



Intersecting realms: Exploring forensic genetics and population structure in human diversity

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INTRODUCTION

Forensic genetics plays a crucial role in the investigation of criminal cases, identification of human remains, and establishment of paternity and kinship relationships. At the heart of forensic genetics lies the analysis of DNA markers, such as Short Tandem Repeats (STRs) and Single Nucleotide Polymorphisms (SNPs), which provide unique genetic signatures that can be used to individualize and differentiate individuals based on their DNA profiles. In addition to its forensic applications, population genetics plays a key role in understanding the genetic structure and diversity of human populations, which has important implications for forensic DNA analysis, ancestry inference, and population history reconstruction.

Population structure refers to the distribution of genetic variation within and between populations, reflecting the demographic history, migration patterns, and evolutionary forces shaping human genetic diversity. By characterizing patterns of genetic variation across different populations, researchers can infer population relationships, ancestry admixture, and population history, providing insights into human evolution, migration, and adaptation. Population genetic studies rely on various statistical methods and computational tools to analyze DNA data, such as Principal Component Analysis (PCA), admixture analysis, and phylogenetic reconstruction, which allow researchers to visualize and interpret genetic relationships among populations.

DESCRIPTION

One of the key applications of population genetics in forensic science is the determination of population-specific allele frequencies and forensic databases, which serve as reference datasets for calculating likelihood ratios and estimating the probability of DNA matches in forensic casework. Population databases contain allele frequency data for DNA markers, such as STRs and SNPs, from geographically diverse populations around the world, enabling forensic scientists to estimate the rarity of DNA profiles and assess the significance of DNA evidence in criminal investigations. Moreover, population databases facilitate the inference of bio-geographical ancestry and identification of unknown individuals based on their DNA profiles, which can aid in missing person cases, disaster victim identification, and cold case investigations.

Forensic genetic studies have revealed substantial genetic diversity and population structure within and between human populations, reflecting the complex history of human migration, admixture, and genetic drift. Global population genetic studies have identified continental-level genetic clusters corresponding to major geographic regions, such as Africa, Europe, Asia, and the Americas, reflecting patterns of human migration and colonization over thousands of years. Within continents, further substructure and population differentiation are

observed, driven by historical events, geographic barriers, and cultural factors influencing gene flow and genetic exchange between populations.

The genetic structure of human populations has important implications for forensic DNA analysis, as population substructure can affect the frequency and distribution of DNA markers within populations, leading to differences in allele frequencies and genetic profiles between subpopulations. Population substructure can also impact the accuracy of ancestry inference and admixture analysis in forensic genetics, as the assignment of individuals to specific population groups relies on reference datasets and assumptions about population history and genetic diversity. Therefore, population structure must be taken into account when interpreting forensic DNA evidence and making inferences about the origins and relationships of DNA profiles.

In addition to its forensic applications, population genetics plays a key role in understanding the genetic basis of complex traits, such as disease susceptibility, drug response, and physical characteristics. By studying patterns of genetic variation across different populations, researchers can identify genetic risk factors for common diseases, such as diabetes, cardiovascular disease, and cancer, as well as pharmacogenetic variants associated with drug metabolism and treatment outcomes. Moreover, population genetic studies have shed light on the genetic basis of human diversity, including traits such as skin color, hair texture, and facial features, which are shaped by natural selection, genetic drift, and cultural factors influencing mate choice and reproductive success.

The integration of population genetics and forensic genetics has led to advances in forensic DNA analysis, ancestry inference, and population history reconstruction, providing valuable insights into human diversity, migration patterns, and evolutionary history. By combining genetic data from forensic casework with population genetic databases and computational tools, researchers can enhance the accuracy and reliability of DNA evidence interpretation, improve the resolution of ancestry inference, and address questions about the origins and relationships of individuals and populations. Moreover, population genetic studies contribute to our understanding of human evolution, migration, and adaptation, highlighting the interconnectedness of genetics, anthropology, and forensic science in unraveling the mysteries of human diversity and ancestry.

CONCLUSION

Population genetics and forensic genetics are intertwined fields that share common goals of understanding human genetic diversity, population structure, and evolutionary history. By studying patterns of genetic variation within and between populations, researchers can infer population relationships, ancestry admixture, and population history, which have important implications for forensic DNA analysis, ancestry inference, and population genetics research. The integration of population genetic data with forensic DNA analysis enhances the accuracy and reliability of forensic evidence interpretation, improves ancestry inference, and contributes to our understanding of human diversity and ancestry.