ON THE VARIABILITY OF GC-SUBTYPES IN INDIA

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In close co-operation with some Indian anthropologists (Indera P. Singh and M.K. Bhasin, Delhi; B.N. Mukherjee and K.C. Malhotra, Calcutta; B.M. Das, Gauhati; and P. Veerraju, Waltair) we are conducting several research projects in order to analyse the distribution of genetic markers in Indian populations. These studies consider a great number of blood group, serum protein and red cell enzyme polymorphisms as well as haemoglobin variants. The results of our Gc subtypings will be reported here briefly.

Up to now a total of 35 population groups from various parts of India have been Gc subtyped (Fig. 1). With the exception of the data from Himachal Pradesh (Papiha 1981, Papiha et al. 1983) and Punjab (Papiha et al. 1982) all the others have been reported by our group; some of them are published already (Walter et al. 1984). Disregarding here the Gc*2 frequencies (which vary among Indian populations between 0.089 in Brahmans from Sikkim and 0.409 in Karbis from Assam) and focusing on Gc*1F and Gc*1S alleles one can see a considerable variability of these two alleles (Fig. 2),which will be described in detail elsewhere. This variability, however, is not due to chance, but was found to be closely associated with language families (Fig. 3): Indo-European and Dravidian speaking populations are forming one cluster (together with the linguistically not classifyable Lambadis, a tribal population from South India), Austro-Asiatic and Tibeto-Chinese speaking another one (together with the Siddis, a South Indian population of Negroid origin). As the first cluster is characteristic by rather low Gc*1F and high Gc*1S frequencies, the other one by high Gc*1F and low Gc*1S frequencies we supposed that this genetic distance pattern might be associated with the racial affiliations of the population groups under study. We therefore have plotted in Fig. 4 the variability of Gc*1F and Gc*1S frequencies in Mongoloid populations from East and Southeast Asia and in comparison that of the language families. The result is clear: Indo-European and Dravidian speaking populations are obviously different from the Mongoloids, whereas Austro-Asiatic and Tibeto-Chinese speakers are falling

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into the Mongoloid range of variability, which applies in particular to the Tibeto-Chinese family, whereas the Austro-Asiatic family is closer to the Indo-European and Dravidian group. This, of course, must be discussed in detail elsewhere. Concluding this one can point out that Indian populations with affinities to the Mongoloid racial group - as the Tibeto-Chinese speakers are - are striking by rather high Gc*1F and low Gc*1S frequencies, whereas those belonging to the Caucasoids (Indo-European and Dravidian speakers) and Australoids, the original inhabitants of India, show the contrary. Thus Gc subtypes prove to be of considerable importance for the analysis of genetic differentiation processes in India.

This is finally also corroborated by the distribution of rare Gc subtype variants in India, as e.g. the Meiteis from Manipur and the Karbis from Assam show Gc 1A8 variants (gene frequency in each of these two populations 0.014), which have also been reported for other Mongoloid populations (Japanese; Constans 1979). One can assume that this rare Gc subtype allele attained to the gene pool of Meiteis and Karbis by gene flow, which is reasonable considering the racial history of the Northeastern parts of India.

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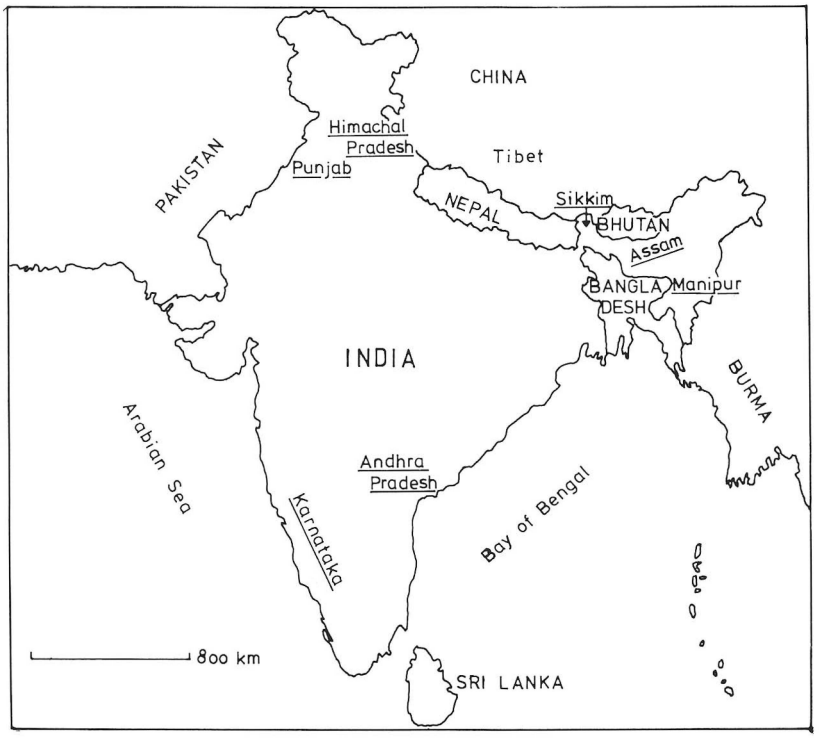

Fig. 1 Location of Indian populations, which have been Gc-subtyped.

