Review Article
Volume 10:7, 2022

Journal of Phylogenetics & Evolutionary Biology

ISSN: 2329-9002 Open Access

Combined Genetic Approaches to Elucidate Relations of Origin, Phenotype, Habitat and Climate Change

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Abstract

Two main approaches, relying on only genetic drift and considering both genetic drift and mutations in equilibrium, are keys in revealing genetic distance and relevance among populations. Genetic relations and histories of communities can be unearthed by utilizing these methods accurately. For this reason, the equilibrium method should be definitely used to identify blood ties and migration waves. F_{ST}, therefore also phenotypes should be utilized in understanding habitats' adaptational effects whereas F_{ST} and phenotypes are not sufficient to disclose blood ties. Thus bonds among migration, genotype, phenotype and origin will be resolved truly. Those are clear phenotypes extremely depend on habitats, especially climates as expected and genotypes hide collective origins over mutational roots. Then formation and evolution areas of populations can be detected via the equilibrium method and F_{ST} respectively. Even rates of genetic drifts can be calculated by measuring the alteration of phenotypes. Moreover some organisms' genes could be regulated stably in the laboratory in part natural manner when habitats' effects on genetic drifts were revealed.

Keywords: Climate • Genotype • Habitat • Migration • Origin • Phenotype

Introduction

Discovering genetic relations among communities is an endeavor of decades in genetics. Through this purpose, many researchers asserted many ideas to yield genetic measures and reveal genetic distances of populations. According to received sources, there are three chief measures of obtaining genetic distances among populations: Fixation index (F_{ST}), minimum genetic distance and standard genetic distance. Whereas three relevant methods are based on evolution, they diverge on a critical point: Minimum and standard genetic distances are calculated by considering genetic drift and mutations in equilibrium while F_{ST} is acquired by taking only genetic drift into account [1,2]. These considerations bring outcomes of respective measures at very different places in terms of genetic distance and relevance.

Since F_{ST} considers only genetic drift meaning changes of allele frequencies [3] and is "the correlation between random gametes within a particular subpopulation relative to the gametes of the total population" equaling $(F_{IT}-F_{IS})/(1-F_{IS})$ where F_{IT} is "the correlation between gametes that unite to produce the individuals relative to the gametes of the total population" and F_{IS} is "the average overall subpopulations of the correlation between uniting gametes relative to those of their own subdivision" [4], it reflects genetic adaptation rather than consanguinity. On the other hand minimum and standard genetic distances exhibit genetic adaptation and consanguinity together in that it depends on genetic mutations suggesting allelic roots [3] alongside genetic drift equaling $(J_x+J_y)/2-J_{xy}$ and $-\ln(J_{xy}/(J_xJ_y)^{0.5})$ respectively where "J_x, J_y and J_{xy} are the arithmetic means of $\sum x_i^2$, $\sum x_i^2$ and $\sum x_iy_i$ respectively; x_i and y_i the sample gene frequencies of the i-th allele in populations X and Y respectively" [2].

Upon already seen, minimum and standard genetic distances considering the named equilibrium will show allelic joint roots of communities, therefore consanguinity, by zeroing non-joint allelic frequencies multiplying them while F_{ST} will mainly express genetic adaptation but not consanguinity much as not multiplying like the just explained. Then it is clear that there are two main approaches in understanding genetic relations of populations: Relying on only genetic drift and considering both genetic drift and mutations in equilibrium. These facts will elucidate how to utilize appropriate methods and infer true results to find true genetic relations among communities out.

Literature Review

Comas and his friends examined mitochondrial DNAs of a number of populations including Central Asian Kazakhs, Kyrgyzs, Uygurs, relatively western White British people and Turks [5]. For this purpose, they analyzed the Central Asian individuals' "hyper variable region I of the mitochondrial control regions" and compared the outcomes with other populations' relevant genetic data from various studies. Genetic distances among the populations were estimated considering genetic drift and mutations in equilibrium [2,6], a neighbor-joining tree was built over those distances as shown in Figure 1A.

