

What's There In Our Genes? A Case For A More Inclusive And Multi-Disciplinary Outlook

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Abstract

EDITORIAL

It seems to be evident from all the data that studies of DNA from human beings, combining both ancient and the modern, give us a hope of finding out the mishmash between the various kinds of pathways, human admixtures have occurred. Sometimes, to understand this process, one has to use the ultimate politically incorrect term 'race.' Thus, one may comment about the different 'races' of human beings, their migrations to different parts of the globe, and their genetic admixtures caused during the course of their journeys and the areas where they stayed. One attempt at looking at these admixtures would be the one by Jean M. Auel¹. However, geneticists feel that looking at gene sequences and then matching them with those they have in their libraries would show how much variation there has been between different groups and the probable causes for these could then be found.²⁻⁵ It was soon found that this created some problems. Genetic admixtures by themselves need not create large differences. Thus, some genes were found to be conserved over long periods of time whereas others changed rapidly giving rise to differences. If one used this as a marker to decide the passage of time, then one could be seriously wrong.

One area which has been developed, is the use of such genetic data of populations to predict the total population in any given time period, especially in the past.⁶ Also, the degree to which inbreeding and consanguinity affect the genetics of the population are also important factors that may be readily checked and used through genetic studies.^{7,8,9}

A study showed that there were genetic indications that early settlers were present in the genes of present day castes and tribes¹⁰. This study was also detailed about its presence among the castes within India.^{11,12} The study was also, to some extent supported by others.¹³

However, arguing against a very closed-systems model, it was soon apparent from some studies that there was some gene flow between castes, tribes as well as some clearly migrant populations from other continents, like the Siddis¹⁴. Also, tribal populations in India seem to have very diverse origins and this does not seem to be very conducive to a common migratory origin of Indian groups.^{15,16}

Some studies had claimed that the Central Asian pastoralists may have formed a strong core group, a state system, which they used to attack the Indian subcontinent, after which they settled within. Genetic studies seem to show that there was only a minor influence of such pastoral groups¹⁷. In fact, it was soon clear that many such studies were influenced by ideological biases of the participating scientists rather than any emerging clear-cut model from the data found.

Scientists also found out that if one used mDNA or mitochondrial DNA, then their searches became better. The mDNA could only have come from the mother and this fact led them to find out the 'Eve' of the human race. Further, mDNA was conserved pretty much over generations only showing very small variations. This made it better for study. Others demanded studies on the Y Chromosome as a marker¹⁸.

Using this arsenal, and the growing database and technologies for gene amplification, purification and analysis, a number of laboratories all over the world began to find out new kinds of linkages and timescales for conducting researches to find out migratory routes of human beings, early colonization scenarios and in some cases even early evolution. These scenarios were then explicated through logical sequences by extrapolating, discussing and concluding from the results of data relating to DNA, often mDNA. Other studies continued with the human

polymorphisms found in such populations and their evolutionary significance.¹⁹⁻²²

One offshoot of such studies has been finding out new polymorphisms in different communities²³.

What has often been ignored is the fact that many of the factors that go into migrations, or changes in gene flows are societal or social factors, that cannot be readily displayed using statistical techniques by molecular biologists, geneticists or even biological anthropologists. Further, inbreeding populations develop their own genetic idiosyncrasies which show up as 'markers'.²⁴ These markers may be traced through their advances into populations in cases of migrations.

For instance, language data has often been ignored unless it had a direct relevance to the research problem itself. In fact, language dissemination and change are becoming important markers showing the spread of populations and the areas that the population had covered on their travels. This would not only show up adjoining, or similar communities, but it might also highlight and add to differences²⁵, thus minimizing mating and providing barriers to reproduction²⁶⁻²⁸. One of the most important barriers to reproduction has always been cultural norms, and these norms have been steadfastly ignored since it does not yield statistically amenable data. Some recent studies, though, have only begun to scratch the surface of such possibilities²⁹.

The mass of data collected by social anthropologists, sociologists and others lies unused by them. Many may form the basis of newer models to explain gene flows, a discovery which has become very rare of late. Models might also be hidden in the oral histories and myths of societies, just waiting for mathematical rigor to expose and enlighten.

Thus, we propose a new rebuilding of this genetic data, using the mass of biological anthropological insights into the issue as well as those ideas used often by social anthropologists as well as prehistorians. We need better reviews, use of both qualitative and quantitative data as well as much more rigorous testing of newer and older models. Only then may we make full use of this large amount of data that has already been collected over the years. What we have described here, for now, presents part of the picture seen from the Indian subcontinent as an example. However, this situation is probably true of other parts of the world as well, perhaps even those areas where it has been assumed that the data is likely to be homogenous. Thus, even biological

anthropologists need to add new sensitivities and methodologies to their studies as their 'Mendelian' populations seem to explode outward into the Tower of Babel that we see among human genetic groups today.

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