Genetic Ancestry and Health

Abstract

Information about genetic ancestry has a great value in health studies and other related areas of expertise such as anthropology, forensics and pharmacogenomics. In this review, we highlight several aspects of health that can be significantly improved by better understanding of genetic ancestry. These observations were made possible based on our own medical genetic research in Asia/Pacific populations (i.e. in particular regarding Maori and Orang Asli of New Zealand and Peninsular Malaysia, respectively). The major objectives of this programme of investigations has been to capture and understand genetic diversity in these populations and subsequently to make recommendations in order to maximise the health benefits of this type of population genetic research.

Keywords: Genetics; Ancestry; Health; Polynesians; Maori; Malays; Orang asli; New Zealand; Malaysia

Abbreviations: HPA: Human Platelet Antigen; HNA: Human Neutrophil Antigen; MICA: Major Histocompatibility Complex class I chain-related gene A; HLA: Human Leukocyte Antigen; KIR: Killer cell Immunoglobulin-like Receptor; SNP: Single Nucleotide Polymorphism

Introduction

Genetic methods play a significant role in many research areas including medicine, forensics and ancestry study. In this respect, we highlight the ways in which knowledge about genetic ancestry has become an important element in health and medical treatments. This viewpoint is largely based on our own experience working on various genetic markers in Asia/Pacific populations such as Maori, Polynesians, Malays and Orang Asli in New Zealand, Pacific Islands and Malaysia. These diagnostic markers include many loci (e.g. HLA, blood group, HPA, cytokines and HNA) that determine transfusion and transplant success, our immune responses to disease and as causal agents in autoimmunity.

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We have completed and reported a comprehensive set of ancestrally informative genetic data across many Asia/Pacific populations. These systems include HLA, MICA, KIR, blood group, cytokine, HNA and HPA [1-20]. These new datasets not only provide special insights into the ancestry of these people, but also is of significant value in health; as recently reviewed by [21-22]. This is because these genes are determinants of transfusion and transplant success or have been directly associated with other immune and important biological functions. For example, matching of HLA markers between patient and donor is important before proceeding with transplant operations. Certain HLA types have also been shown to be contributing factors in the pathogenesis of various diseases [23]. In the following subsections, we will discuss several aspects of health which can be significantly improved based on our understanding of ancestry and genetic diversity in Maori, Malays, Orang Asli and several Polynesian sub-populations.

Allelic variations and disease prevalence: Many diseases have been mapped to particular regions of the human genome and certain allelic types have been associated with high risk of disease susceptibility. In this context, relative risk of autoimmune diseases can be predicted from the prevalence of particular antigen types in a population. For example, medical conditions such as ankylosing spondylitis and rheumatoid arthritis are rare in Maori/Polynesians, but relatively common among Europeans. They are typically associated with the HLA-B*27:05 and HLA-DRB1*04:01 allele types in Europeans and HLA-B*27:04 and HLA-DRB1*04:05 in Asians/Polynesians, respectively [24-26]. The HLA-B*27:04 and HLA-DRB1*04:05 alleles are quite rare in Polynesians (0-0.01 and 0.02-0.08, respectively) which may explain the unusually low occurrence of ankylosing spondylitis and rheumatoid arthritis in Maori/Polynesians [5].

Candidate genes for disease study: Many genetic markers characterized in various populations across the globe are now available as population datasets and can be readily retrievable from public databases; e.g. see [8] for Allele Frequencies.net and [27] for IPD – Immuno Polymorphism Database. These datasets can be used not only as a reference standard for disease association studies (see later), but also provide important resources to search for candidate susceptibility genes in disease studies. A good candidate gene(s) will be one with greatest differences in allele frequency among populations, including between ethnically related populations which show different schedules of disease prevalence. This is one of the main molecular signatures of the highly polymorphic immune system genes, where patterns of allelic variation at population level are shaped by local demographic or selective factors; e.g. see [17,28].

Donor recruitment: In general, compatible donor for a particular patient might best be recruited from his/her own group or other
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Our various surveys have tested many loci; see [5,7,20]. Our experimental design proved to have value in forensic DNA studies and pharmacogenomics [22,34-37]. The major challenges ahead are to investigate, describe and understand genetic variability in order to maximise the health benefits of population genetic research.

References


