

Haplowebs: a graphical method for species delimitation

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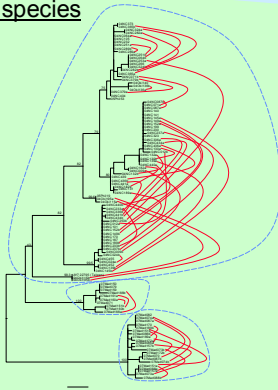
Phylogenetic approaches to species delimitation fail to distinguish species whose haplotypes or alleles are not reciprocally monophyletic (as for at least 25% of all animal species, probably even more among plants).

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).

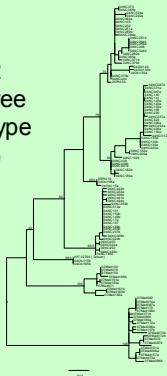
Three putative species

ITS2
haploweb
(haplotype
web)



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

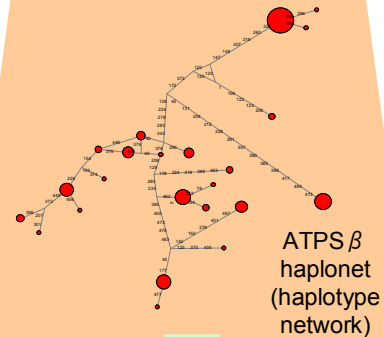
ITS2
haplotree
(haplotype
tree)



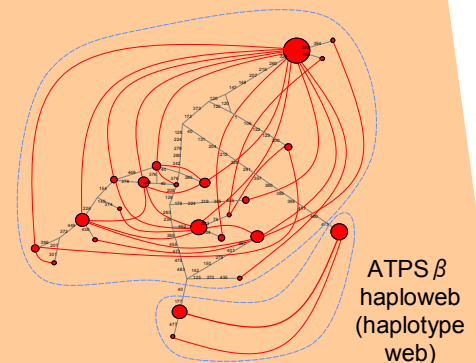
From haplotree to haploweb

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

From haplonet to haploweb



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



Two putative species

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.

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