GENETICS

HAP WORLD MAP?

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A new study of 12 Mb DNA sequence in 927 individuals representing 52 populations now finds good portability of of tag SNPs between the 4 hapmap groups and any of the 52 populations (except some African populations like the Mandenka, Bantu, Yoruba, Biaka Pygmy, Mbuti Pygmy and San). The paper has some exceptional well done graphics – and I am quite happy that the resolution of European nations leaves some gaps for our forthcoming ECRHS papers (a poster had already been on display at the 3rd Annual International HapMap Project in Cambridge, Massachusetts).

“Die Botschaft hörâ€™ ich wohl, allein mir fehlt der Glaube” (Goethe, “I hear the message well…”). The usefulness of tagSNPs in disease association studies still remains to be shown (I still renember comments like cr.. map). At present I neither believe in rare variants nor in common common variants but a permanent reshuffling of rare, frequent and highly abundant variants. Yea, yea.