

MCB 142 Discussion

Hana Lee

November 25, 2008

1 Hardy-Weinberg

Hardy-Weinberg equilibrium occurs under the following assumptions:

- Large (infinite) population
- Random mating
- No new mutations
- No migration
- No genotype-dependent differences in fitness

If the above assumptions hold true, then we can assume that the population achieves Hardy-Weinberg genotype frequencies in one generation and maintains those genotype frequencies in subsequent generations. Allele frequencies remain unchanged from generation to generation.

Selection and genetic drift are both mechanisms by which allele and genotype frequencies can change over time in a population.

2 Selection

Natural selection changes allele frequencies because not all genotypes have the same reproductive fitness.

To calculate the change in allele frequencies, look at the relative viabilities of the different genotypes. For a biallelic gene with alleles A and a :

$$\bar{w} = p^2 w_{AA} + 2pq w_{Aa} + q^2 w_{aa} \quad (1)$$

$$\Delta q = \frac{pq (q (w_{aa} - w_{Aa}) + p (w_{Aa} - w_{AA}))}{\bar{w}} \quad (2)$$

The rate at which Δq (i.e. allele frequency of a) decreases with time depends on q (i.e. the initial allele frequency of a). Hence, rare recessive lethal alleles will never completely disappear from the population. The rate also depends on s , so if there is a strong selection against an allele, the allele frequency can change rapidly.

There is also balancing selection, which maintains genetic variation:

- Heterozygous advantage ($q_e = \frac{t}{s+t}$)
- SI and MHC loci
- Mutation-selection balance ($q = \sqrt{\frac{\mu}{s}}$)

3 Genetic Drift

On average, random mating does not cause change in allele frequencies, but small populations are subject to random deviations. The variance in frequency, where p is the initial frequency of a particular allele and N is the population size, is:

$$\sigma^2 = \frac{p(1-p)}{2N} \quad (3)$$

The time to fixation or loss for a neutral allele is $4N$ generations. The probability of fixation is equal to its initial frequency.

Genetic variation is maintained through the mutation-drift balance. Given π , the average pairwise difference in sequence, or S , the number of segregating sites, and μ , the mutation rate, the following equation allows us to estimate the population size:

$$\pi = 4N\mu L \quad (4)$$

$$S = 4N\mu L \sum_{i=1}^{n-1} \frac{1}{i} \quad (5)$$