Mergen and her friends also examined mitochondrial DNAs of the populations mentioned above [7]. For this purpose, they analyzed the Turks' "hyper variable segment I of the mitochondrial DNA's noncoding regions" and compared the outcomes with other populations' relevant genetic data from various studies. Genetic distances among the populations were estimated considering again genetic drift and mutations in equilibrium [2,6], a neighbor-joining tree was built over those distances utilizing "the NEIGHBOUR program in the PHYLIP 3.5c software package" as shown in Figure 1B.

Distinctively Hodoğlugil and Mahley studied autosomal chromosomes of Turks and Kyrgyzs and compared those with other populations' relevant genetic data [8]. Genetic distances among the populations were estimated by F_{ST} based on just genetic drift over "the smartpca function of EIGENSTRAT" and a neighbor-joining tree was built over those distances "in MEGA4 utilizing the neighbor-joining method" as shown in Figure 2A. As for Pankratov and his friends, they compared single nucleotide polymorphisms (SNPs) of whole genomes of many populations including the French, Germans, Turks, Altais, Mongols, Kyrgyzs, Uygurs and Kazakhs as shown in Figure 3 [9]. Genetic distances among the populations were estimated by principal component analysis (PCA) over "the smartpca program implemented in EIGENSOFT package" as shown in Figure 4B and the PCA results worked out in concordance with F_{ST} values based on only genetic drift.

Depending on the collective results of the past studies considering

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Date of Submission: 04 July, 2022, Manuscript No: jpgeb-22-66526; **Editor assigned:** 06 July, 2022, PreQC No: P-66526; **Reviewed:** 18 July, 2022, QC No: Q-66526; **Revised:** 23 July, 2022, Manuscript No: R-66526; **Published:** 30 July, 2022, DOI: 10.37421/2329-9002.2022.10.226

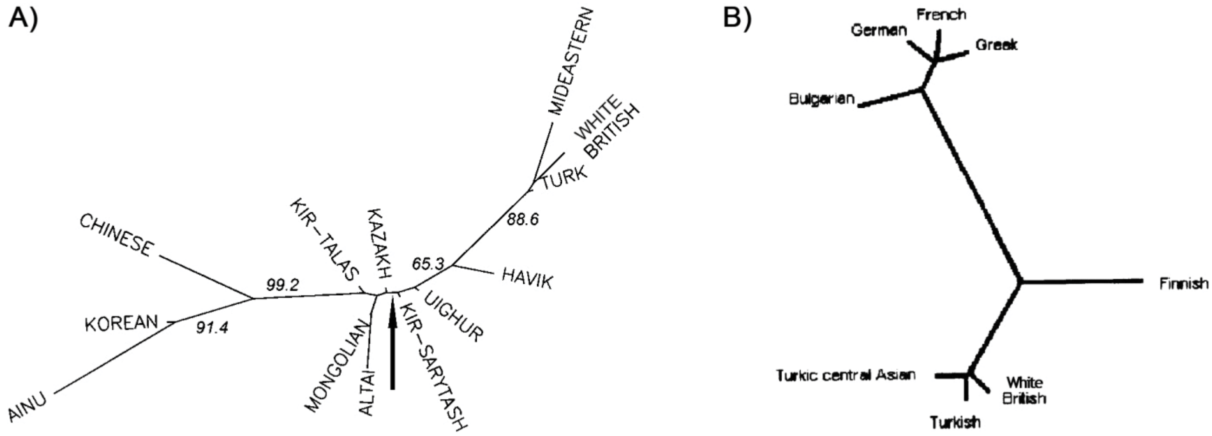

Figure 1. Neighbor-joining trees relative to the method of genetic drift and mutations in equilibrium. **A)** Some East Asian and western populations. Kir abbreviation means Kyrgyz. Talas and Sarytash are settlements of origins of Kyrgyz samples. Mongolian and Uighur denotes Mongol and Uygur respectively. Arrow in bold indicates separation node of some African populations largely away from other communities. **B)** Some Asian and western populations. Turkic central Asians are Kazakhs, Kyrgyzs and Uygurs.

