Phylogenetic approaches to species delimitation fail to distinguish species whose haplotypes or alleles are not reciprocally monophyletic (as for at least 25% of all animal species, probably even more among plants).

Population genetic approaches can delineate species that are not monophyletic, but require analyzing large numbers of individuals (typically hundreds) and of independent markers (typically 10 or more).

Hence the need for an intuitive, graphical method to delineate reproductively isolated populations from haplotype trees (haplotrees) or haplotype networks (haplonets).

From haplonet to haploweb

Add connections (red curves) between haplotypes (alleles) found co-occurring in heterozygous individuals

From haplotree to haploweb

Haplowebs simultaneously display the evolutionary relationships between haplotypes in a population and the co-occurrence of these haplotypes in heterozygotes.

This makes it possible to delineate graphically groups of haplotypes that never co-occur in heterozygotes and therefore probably belong to different species.

Some markers, however, may be insufficiently variable to distinguish between closely related species, whereas some others may be experiencing selection: hence, reliable species delimitation is better achieved by comparing haplowebs obtained from several independent markers.