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ABSTRACTS - Oral Presentations

Population genomic study of an introduced ectomycorrhizal fungus *Suillus luteus*

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Suillus luteus is one of the most widely-introduced ectomycorrhizal fungi in the world. During the forestation of pine around the world, *S. luteus* has been introduced to North America, South America, South Africa and Oceania from its native Eurasian distribution. We sequenced 153 *S. luteus* genomes from native and introduced populations. Phylogenetic analysis indicates that *S. luteus* populations from Australia, New Zealand, and South America each possess novel SNPs that place them into well-supported monophyletic clades. Australia and New Zealand form a single clade in the ML tree, suggesting either shared common ancestry, or recent admixture. PCA and admixture analysis support the populations in exotic areas clustered together at continental level, and that all exotic population are divergent from European source population except North American individuals. Both PCA and admixture analysis imply Australia population and New Zealand population have undergone recent admixture. These results suggest that (1) exotic populations on different continents are descended from independent colonization events (2) Australia and New Zealand likely represent two independent introduction events, while subsequent migration homogenize the genetic components (3) North American population has similar genetic components as European populations, probably reflecting recent history of introduction followed by limited population expansion and reproduction.