Phylogenetic bioprospecting for medicinal plants

Author: Giovanni Zecca[1]*, Elisa Toini[1], Massimo Labra[1], Fabrizio Grassi[1]
*lead presenter: giovanni.zecca@unimib.it
1 University of Milano-Bicocca, Milan, Italy

For millennia, plants have been a vital source of compounds useful for human health. While botanicals remain a cornerstone of modern pharmacology, identifying promising species within the vastness of plant diversity is a persistent challenge. Traditional bioprospecting is often slow, resource-intensive, and largely restricted to a few well-studied groups.

To address these issues, we developed a new methodological framework that leverages molecular phylogenetics to speed up the screening of plant species with untapped medicinal potential. Central to our approach is the introduction of *pm4mp*, an open-source R package designed to streamline the identification of bioactive candidates by integrating new analytical methods with existing ones. Capable of handling large-scale phylogenetic data, our workflow allows researchers to extract specific evolutionary clusters where beneficial properties are most likely to be concentrated and to assign prioritisation values to each species.

We validated the effectiveness of *pm4mp* by analysing medicinal data across 10 diseases, mapped against a comprehensive phylogeny of over 30,000 land plants. Our findings demonstrate that these new methods represent a substantial enhancement over existing approaches for plant bioprospecting.

Beyond its technical utility, this framework facilitates a more targeted approach, reducing the time and costs associated with research while minimizing the environmental impact on biodiversity. Ultimately, our study provides a robust, data-driven strategy to promote sustainable drug discovery.