

Genetic diversity within *Colletotrichum lupini* and its virulence on white lupin (*Lupinus albus*)

Key findings

- Multi-gene phylogeny distinguishes four groups within *C. lupini*
- Culture-based morphology distinguishes seven groups within *C. lupini*
- Highest genetic diversity is found in South America
- The most aggressive and widespread strains belong to phylogenetic group 1 and suggest to be the main cause of the current anthracnose epidemic of white lupin

Background Information

White lupin (*Lupinus albus*) is a grain legume known for its high protein content and quality, efficient nutrient acquisition and health benefits. Its high yield potential could make it a sustainable alternative to soybean in cooler regions. However, the anthracnose causing air- and seed-borne fungal pathogen *Colletotrichum lupini*, threatens lupin cultivation worldwide. We analysed the genetic and morphological diversity of globally-collected *C. lupini* isolates by multi-gene sequencing and culture-based morphology. Virulence assays were performed with strains representing different genetic groups.

Further research

- Increase South American *C. lupini* collection
- Improve phylogenetic resolution by 3D-RAD sequencing
- Test virulence on different white lupin genotypes and lupin species

Figure 2 – Genetic diversity within *C. lupini*.

A: Maximum likelihood tree inferred from the combined ITS, TUB2, GAPDH and APNMT1 sequence datasets. Bootstrap support values (>60%) and Bayesian posterior probabilities (>0.95) are given at each node. Subgrouping within group 1 is based on morphological differences.
B: Representative twelve day old *C. lupini* cultures on potato dextrose agar for different genetic groups.