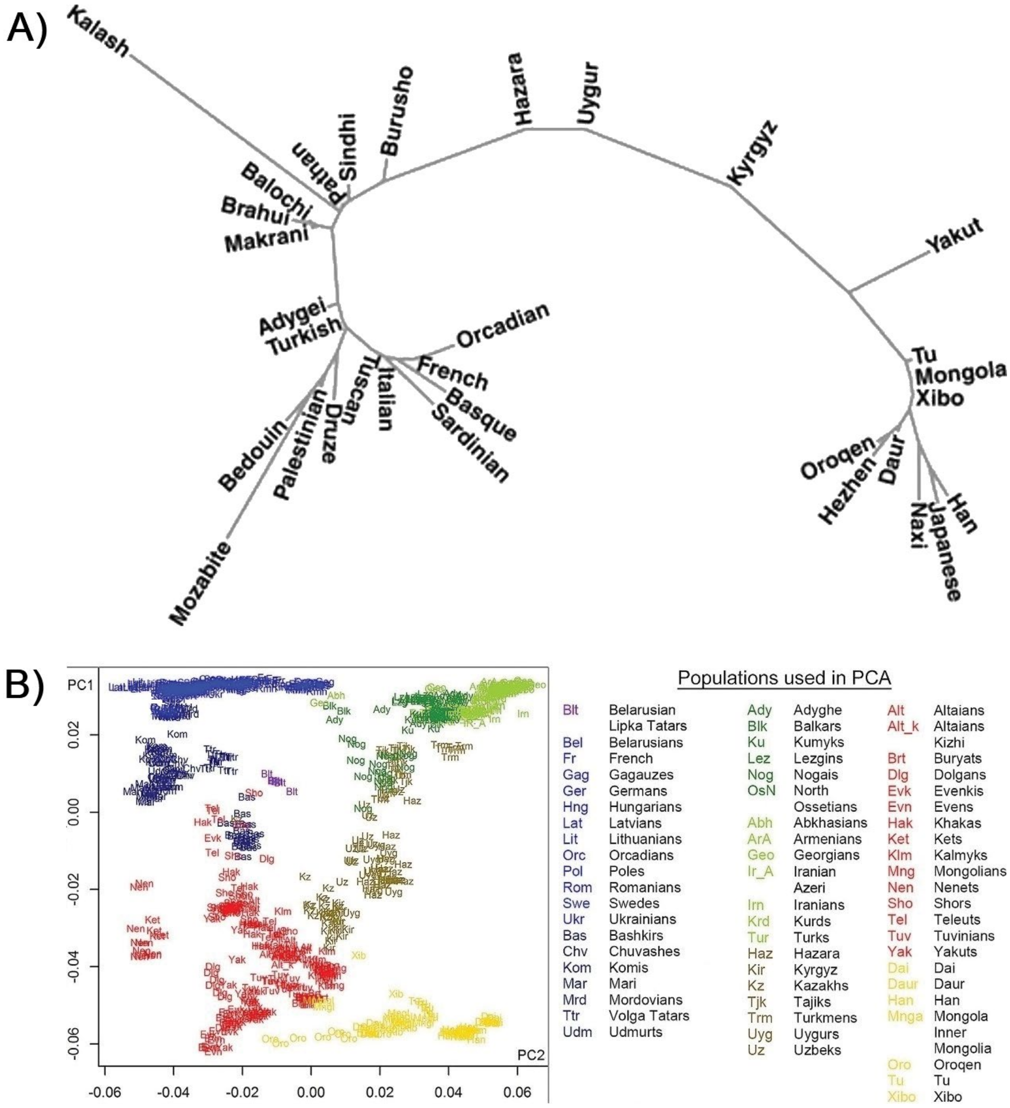

Figure 2. A) Another neighbor-joining tree relative to pairwise F_{ST} of some Asian and western populations. **B)** PCA representing F_{ST} values of some Asian and western populations. PC1=3.8, PC2=0.6. Each abbreviation denotes one individual.

genetic drift and mutations in equilibrium, the French and Germans form a single cluster. Besides Altais, Kazakhs, Kyrgyzs, Mongols, Uygurs and Turks form another single cluster. Both clusters are in terms of genetic distance and isolated from each other as shown in Figure 4A. Further depending on the collective results of the studies considering only genetic drift; the French, Germans and Turks form a single cluster. In addition, Kyrgyzs and Uygurs form another single cluster. Both clusters are in terms of genetic distance and isolated from each other as shown in Figure 4B. In terms of genetic distance again, just mentioned clusters demonstrate that Turks are closer to the French than Kyrgyzs and Uygurs according to FST values while they seem, in comparison of FST values, much closer to these Central Asians than the French according to method of genetic drift-mutations equilibrium.

