



Palaeointeractomics

The genome of laboratory model plant and widespread wild flower *Arabidopsis thaliana* contains around 30,000 protein coding genes, around one and a half times as many as a human's. Some proteins are recently evolved and unique to the plant, but most have identifiable orthologs in other species, including our own. In the diagram, nodes represent *Arabidopsis* proteins, and edges represent pairwise physical interactions between proteins measured by yeast two-hybrid laboratory experiments or curated from the literature. Node size represents the number of a protein's interacting partners. Since plants first emerged from the sea, around 400 MYA, their genomes have doubled in size a number of times through duplication events, and undergone considerable subsequent interactional rewiring. As proteins from duplicated genes diverged over evolutionary time, the number of interacting partners shared in common between a duplicated pair decreased, rapidly at first then more slowly. Node colour represents estimated time since the most recent common ancestor of extant organisms across the tree of life whose genomes contain an orthologous gene. The red and brown proteins are the ones we share with the plants. Evolutionary footprint ages are estimated by an integration of fossil and genetic evidence. Tectonic projections are courtesy of Ron Blakey, tectonic interactions themselves partly inferred from the distribution of plants and their fossils across continents.

Interactome data from **Arabidopsis interactome mapping consortium, (2011), Science 333(6042).**

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