom = ____

Fair Die problem:

Roll die 120 times:

	observed	expected		
"1"	23	20	$3^2 \div 20 =$	0.45
"2"	10	20	$10^2 \div 20 =$	5
"3"	35	20	$15^2 \div 20 =$	11.25
"4"	18	20	$2^2 \div 20 =$	0.45
"5"	14	20	$6^2 \div 20 =$	0.2
"6"	20	20	$0^2 \div 20 =$	0

17.35

Degrees of freedom = ____

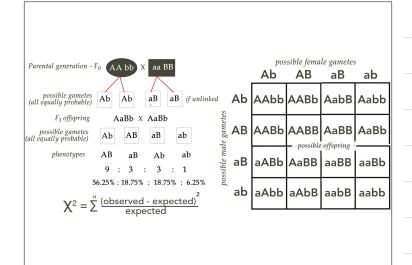
Chi square analysis Chi-Square (χ^2) Distribution Area to the Right of Critical Value Degrees of -Freedom 0.90 0.10 0.05 0.025 0.01 0.99 0.975 0.95 0.001 0.004 0.016 2,706 3.841 5.024 6.635 0.004 0.103 0.352 0.711 4.605 6.251 7.779 0.211 0.584 5.991 7.815 7.378 9.348 0.051 9.210 3 0.115 11.345 13.277 0.216 1,064 9,488 11.143 0.554 0.831 1.145 9.236 11.07112.833 15.086 0.872 1.237 2.204 12.592 14.449 16.812 1.635 10.645 2.167 2.733 3.325 12.017 13.362 14.684 14.067 15.507 16.919 1.239 1.690 2.833 16.013 18.475 2.180 2.700 20.090 21.666 1.646 2.088 3.490 4.168 17.535 19.023 2.558 3.940 4.865 15.987 18.307 20.483 23.209

17.35

Mendel's data

Results of all of Mendel's monohybrid crosses

	Parental phenotype	F ₁	F ₂
1.	Round×wrinkled seeds	All round	5474 round; 1850 wrinkled
2.	Yellow×green seeds	All yellow	6022 yellow; 2001 green
3.	Purple×white petals	All purple	705 purple; 224 white
4.	Inflated×pinched pods	All inflated	882 inflated; 299 pinched
5.	Green×yellow pods	All green	428 green; 152 yellow
6.	Axial×terminal flowers	All axial	651 axial; 207 terminal
7.	Long×short stems	All long	787 long; 277 short
			Griffiths et al., 2000



Mendel's (tentative) conclusions	
alleles seggregate	
Genes exist in different versions (alleles). Adults have two copies of each gene (diploid) Gametes produced by adults have one copy of each gene (haploid), a single allele for each gene An allele must be dominant or recessive.	
Alternatives to Mendel's conclusions	
Genes exist in different versions (alleles).	
Adults have two copies of each gene (diploid)	
Gametes produced by adults have one copy of each gene (haploid), a single allele for each gene	
An allele must be dominant or recessive.	
	1