

A reconciled version of the cork oak tree genome-scale metabolic model

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Quercus suber, commonly known as cork oak tree, is an evergreen tree which produces a thick bark (also known as cork) with multiple (a)biotic stress resistance properties (1). Due to cork's natural characteristics, such as the low weight, excellent insulation and low permeability, the cellular structure has a significant economic value as it has multiple applications. For instance, it can be used as a wine bottle sealant and insulation boards (2,3). Additionally, cork is harvested periodically throughout the tree's lifetime (4). Nevertheless, the cork's quality can only be properly assessed after 40 years of tree growth, which makes the identification of metabolic traits, associated to high-quality cork, of the utmost importance (5).

Genome-Scale Metabolic (GSM) models comprise both genomic and metabolic information and can predict the phenotypic behavior of an organism when subjected to distinct environmental conditions (6). Therefore, a reconstructed GSM model of the cork oak tree can point to metabolic properties related to cork quality. Additionally, *in silico* metabolic engineering strategies could lead to the development of metabolically enhanced trees.

The current *Quercus suber* leaf model, reconstructed within *merlin* (7), contains 3126 reactions, 2648 metabolites, 7258 genes and was subjected to extensive manual curation, while the biomass and energy requirements were revamped. *In silico* simulations, using Flux Balance Analysis (8), accurately predict the phenotypic behavior of the leaf cell when exposed to phototrophic and heterotrophic conditions.