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Errata

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The population genetics of *Trypanosoma brucei* and the origin of human infectivity

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Figure 1 contained some incorrect symbols. The amended figure and its caption are reproduced below.

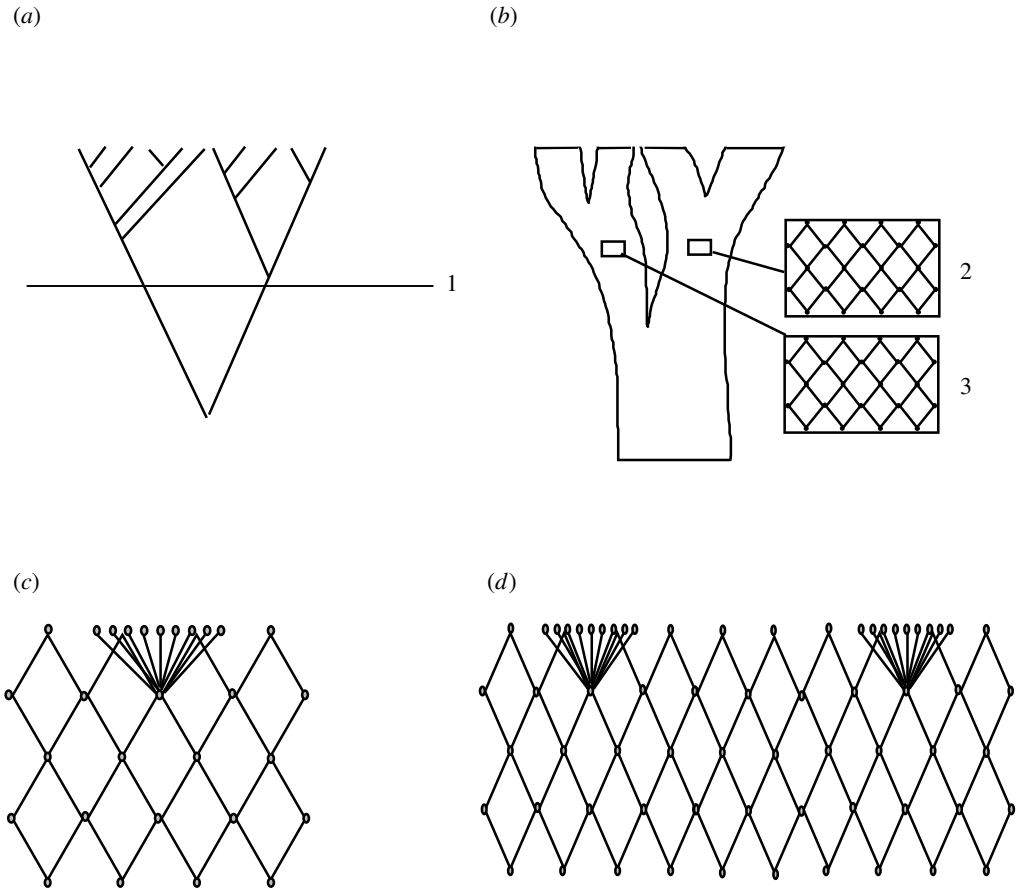

Figure 1. Diagrammatic representations of different population genetic structures (adapted with permission from Maynard Smith *et al.* (1993)). (*a*) *Clonality*. Clonality can be defined as a population in which genetic exchange is limited to such an extent that it is not sufficient to break up associations between alleles at different loci resulting in strong linkage disequilibrium. A dendrogram of genotype similarity would resemble an evolutionary tree, with no recombination occurring between isolates in the same or different branches of the tree. A clonal population does not imply that all isolates from this population are identical. If, for example, samples were taken at time-point 1 two clonal genotypes would have been identified. (*b*) *Panmixia*. In a panmictic population sexual recombination occurs frequently between individuals within the population. It must be remembered, however, that a species can consist of a number of populations, which can be subdivided into subpopulations due to a variety of different factors such as host-specificity and geographical isolation. Within each subpopulation, sexual recombination could occur frequently between isolates from within the same lineage as shown, but rarely, if at all, between different subpopulations. The analysis of polymorphic markers in such subpopulations would reveal a population in agreement with Hardy–Weinberg predictions and no significant linkage disequilibrium. However, if samples from two discrete populations were examined, i.e. if isolates from different subpopulations are combined, for example populations 2 and 3, deviation from Hardy–Weinberg predictions and linkage disequilibrium would be observed. (*c*) *Epidemic*. An epidemic population structure results from a combination of panmictic and clonal effects. The population has a basic panmictic population structure, but occasionally one or more genotypes, which are particularly suited to the environmental conditions, expand clonally to dominate the population. Superficial analysis of such populations would give the appearance of a clonal population structure (i.e. strong linkage disequilibrium and deviation from Hardy–Weinberg predictions) as the expansion of one or two genotypes would obscure underlying frequent genetic exchange in the population. However, reanalysis of the same data once the frequency of the common genotype(s) has been normalized would reveal the underlying nature of the population (i.e. no significant linkage disequilibrium and agreement with Hardy–Weinberg predictions). (*d*) *Different epidemic foci*. It is likely that different subpopulations, for example from different geographically isolated regions, have different clonally expanded genotypes or that over time different genotypes can come to dominate the population.

