Using the Hardy-Weinberg Equations to find Frequency

1. Determine number and frequency of each phenotype in population
2. Use the frequency of non-tasters(q2) to find q.
3. Use p+q = 1 to find p.
4. Use p, q values to find genotype frequencies: p2 + 2pq + q2 = 1
5. Use genotype frequencies and population size to find # students/genotyype.
6. If expected frequencies = observed frequencies then population is not evolving (no change in p, q frequency)

Punnett square

	A	a
A	AA (p^2)	Aa (pq)
a	Aa (pq)	aa(q^2)

SODIUM BENZOATE

	Taster		Non-Taster	Total	steps
# in population	11		4	15	survey the population
phenotype frequency				1.00	divide part by whole
allele frequency				1.00	solve for q; then use p+q = 1 to find p
genotype	Homozygous dominant (p^2)	Heterozygous (2pq)	Homozygous recessive (q^2)	n/a	
genotype frequency				1.00	p^2 + 2pq + q^2 = 1
# in population				15	frequency * total population

THIOUREA

	Taster		Non-Taster	Total	
# in population	14		2	16	survey the population
phenotype frequency				1.00	divide part by whole; this is q^2
allele frequency				1.00	solve for q; then use p+q = 1 to find p
genotype	Homozygous dominant (p^2)	Heterozygous (2pq)	Homozygous recessive (q^2)	n/a	
genotype frequency				1.00	p^2 + 2pq + q^2 = 1
# in population				16.0	frequency * total population

PTC

	Taster		Non-Taster	Total	
# in population	15		1	16	survey the population
phenotype frequency				1.00	divide part by whole
allele frequency				1.00	solve for q; then use p+q = 1 to find p
genotype	Homozygous dominant (p^2)	Heterozygous (2pq)	Homozygous recessive (q^2)	n/a	
genotype frequency				1.00	p^2 + 2pq + q^2 = 1
# in population				16	frequency * total population