

Supplementary Material S2

Nutritional Assessment of *Lactarius drassinus* and *L. controversus* from Cold Desert Region of Northwest Himalayas for Their Potential as Food Supplements

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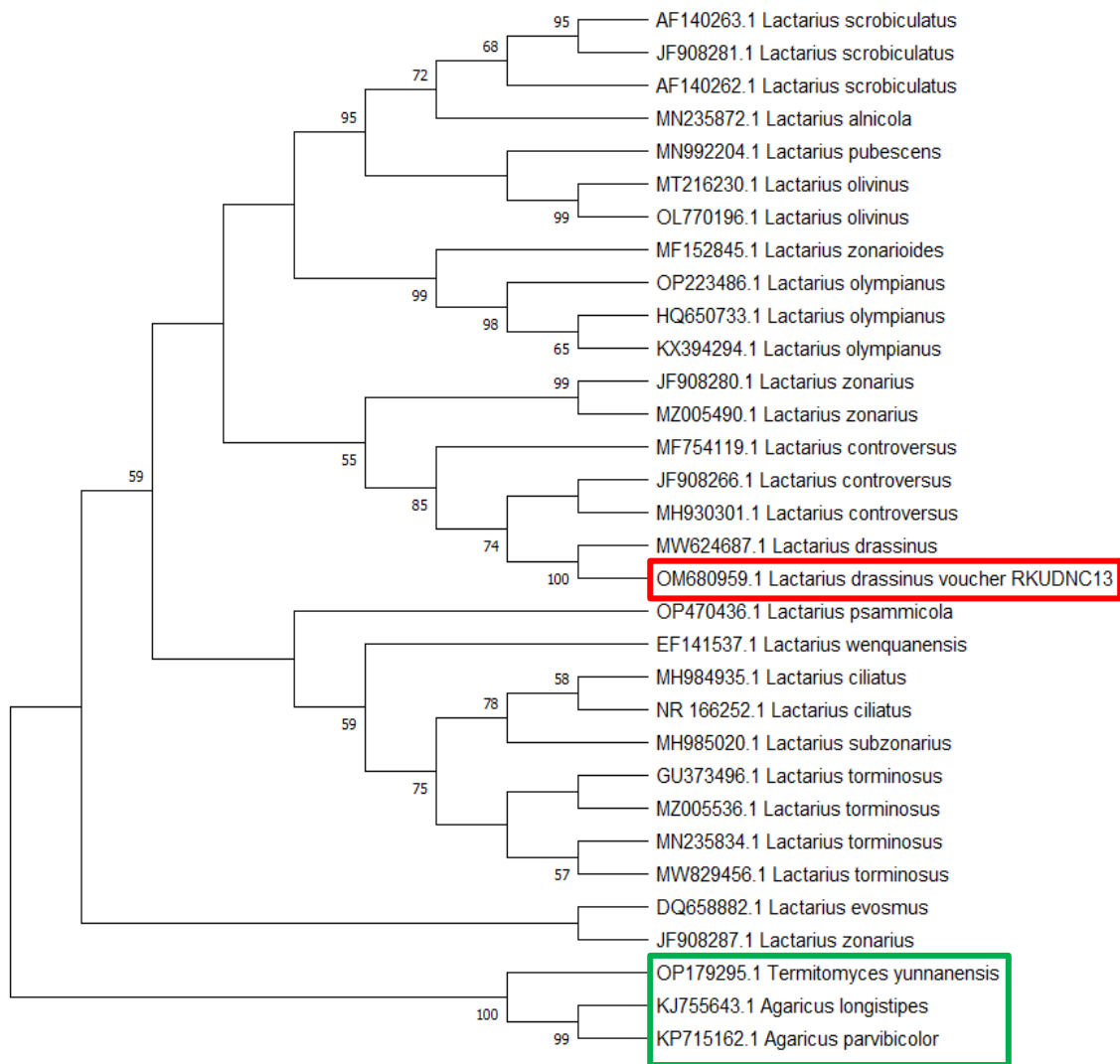


Figure S1. Neighbor-Joining tree constructed using sequences of internal transcribed spacer (ITS) region of the rRNA of *Lactarius* spp. The bootstrap consensus tree inferred from 1000 replicates is taken to represent the evolutionary history of the taxa analyzed. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. The evolutionary distances were computed using the Kimura 2-parameter method and are in the units of the number of base substitutions per site. The rate variation among sites was modeled with a gamma distribution. *L. drassinus* is highlighted in red and the outgroup (*Termitomyces yunnanensis*, *Agaricus longistipes*, and *A. parvibicolor*) in green.