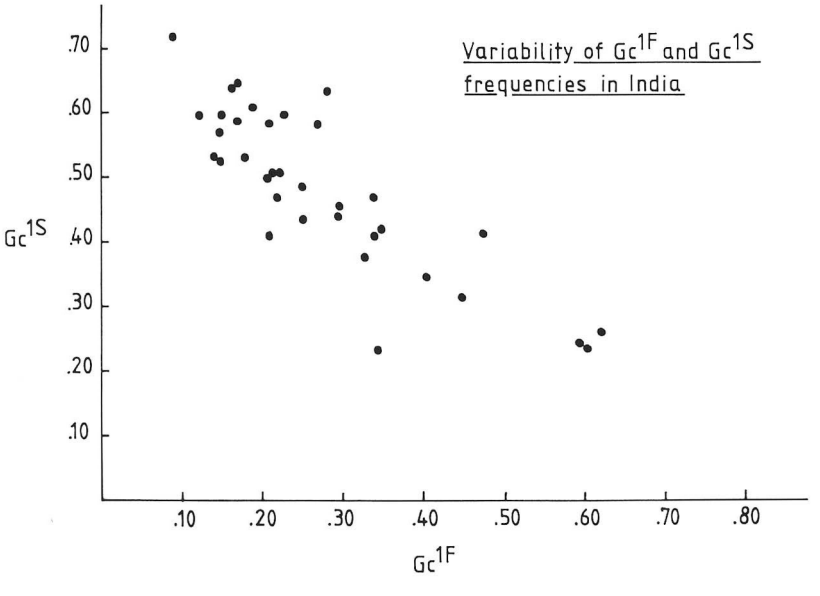

Fig. 2 Variability of Gc^{1F} and Gc^{1S} frequencies in India.

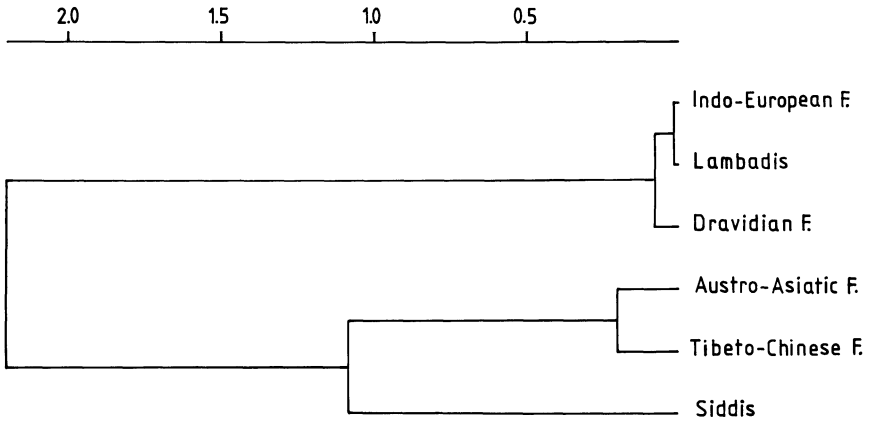

Fig. 3 Genetic distances among language families.

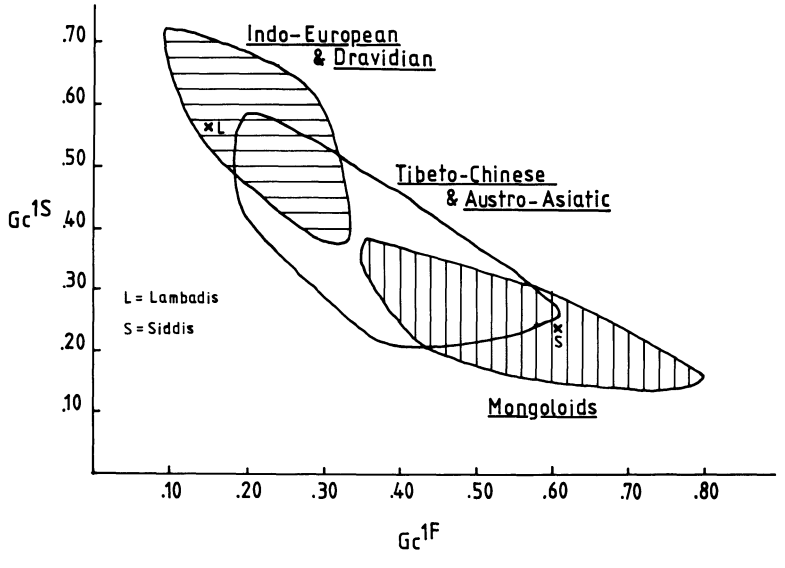

Fig. 4 Variability of Gc^{1F} and Gc^{1S} frequencies in Mongoloids as compared with language families.