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TraceAncestor: a Tool to Infer Unphased Phylogenomic Karyotypes of Admixed Plant Genomes

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For many plants, including citrus (Figure 1), reticulate evolution results in admixed mosaics of large genomic fragments from the ancestral taxa. For those plants, we developed a pipeline called TraceAncestor in order to infer phylogenomic karyotypes from GBS or re-sequencing sequence data and diagnostic SNPs (DSNPs) of the ancestral taxa.

TraceAncestor is based in the relative read numbers of ancestral alleles in successive genomic windows (Figure 2). It allows the user to define the number of DSNPs per window, the sequencing error rate and the threshold for LOD values of the maximum likelihood test. There is no limit to the number of ancestral taxa considered (which is automatically defined by the reference matrix of DSNPs).

TraceAncestor allowed revealing for the first time the origin and phylogenomic karyotypes of several cultivated Citrus (Ahmed et al. 2019) such as diploid bergamot Citrus bergamia, and triploid ‘Tahiti’ lime, C. latifolia (Figure 3).


This pipeline is available as a Galaxy workflow at: http://galaxy.southgreen.fr/galaxy/

and for download at: https://github.com/SouthGreenPlatform/galaxy-wrappers/tree/master/Galaxy_SouthGreen/traceancestor