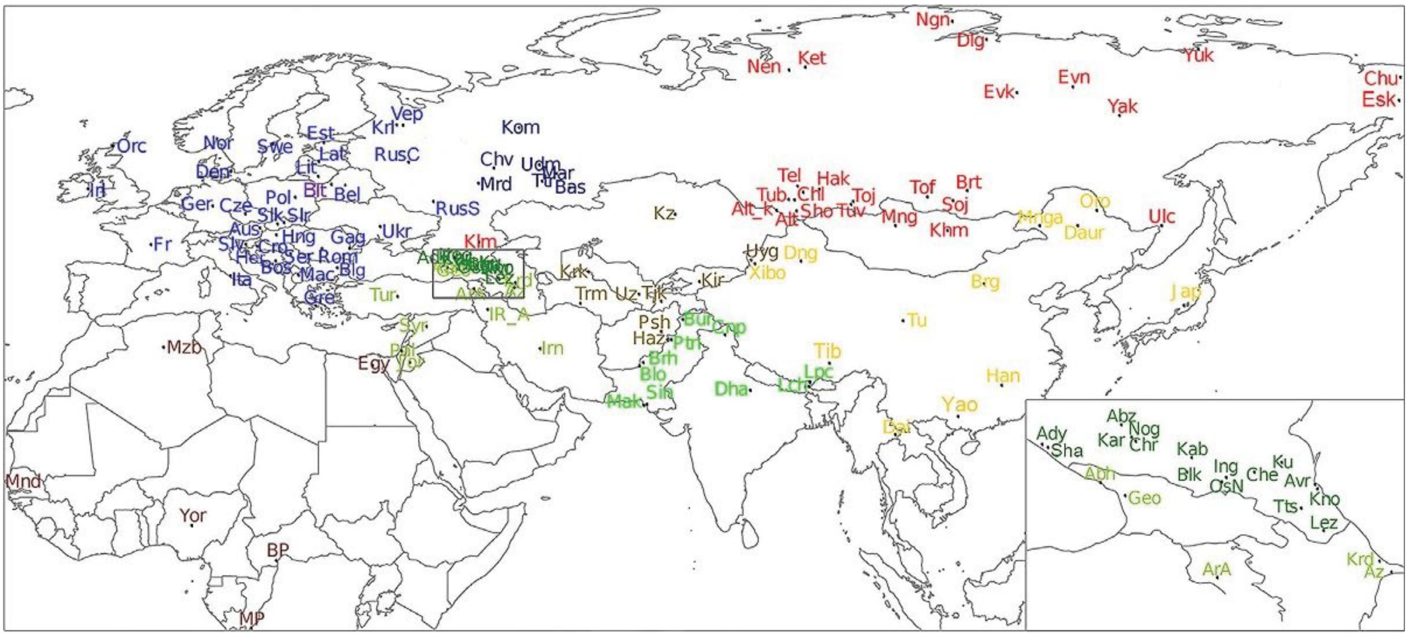

Figure 3. Map produced in R v3.1.1 utilizing "maps" and "mapproj" packages exhibits geographical origins of populations mentioned in this study. Fr, Ger, Gre, Blg, Tur, Kz, Kir and Uyg denote French, German, Greek, Bulgarian, Turkish, Kazakh, Kyrgyz and Uygur respectively (see Figure 2B for meanings of other abbreviations).

