PHASE 3 LAB REPORT

Purpose

Determining Human recessive and Dominant Genes

Introduction

Punnett square on dwarfism

	½ D	½ d
½ D	¼ DD	¼ Dd
½ d	¼ Dd	¼ dd

key:- DD-dwarf
Dd- heterozygous
dd- Normal human

Genes possess two alleles that are one inherited from the mother and another from the father. Inheritance of alleles in a gene is by luck one gene may have different numbers of alleles. Parents possess any either the recessive or dominant genes. (Goswami, 1976)

Certain genes i.e. Tongue rolling ability may have a recessive and dominant gene. In such cases, tongue rolling ability may be called dominant allele(R) while the inability to roll the tongue may be presented by recessive gene(r). All parents possess any of the combination alleles; aa, Aa or AA. (Judd, 2010) Therefore, the probability of inheriting either a recessive or dominant gene is half. Unexpected outcome is dwarfism allele in human is dominant, whereas recessive allele is represented by normal growth. In such instances if one inherit both the alleles both the dwarfism and normal growth traits. Various examples may be used to examine this; e.g. eye color dominant traits may be presented brown eyes while recessive traits may be expressed by hazel, grey, blue or green eyes. (Curl, 1961)

Hypothesis

Unexpected outcome is dwarfism allele in human is dominant, whereas recessive allele is
represented by normal growth.

Methods

Main methods applied are sequencing and mapping. Sequencing refers to the determination of DNA exact base pairs. Mostly chromosome size in humans varies between 55,000,000 to about 300,000,000 pairs. Arranged in order and similarity of base pairs helps the sequencing procedure in determining alleles.

Mapping entails segmenting chromosomes into small portions that

can be characterized and propagated. Also, involves arranging them to match their chromosomal locations.

Results/Outcomes and Discussion.

Sequencing procedure was used in determining the relationship between chimpanzee and humans. It was found that around three billion base pairs are equal to the human genome. 99.7% of the base pairs confirm that human and chimpanzee genes are identical. This is because humans share more than 99% of base pairs with chimpanzee. Genetic gap between chimpanzee and human is then confirmed to be equally linked.

References

1. Curl, S. E., Comfort, J. E., & Lasley, J. F. (1961). ***Dwarfism in beef cattle and the influence of dwarfism genes on physiological response to hormone-induced stress.*** Columbia, Mo: University of Missouri, College of Agriculture, Agricultural Experiment Station

2. Goswami, P. N. (1976). ***Effect of dwarfing genes on yield and its components in pearlmillet (Pennisetum Typhoides).***

3. Judd, S. J. (2010). ***Genetic disorders sourcebook: Basic consumer health information about heritable disorders, including disorders resulting from abnormalities in specific genes.*** Detroit, MI: Omnigraphics