International Journal of Scientific Research in Science and Technology
Available online at : www.ijsrst.com
OPEN ACCESS
Print ISSN: 2395-6011 | Online ISSN: 2395-602X
doi : https://doi.org/10.32628/IJSRST24112109

Population Genetics : A Review

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ARTICLEINFO

Article History:
Accepted: 12 April 2024
Published: 22 April 2024

Publication Issue :
Volume 11, Issue 2
March-April-2024

Page Number :
746-748

ABSTRACT

Genetics is the study of genes and genetic variations alongwith the hereditary characteristics of an organism. Genetics is a central pillar of biology. It overlaps with other areas, such as: Agriculture, Medicine, Biotechnology. Genetics involves studying:
Gene structure and function
Gene variation and changes
How genes affect health, appearance, and personality.
Population genetics studies genetic variation within and among populations, based on the Hardy-Weinberg law, which remains constant in large populations with random mating and minimal mutation, selection, and migration.

Keywords : Genetics, Genes, Population, Roadmap, Epigenetics, Biochemical, Hardy-Weinberg Equilibrium, Myocardial Infraction.

I. INTRODUCTION

Genetics is the primary branch of biology that focuses on the study of genes and hereditary characteristics. The recent exploration in the field of genetics have led Biology to a new direction as humans have exploited genetics in various ways leading to benefits of mankind. Population genetics is a branch of genetics that focuses on the study of genetic variation within and among different populations. It's a part of evolutionary biology. Population genetics studies:

- Genetic differences within and between populations
- Evolutionary factors that explain genetic variation
- Adaptation, speciation, and population structure
- Changes in genetic composition that result from various factors, including natural selection.

This article is a review of various traits transferred in a population of a particular area.

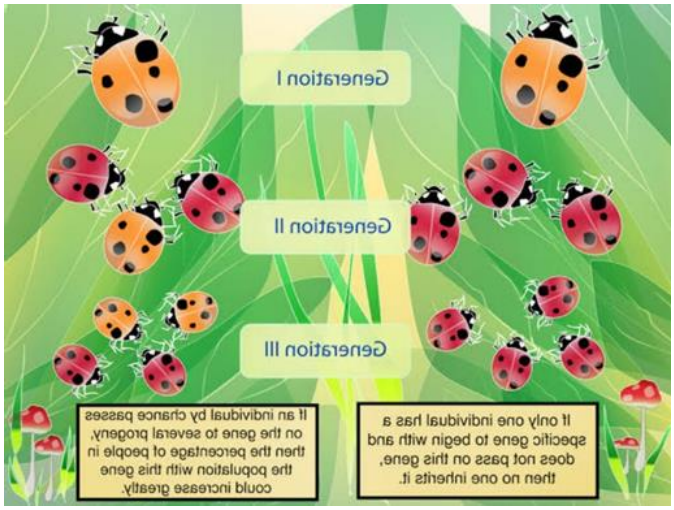

Fig 1. Flow of genes in a population – two modes.

This review article is about seven research articles about population genetics. The research article about the geography of genetics examines patterns in referrals to a British cancer genetics service, focusing on familial cancers. Between 1998 and 2006, the Cancer Genetics Service for Wales received nearly 11,000 referrals for patients in Wales. Deprivation scores were assigned using postcodes, and referral rates per 10,000 head of population were presented. The study found correlations between the number of GPs, patients referred, and deprivation, with deprivation decreasing as deprivation increased. Changes in referral sources, types of cancer, and referral centers revealed an inverse relationship between deprivation and health service availability. (Kevin McDonald, 2008) The other research about detecting significant genotype- phenotype association on rules in bipolar disorder (BD) faces challenges in explaining its high heritability. To address this, a novel data mining procedure using existing GWAS data was proposed. This method identifies undetected genotype-phenotype relationships, using association rule mining to identify frequent patterns. The study extracted 20,882 candidate association rules from three independent datasets from 2835 BD patients. (Rene Breur, 2018) The study of population data and genetic diversity analysis of 17 Y-STR loci in Saudi population ,the Y chromosome polymorphism is extensively studied for human migrations, population genetics, forensic applications, and paternity analysis, but its genetic lineage and structure in Saudi Arabia are limited. (Ahmed Ch.Kassab, 2020) The association study between asthma and single nucleotide polymorphisms of ORMDL3,GSDMB and ILLRLL genes in an Algeria population analyses four key single nucleotide polymorphisms (SNPs) were selected based on previous studies and linkage disequilibrium patterns. These polymorphisms were genotyped using Taqman PCR. Allelic discrimination assays were performed in duplicate using a Taqman MX3005P machine. The data was quality controlled to ensure correct SNP calling and the last cycle was set to 35 for specificity. The genotyping process involved denaturation, annealing, and HEX and FAM fluorescent levels. (Mouna Ziani, 2021) The analysis of 27 Y – chromosomal STR loci of the Mestizo Peruvian population studies sex differences in human survival have been extensively studied, revealing biological determinants that promote female longevity and environmental factors that can modulate the sex gap. This review aims to summarize the role of genetic and epigenetic mechanisms in promoting female advantage from early life and in including he gap in survival and ageing. Evidence shows that innate mechanisms common to all males and females play a major role in sex differences in lifespan, while variable genetic and epigenetic patterns can affect survival gaps. (Vincenzo Lannuzzi, 2023)The authors propose a roadmap to integrate genetics in the Electronic Patient Record in Family Medicine and clinical research, aiming to improve genomic literacy, register family history, add codes to ICPC chapters, and create unambiguous multidisciplinary guidelines for referral. They also propose automatic alerts to help general practitioners identify patients at risk. (Elisa JF Houwink, 2013)The study investigates genomic diversity in Gujarat's Rabari population using 20 autosomal genetic markers. Using bio-statistical software programs, the study compares Cervus, Genepop, and Fstat packages. The analysis is performed on 50 unrelated blood samples of healthy male individuals. DNA was extracted using organic extraction, and 20 autosomal STR loci were amplified using PowerPlex 21 kit and detected on a 3100 Genetic Analyser. (Aditi Mishra, 2021)

The Hardy – Weinberg equilibrium makes the base of population genetics and it states that allele and genotype frequencies in a population will remain constant from generation to generation in the absence of other evolutionary influences. This state is not possible idealy but it proves helpful in calculating the allelic frequencies of the given population as the equation of Hardy -Weinberg equilibrium give an expression –

$$P2+ 2pq+q2 = 1.$$

Where,

- p = Frequency of homozygous dominant genotype.
- q = Frequency of homozygous recessive genotype.
- pq = Frequency of heterozygous genotype.

Basically, genotype is the genetic makeup of an organism.

We can study the rate of evolution in the particular population with the help of this study. The diversity, the genetic makeup; in short population genetics prove an important role in the various areas.

II. CONCLUSION

Population genetics can provide insight into ecological and evolutionary processes (i.e., mutation, genetic drift, natural selection, and migration) relevant to vector-borne disease transmission by examining spatial and temporal patterns of genetic variation in insect vectors. It have vast applications in the medicine, physiology, etc so this review summarized about population genetics will surely help new researchers to study population genetics in a convenient way or further research.

III. ACKNOWLEDGEMENT

We express our gratitude to the Department of Forensic Science at Yashwantrao Chavan Institute of Science, Satara, India, for their invaluable guidance and cooperation.

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