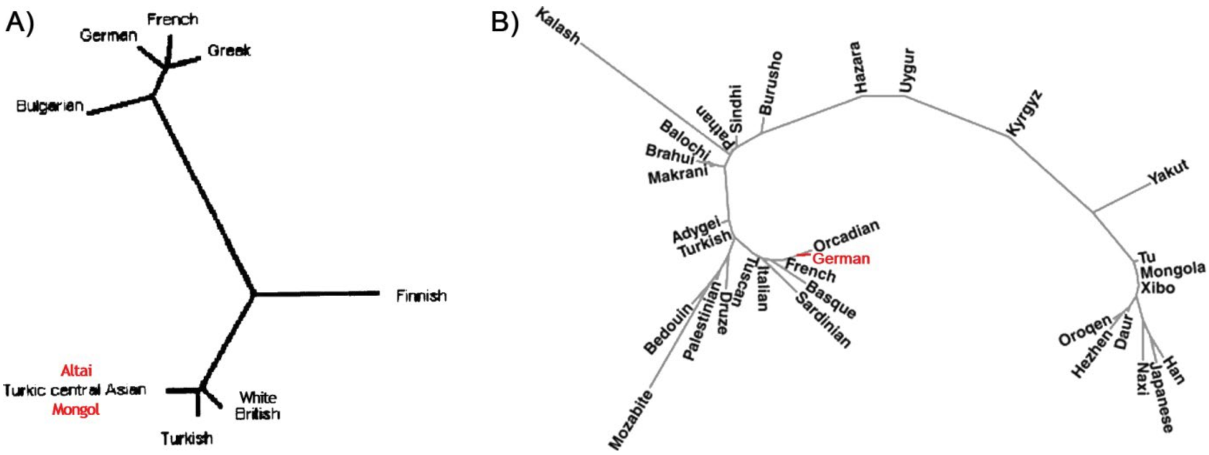

Figure 4. A) Probable consanguinity tree of various populations by the method of genetic drift-mutations equilibrium. The figure was drawn combining reference studies proportionally. Greeks and Bulgarians are demonstrated genetically far away from Turks although these three are geographically very close populations to each other (see Figure 4). **B)** Probable genetic adaptation tree of various populations by F_{ST}. The figure was drawn transferring German data in Figure 2B onto Figure 2A proportionally. The German segment's node, length and inclination were estimated averaging French and Orcadian segments' these features.

Results of FST and the equilibrium method are very different. Since different habitats bring about different needs for genetic inheritance, mutations [3,10], hence distinct alleles and genetic drifts for populations over periods, separated populations arrive at different genetic structures in terms of allele frequencies. For this reason, communities' relative FST values would work out away from each other by the time when they live in distinct areas even if all individuals are blood relations. Similarly, communities' relative FST values would work out close to each other after centuries when they live in sufficiently similar areas even if individuals have no common lineage.

However the same meaning cannot be inferred like FST for the equilibrium method in that it takes mutational roots into account of genetic distance computation. As long as roots of genetic mutations are input toward computations, branches denoting genetic divergence would arise from the same nodes for consanguineous communities and these branches would not end on different clusters unless very severe genetic drift takes place within one of the populations. Since habitats produce adaptations and adaptations produce genetic drifts, it is expected that geographically separated populations who had admixed fully with each other would be in distinct phenotypes following centuries. It is known as environmental adaptation that different living spaces alter individuals into beings with different phenotypes such as body size and skin color [11,12]. Hence suchlike phenotypes cannot unearth individual or collective consanguinity yet can reveal adaptive abilities, suggest adaptation tendencies and therefore yield rates of genetic drifts.

Indeed extreme differences are phenotypically realized among Turkic Central Asians, Mongols, Turks and the White British even at first glance although they are genetically identified far close on Figure 4A. In addition, such that the British, Finns are demonstrated closer to name Asians than the French and Germans on the same figure though their apparent phenotypes exist more similar to the Europeans than the Asians.

On the other hand, the French and Germans are exhibited closer to Turks than Kyrgyzs and Uygurs in Figure 4B. Presumably, as named Europeans' apparent phenotypes seem more similar to Turks than other Asians [13-16], respective FST outcome on the tree may indeed reflect true characteristics of adaptation and genetic drift in these populations in several aspects. Then populations' blood ties can be disclosed per the equilibrium method and not FST. Yet some migration patterns of communities, for instance routes where individuals had separated in history, could be resolved by utilizing FST. At this point, detecting habitats' adaptational effects will be important. If these effects are exactly revealed, basic organisms' genes may be arranged more stably under laboratory conditions ceding recombination to those beings. Suchlike part natural processes could be invented for genetic engineering.