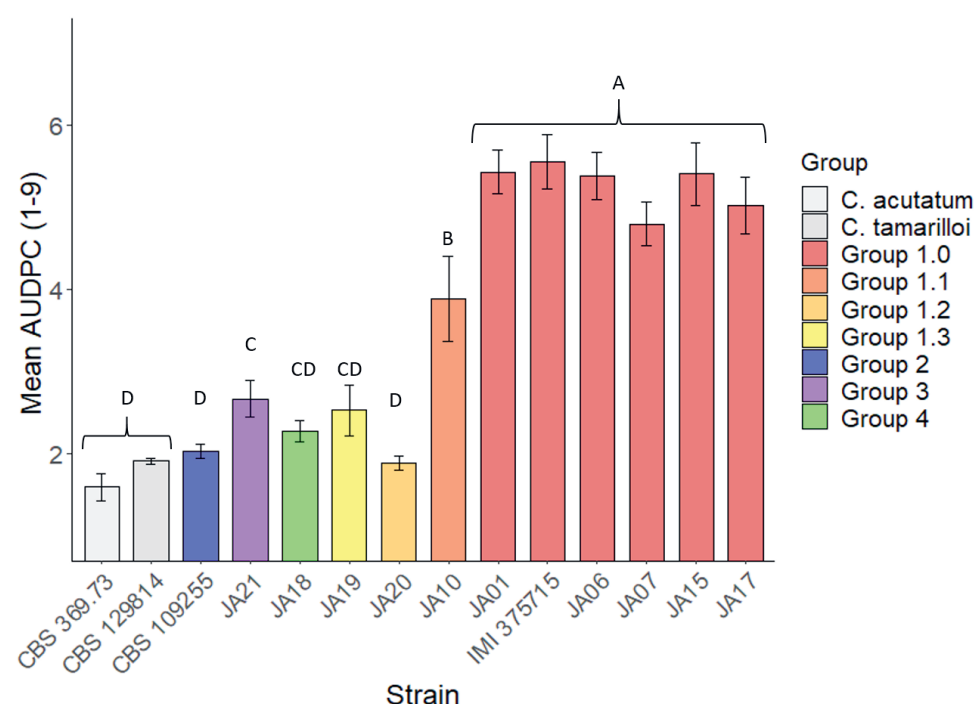
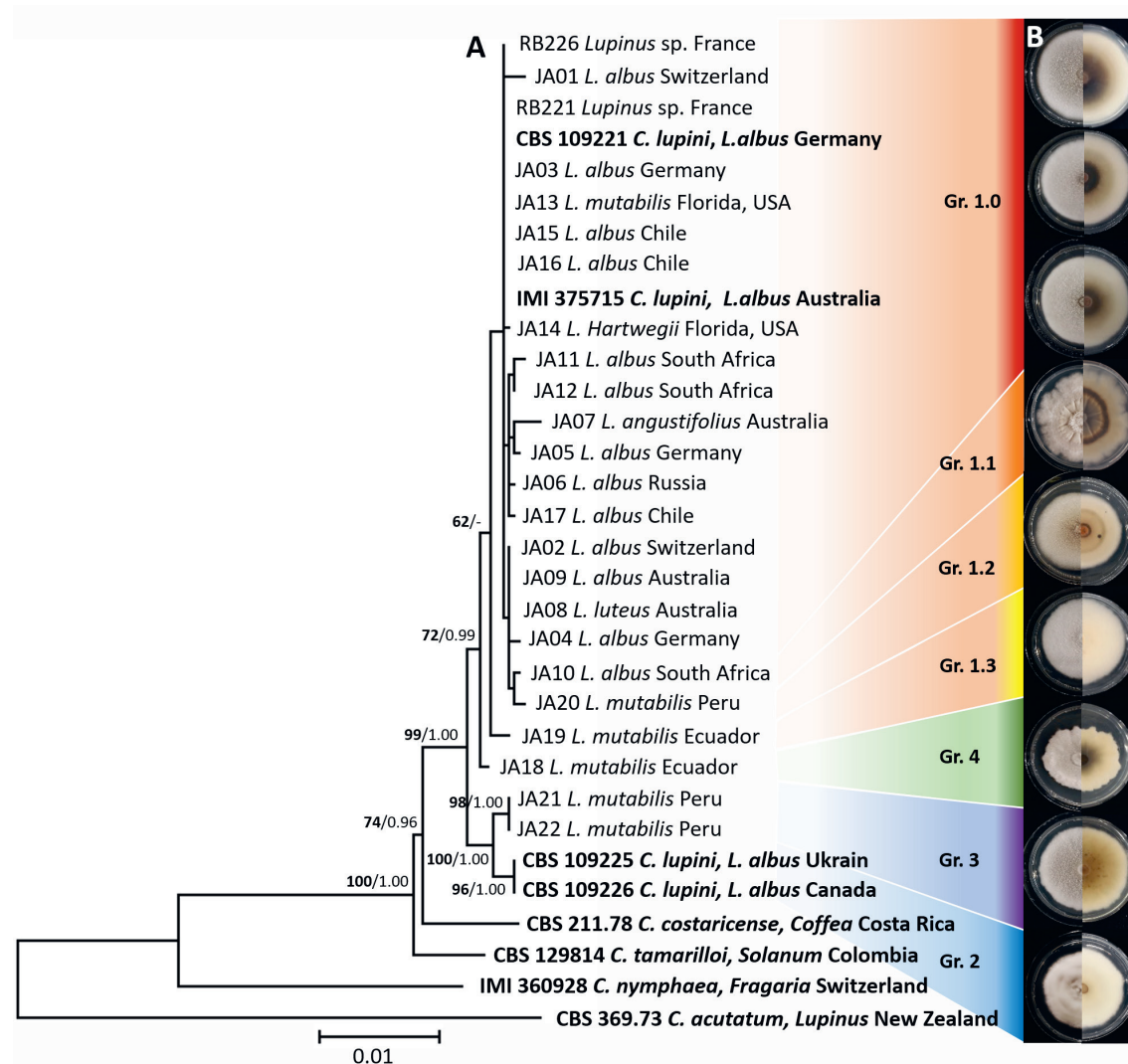


Figure 1 – Virulence of *C. lupini* strains on white lupin.

Errors bars show the standard error of the means. Different letters show significant differences between genetic groups (Tuckey-HSD, $p < 0.05$). AUDPC = Area under disease progress curve.



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