

Human plasma protein polymorphisms and the persistence of cultural diversity

Recently, Laitin et al. (1) reported on the roots of cultural diversity. Geographic axis ratios for individual countries help to understand the diversity of language, showing more diversity in north–south oriented countries. We believe that genetic factors related to vitamin requirements also should be taken into account as confounders. Human long distance migration has been limited by availability of vitamin C and D. Biological half-life of vitamins C and D in man is largely determined by genetic polymorphisms of plasma proteins such as haptoglobin (Hp) and vitamin D binding protein (DBP) (2, 3). These polymorphisms are in a state of transient gene equilibrium, proving their major role as a genetic migration driver.

Variation in DBP allele frequencies in different geographic areas is correlated with skin pigmentation and sunlight exposure. Because sun exposure depends on latitude, DBP allele frequency gradients all over the planet show a north–south orientation. Evolution in DBP helps to store vitamin D during the long winters at high latitudes. Little dietary vitamin D was available, causing poor calcium absorption. Northern populations were vulnerable to rickets and osteomalacia. Pelvic deformities made births difficult. The gradual extinction of the Greenland Viking colony is an example; skeletal evidence shows that bone diseases were common among this population.

Similarly, Hp allele gradients show a marked north–south distribution (4) that is hardly affected by crossing the world's biomes (5) and crossing the malaria belts. Populations with a high Hp1 allele frequency show better in vivo vitamin C stability. The effect of the Hp polymorphism on vitamin C metabolism offers an explanation as to how, during the course of human history, some populations with a high Hp1 allele frequency have been able to migrate successfully over long distances with less casualties to scurvy, and some genetically

privileged nations (in terms of vitamin C stability) could advance to colonizing empires with a global presence (2). Particular regions that are difficult to access (e.g., the east–west oriented Papua New Guinea, where 841 different languages are spoken, showing a high cultural diversity) are characterized by sharp Hp1 allele gradients (4). The core of the Mongolian Empire was the huge Eurasian Steppe that stretches from the Khingan Mountains in the east to the Carpathians in the west. The Mongols were steppe warriors, and they were able to rapidly extend their influence. Because of a very high Hp2 allele frequency and consequent susceptibility to scurvy (5), they had little alternative than to move along a west–east axis. Zheng He's expeditions (1405–1433) (which would have given China unique opportunities to expand in other directions) were eventually discontinued (5) after facing huge nutritional problems.

Apart from cultural, technological, and political variables, genetic factors such as plasma protein polymorphisms also may have played a major role in human mass migration, in which some populations have been more favored than others. Geographical gradients may partly reflect genetic maps. When fine-tuning cultural diversity models, we therefore propose to also take into account these major genetic driving mechanisms.

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Author contributions: J.D., M.S., M.L.D.B., M.L., and M.T. wrote the paper.

The authors declare no conflict of interest.

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