In addition, probable consanguinity between the French and Germans, such as their probable genetic adaptation in Figure 4B, had worked out very close as shown on Figure 4A. This presumably means they occurred and evolved in identical areas. On the other hand, probable consanguinity between Turks and Uygurs had worked out very close on Figure 4A whereas their probable genetic adaptation was demonstrated away in Figure 4B. This presumably signifies they formed in identical areas yet evolved in distinct land. All these data provide important insights to comprehend how genetic drift, therefore also habitats, can alter populations and generate distinct communities in evolutionary history. Distinctions of populations would signify basically just changes of allele frequencies under mild genetic drift and nearly rupturing of blood ties under severe genetic drift. At this point, it is a question mark that genetic distance in what degree nearly ruptures blood tie between communities.

Inferring from previous statements, phenotype should replace race in which expressing skin color and country of origin as a description of suspects to correct a forensic misuse and catch more accurate descriptions. Moreover chief reason for genetic drift should be searched in correspondence with climatic differences among regions. Upon easily estimated, climate may essentially affect dietary habits, biochemical processes at organisms and various social preferences of individuals over especially its components of humidity, temperature and solar radiation. Even populations with close minimum and/or standard genetic distance but away FST values relative to each other who lived in same area and different ages would suggest a major climate change in their land. Consanguinity alongside divergent adaptation will be a useful gauge for monitoring climate changes in common locations throughout history.

In that case allele frequencies are likely to depend on habitat to a large degree via new mutations and pre-existing traits. Then habitats, by themselves, may form and change general phenotypes of populations even if communities are completely isolated from all outer individuals. However, of course, this phenomenon would arise in a form of process. Hence phenotypes would shift toward other phenotypes slowly and interestingly within isolated populations changed their habitats.

As a matter of fact consanguineous individuals who have very distinct allergies, predispositions of chronic diseases, genetic defects, body proportions, hair spread, blood groups, hair colors, eye colors and skin pigmentation from each other will seem with significant frequencies inside same communities over time due to effective genetic drifts stemmed from surroundings. Furthermore these differences will present populations who have very diverse individuals in many aspects such as just mentioned traits, so that, even isolated communities who had been fully admixed in and phenotypically homogeneous once upon a time will alter into preserved phenotypic ragbags after split and geographically separated. This expected phenomenon is briefly habitational transition phenotypes and may be observed individually and collectively.

Besides it is not certain these ragbags will alter into new homogeneous populations in their new habitats since initial genetic homogeneity of them would reflect itself always even in exiguous percentages of phenotypes if initial habitats had continued on those populations for adequately long duration. Possibly respective duration is not definite and depended on population and habitat characteristics. In the bargain, as different types of climates exist in a habitat, these will intensify habitational transition phenotypes and complicate thoroughly habitational phenotypes rehomogenization for populations upon explained before. Phenotypes which stemmed from genotypes act probably in that way and adaptive radiation can be understood better through these inferences.

Eventually genetic admixtures, blood ties and migration waves pertaining to populations can be detected per the equilibrium method. Using just FST is not sufficient for these purposes. Similarly haplotypes and haplogroups cannot reveal respective phenomena by themselves as well. So, same alleles and mutations can form in different areas and distinct populations. Also these are surely urban myths that blood ties of communities will approach each other unavoidably as their geographic locations draw near and a population's main genetic origin is consistent with its name. So, the Bulgarian name is acknowledged Turkic [17,18].

Conclusion

Yet it is clear that populations' phenotypes can approach each other as their geographic locations draw near. Besides, autosomal chromosomes' comparative outcomes based on the equilibrium method must combine with anthropology, ethnology and philology to ascertain blood ties of communities. As for genetic regulation, it could advance utilizing surroundings-adaptations relations deeply.

Of course, explained genetic distance approaches rely on several assumptions. Hence these methods can easily err in various points. However several facts regarding civilization history may be unearthed via those approaches. Even perhaps the known history of nations will be rewritten truly next time through these methods.

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How to cite this article: Pala, Yasin M. "Combined Genetic Approaches to Elucidate Relations of Origin, Phenotype, Habitat and Climate Change." J Phylogenetics Evol Biol 10 (2022): 226.