

POPULATION GENETICS and USING HARDY WEINBERG-Practice "Type I" Question
ANGELL*BIO 150
KEY

Imagine we head into Northfield and count the number of people with each genotype.

- 1460 individuals of type MM
- 2550 of type MN
- 0 individuals of type NN!

What are the allele frequencies of the M and N allele in this population (basically you are "applying the Hardy Weinberg Principle)

Total number of individuals in the population...4,010. Total number of alleles at this locus in the population....8,020.

Frequency of M (p) = $(1460+1460+2550)/8,020 = .682$

Frequency of N (q) = $2550/8,020 = .318$

Now calculate the expected genotype frequencies. These are the frequencies you would expect to see if "nothing" is going on in the population (no selection, no gene flow, or migration, no inbreeding (like mating with like for example if all homozygous recessive NN genotypes only chose to mate with other NNs). Show your work.

What would we expect the genotype frequencies to be??

Expected Freq of MM $(.682)^2 = .465$

Expected Freq of MN $2(.682)(.318) = .434$

Expected Freq of NN $(.318)^2 = .101$

Notice they should add up to 1!

Now calculate the genotype frequencies in the actual population in Northfield using the numbers above.

Actual genotype freq MM = $1460/4010 = .364$

Actual genotype freq of MN = $2550/4010 = .636$

Actual genotype freq of NN = $0/4010 = 0$

Is this population in Hardy Weinberg? (compare the two!) Ummm no it is not in HW! We are totally lacking the NN genotype...wow what could be happening?

You should go straight to the assumptions of the HW theorem...what were they?

One obvious possibility is selection against the NN individuals. Perhaps NN individuals are born but just don't survive.

If the population is super small (which it really isn't) you might suspect genetic drift is happening, but that doesn't really fit this scenario.

If you just had way too many of the MMs relative to the other it might be that a neighboring population that is all MMs is flooding individuals with their MM genes into this Northfield population. This would be gene flow.

If you had a lot of extra MNs compared to what you would expect you might think about heterozygote advantage where the heterozygote has higher fitness than either the MM or NN.