Screening for recessive diseases – A valuable investment for future generations of South Asia

Padmalatha S Rai¹, Kumarasamy Thangaraj², Kapaettu Satyamoorthy⁠*¹

¹School of Life Sciences, Manipal University, Manipal, India; ²CSIR-Centre for Cellular and Molecular Biology, Hyderabad, India

*Corresponding author e-mail: ksatyamoorthy@manipal.edu


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South Asia is the land of traditions and rightfully so, the innumerable pockets of endogamous groups provide extensive population diversity in the world with several ethno-linguistic groups that present a significant challenge to implement translational genome based medicine. In India alone, there are 4635 anthropologically well-defined endogamous populations [Tamang and Thangaraj, 2012; Mastana, 2014]. Impact of such endogamy has been recently demonstrated by Nakatsuka and colleagues, which was published in the September (2017) issue of Nature Genetics [Nakatsuka et al, 2017]. The authors have identified that about a third of populations in South Asia have had strong founder events / population bottlenecks, which are responsible for a high rate of population-specific recessive disease in South Asia. They have analysed samples from more than 2,800 individuals from over 275 distinct South Asian groups from India, Pakistan, Nepal, Sri Lanka, and Bangladesh using about 600,000 genome-wide markers. This highlights the divergence of individuals arising from same ancestors to different subgroups leading to founder events [Reich et al, 2009]. The founder event can be attributed to loss of genetic variation in a newly established sub group of small number of individuals from a larger population. Studies on founder groups of Ashkenazi Jews, Finns, Amish, Hutterites, Sardinians, and French Canadians of European ancestry has led to identification of numerous disease causing recessive mutations and prenatal screening for these mutations have decreased the disease burden [Arcos-Burgos and Muenke, 2002; Lim et al, 2014]. Hence, the persistent founder events in South Asian populations provide an opportunity for decreasing disease burden.

The authors have thoroughly analyzed the data collected from endogamous groups in South Asia and combined it with previously reported data; thus, providing information about subgroups originating from Indo-European, Dravidian, Austroasiatic, Tibeto-Burman ancestry. The method utilized an algorithm to study the founder event by analyzing wide stretches of DNA in approximately 100 generations originating from a common founder. This involved computation of identity by descent (IBD) scores between DNA segments of two genomes, which were later normalized according to sample size [Arcos-Burgos and Muenke, 2002]. Out of a total of 263 unique groups in South Asia, authors have found 81 groups with IBD scores greater than those of both Finns and Ashkenazi Jews. It is interesting to note that other groups outside of South Asia such as the Hutterites, Amish, and individuals of the Saguenay–Lac Saint-Jean section have also shown founder events leading to the unearthing of dozens of novel disease-causing variations despite their small census sizes. The evidence provided by Nakatsuka and colleagues [Nakatsuka et al, 2017] provides a screening opportunity to reduce disease saddle in South Asia. Proactive surveys in community-based programs, screening for congenital diseases in vulnerable groups with strong founder effects can be profitable gene mapping approach considering the advances in the post genomic era. With some social beliefs, sentiments and ethics in the way, research programs like these can still become a crucial factor for the establishment of modern medical genetics and provide health benefits. Mapping recessive disease mutations are important in communities undergoing social marriage practices, particularly in South Asia to construct large blinded and confidential database for recessive disease-causing mutations earlier recognized to segregate at high rate. Finally, there is a need for health care providers to fully comprehend and embrace the genetic and genomic advances that have been sweeping the scientific community in every area of health care since the turn of the century.

We know more about gene-environment interactions, autosomal dominant, autosomal recessive, X-linked, chromosomal abnormalities, chronic multifactorial, and congenital abnormalities that affect a substantial percentage of live births is because of the advances in genomic information. Arguably, patients with the sickle cell disorders
suffer from many other complications and much remains to be done from public health perspective despite the advances in its diagnosis. Our burden of neurological disease is an ‘Achilles heel’ associated with cognitive adaptations. Microbiomics established concurrently with the development of genome technologies and dysbiosis is now reported to cause number of disorders including diabetes, obesity, periodontal disease, inflammatory bowel disease, and increased the risk for cancer. The ever-growing role of genomics in health disparities, despite being complex, will tell us genetic and environmental variations that influences health status or disease burden.

Application of epidemiological studies with advances in genomic research to a large extent has promised to address heritability impacted by environmental, behavioral influences and phenotype variance. Conceptually, by integrating “nature and nurture” with biosocial perspective to elucidate identity by descent with data science can help prevention of diseases and health related problems in the human population [Brand et al, 2016]. The information can be utilized to predict the compatibility of the potential couple about carrier status for a condition. Although applied in Ashkenazi Jews, awareness among South Asian communities is still lacking. The lessons are clear. We must incorporate our expertise in the field of community medicine, genetics, genomics and information and communication technologies (ICT) to forge a viable and strong partnership for disease prevention. Feasibility and goal of this ultimate endeavor can only be tested to identify gaps and priority areas by engaging standards accepted in developing nations. However, innovative steps are required to foresee and implement based on the local needs. The main strength of these genetic approaches has been the identification of vulnerable groups in the subset of the population. The work conducted by Nakatsuka and coworkers [Nakatsuka et al, 2017] have shown a potential of genetic mapping to save the life in near and far off future by valuable investments into community-based screening and evaluations.

References


