CONCEPT OF GENE POOL AND GENE FREQENCY

(Pg semester II – CC-8)

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GENE POOL

A gene pool is the collection of different genes with in an interbreeding population. The concept of a gene pool usually refers to the sum of all the alleles at all of the loci within the genes of a population of a single species. It includes both genes that are expressed, and those that are not.

A population that has a large and diverse gene pool tends have increased biological fitness and is usually able to adapt to and survive throughout pressures caused by rapid changes in environmental conditions or disease. Although individuals may die in such situations, a diverse population often contains enough genetic variation so that there will be an availability of suitable genes that are necessary for survival. This is the basic concept behind the theory of natural selection.

A population with a narrow gene pool containing low diversity is more likely to suffer from reduced fitness when affected by stresses and is more likely to become extinct. This is either due to a low availability of alleles that are necessary for an organism to survive under certain conditions, or due to the consequences of inbreeding. When there is less variation between available alleles, there is a

greater probability that a harmful allele, which causes a deformity or disease, will increase in frequency.

Over time, the size of any gene pool can change through natural selection, gene flow and genetic drift. The size may increase when a gene mutation occurs and survives, and decrease when alleles are removed, e.g. when a population goes through a bottleneck.

There can be several variations of each allele for each gene, some of which are dominant alleles and some of which are recessive alleles. Within genes, each allele variant occurs at a particular frequency, at a particular time. When small changes to allele frequency occur this is known as microevolution, large changes, or an accumulation of small changes results in macroevolution, both of which can result in speciation.

The genetic variation within the population is characterized by differences in allele frequency and determines the relative frequency of each phenotype displayed in a population. The phenotype of an individual is determined by its own gene.

Examples of Gene Pool

Humans

Every human being on Earth is able to interbreed with one another as a single species. The human gene pool is therefore made up of every allele variant of the approximated 19,000-20,000 human genes within our DNA.

GENE FREQUENCY

The gene frequency is the number of individual alleles of a certain type, divided by the total number of alleles of all types in a population. In simple terms, the allele frequency describes how common an allele is within a population.

GENE FREQUENCY OVERVIEW

The gene frequency is different from the phenotypic ratio in that it accounts for all alleles, even if they are recessive and are “hidden” within carrier organisms. The phenotypic ratio only describes the phenotypes, or actual physical features that are present within a population. To find the allele frequency, scientists must consider heterozygous individuals, which may be hiding a recessive allele.

Gene frequency is most commonly calculated using the Hardy-Weinberg equation, which describes the relationship between two alleles within a population. When more than two alleles are present, scientists must use more complex methods to determine the actual allele frequency. Allele frequency can change over time as evolution acts upon a population and the population adapts by increasing or decreasing the frequency of certain alleles.

Calculating gene frequencies is a complex topic, which combines aspects of math and genetics. In general, all of the alleles in a population add up to 100%. So, we can use mathematical formulas to predict and determine the allele frequency of an allele in a population.

CALCULATE GENE FREQUENCY

To find the number of alleles in a given population, you must look at all the phenotypes present. The phenotypes that represent the allele are often masked by

dominant and recessive alleles working in conjunction. To analyze the gene frequency in a population, scientists use the Hardy-Weinberg (HW) equation. The Hardy-Weinberg equation is written as follows: $1 = p^2 + 2pq + q^2$

P and q each represent the allele frequency of different alleles. The term p^2 represents the frequency of the homozygous dominant gene. The other term, q^2, represents the frequency of the homozygous recessive gene.

While it would be impossible to count all of the hidden gene, it is easy to count the number of recessive phenotypes in a population. Recessive phenotypes are caused by two recessive alleles. Therefore, q^2 can be easily observed by dividing the total number of recessive phenotypes by the total number of individuals. Let's look at an example of how we can use this information to calculate the allele frequency of any given allele.

GENE FREQUENCY EXAMPLE

In a simplified scenario, p and q are the only alleles in the population, and the population is not developing any mutations. If this is the case, the sum of the gene frequencies of p and q must equal 1 because with only two alleles the combined frequency must equal 100%.

Finding q

In this example, consider a hypothetical population of rabbits. A certain recessive allele within rabbits causes the rabbits to be white, while all of the other rabbits are black. Only a rabbit with two recessive alleles for a particular gene will be white.

When we observe the population, we find that there are 16 white rabbits and 84 black rabbits.

Since we already know what q^2 is simply by observing the population, we can take the square root of q^2 to find q. In this case, the white rabbits contain two recessive alleles. The white rabbits account for 16 of the 100 total rabbits. In a percentage, this is exactly 16%, or 0.16. This number is equivalent to q^2. Taking the square root, we find that the allele frequency of q (white) is 0.4, or 40%.

Finding p

Once we know q, we can simply subtract q from 1 to find the frequency of p. This works only in a simplified scenario, where p and q are the only alleles and account for 100% of the total alleles. In this case, p will be equal to 60% of the alleles, or 0.6