

**Investigation of 12 X-STR loci in Mongolian and Eastern Han populations of China
with comparison to other populations**

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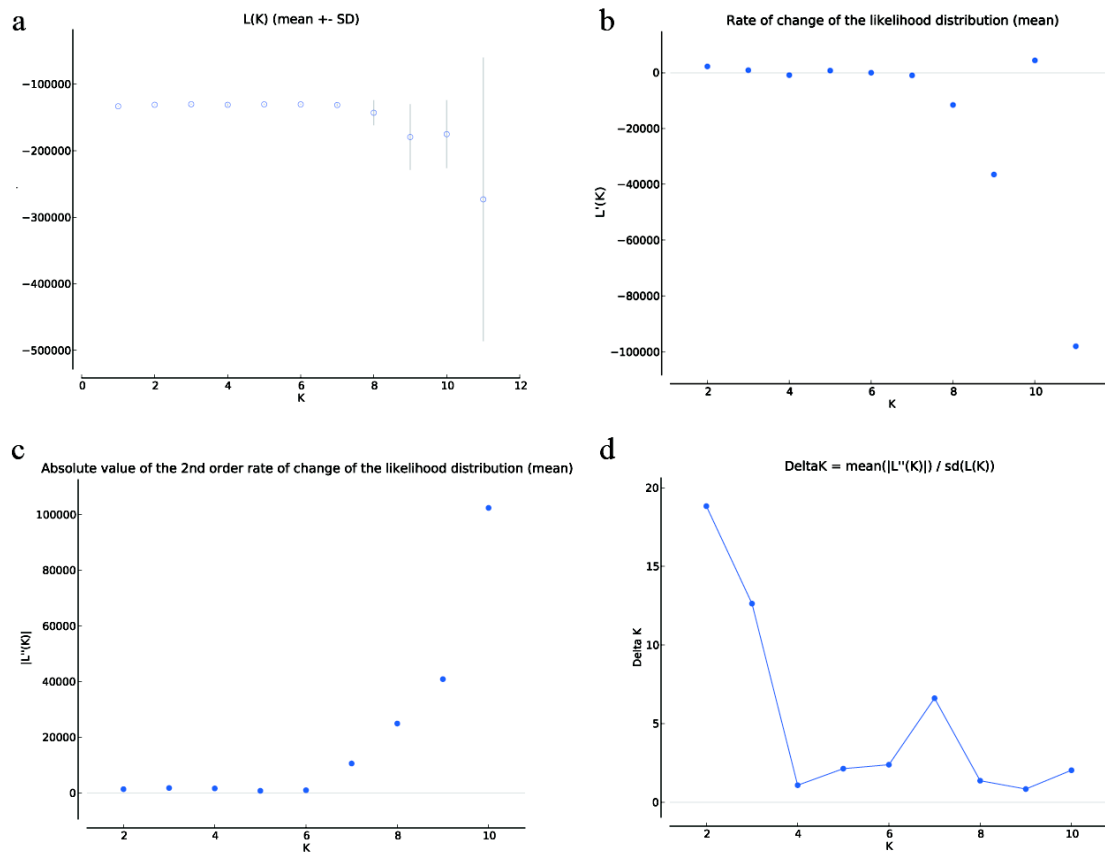
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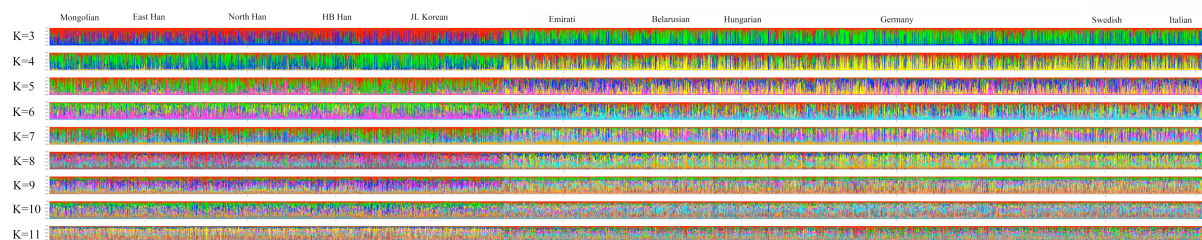
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Supplementary information:



Supplementary Figure S1. Graphical method used to detect the true K value. (a) Mean $L(K)$ ($\pm$ SD) over 10 runs for each K value. (b) Rate of change of the likelihood distribution (mean $\pm$ SD). (c) Absolute values of the second order rate of change of the likelihood distribution (mean $\pm$ SD). (d) ΔK calculated as $\Delta K = \text{mean}(|L''(K)|) / \text{sd}(L(K))$. The modal value of this distribution is the true K (*) or the uppermost level of structure, here 2 clusters.



Supplementary Figure S2. Estimated population genetic structure of Mongolian, Eastern Chinese Han and the nine other populations when $K=3-11$.

Supplementary Table S1. Haplotype frequency in Mongolian males (N=116).

Supplementary Table S2. Haplotype frequency in Eastern Chinese Han males (N=200).

Supplementary Table S3. Allelic frequency in the Mongolian population (N=232, female=116, male=116).

Supplementary Table S4. A total of 11 Chinese population groups and their sample sizes for 12 X-STR population comparisons.

Supplementary Table S5. Average F_{ST} based on allele frequencies among 11 Chinese populations.