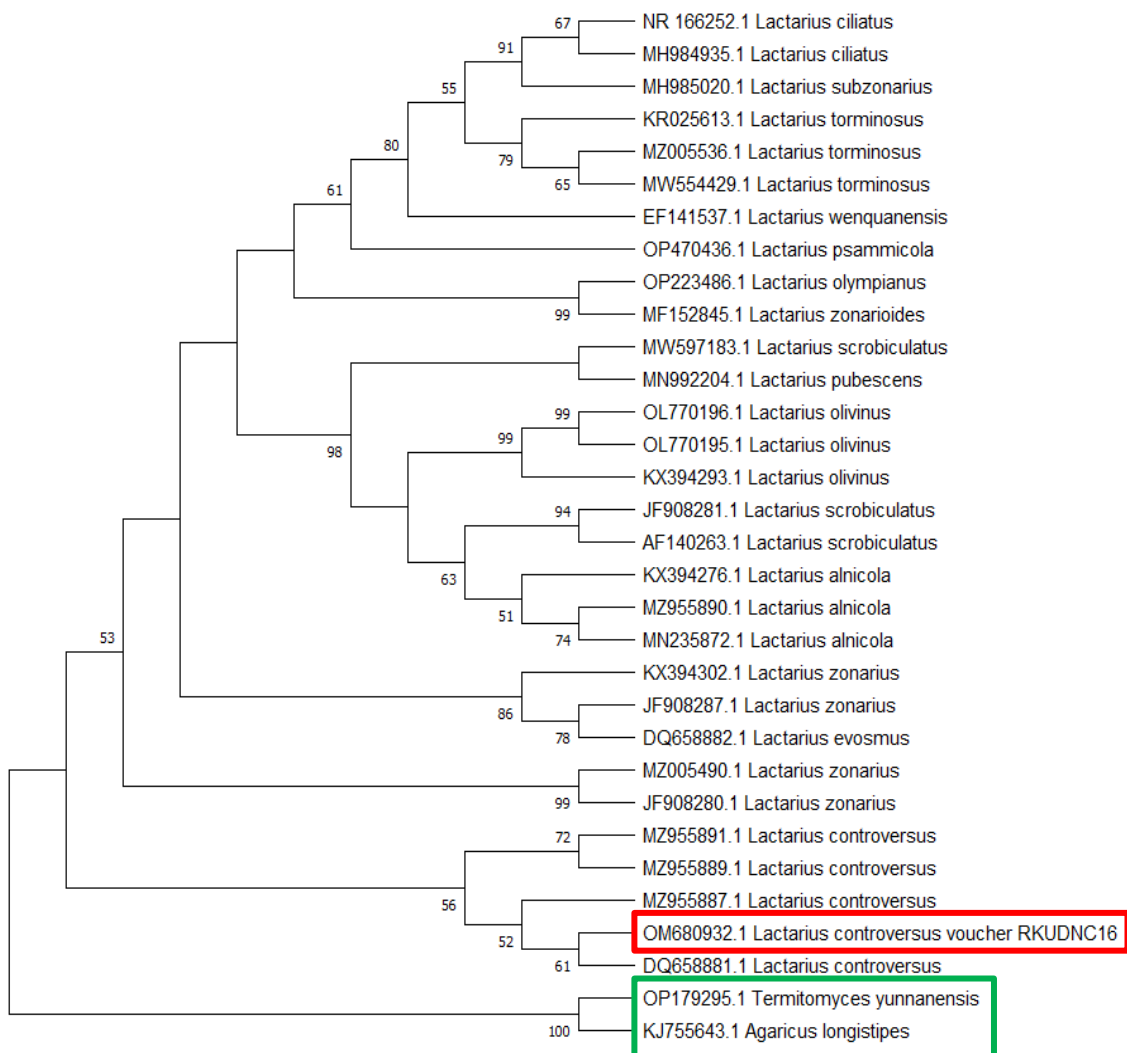


Figure S2. Neighbor-Joining tree constructed using sequences of internal transcribed spacer (ITS) region of the rRNA of *Lactarius* spp. The bootstrap consensus tree inferred from 1000 replicates is taken to represent the evolutionary history of the taxa analyzed. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. The evolutionary distances were computed using the Kimura 2-parameter method and are in the units of the number of base substitutions per site. The rate variation among sites was modeled with a gamma distribution. *L. controversus* is highlighted in red and the outgroup (*Termitomyces yunnanensis* and *Agaricus longistipes*) in green.