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Ice nucleation activity in the widespread soil fungus *Mortierella alpina*

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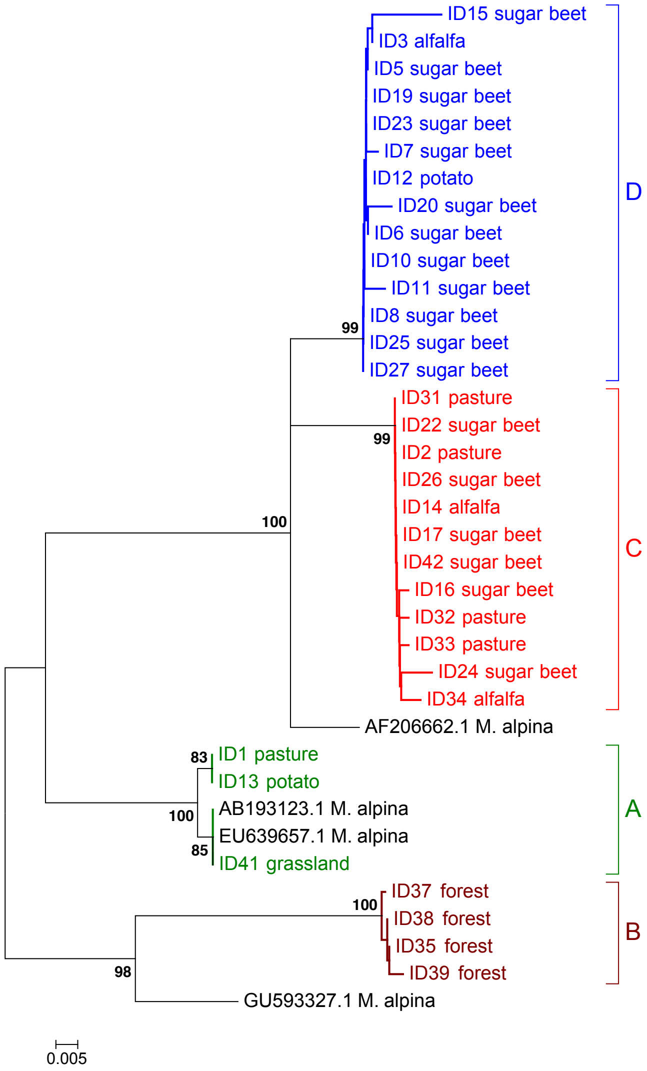

FIG S1 Neighbor-Joining tree based on GLELO DNA sequences. The evolutionary distances were computed using the Kimura 2-parameter method (Kimura, 1980); units are the number of base substitutions per site. The rate variation among sites was modeled with a gamma distribution (shape parameter = 0.34). Node support above 75% is given.

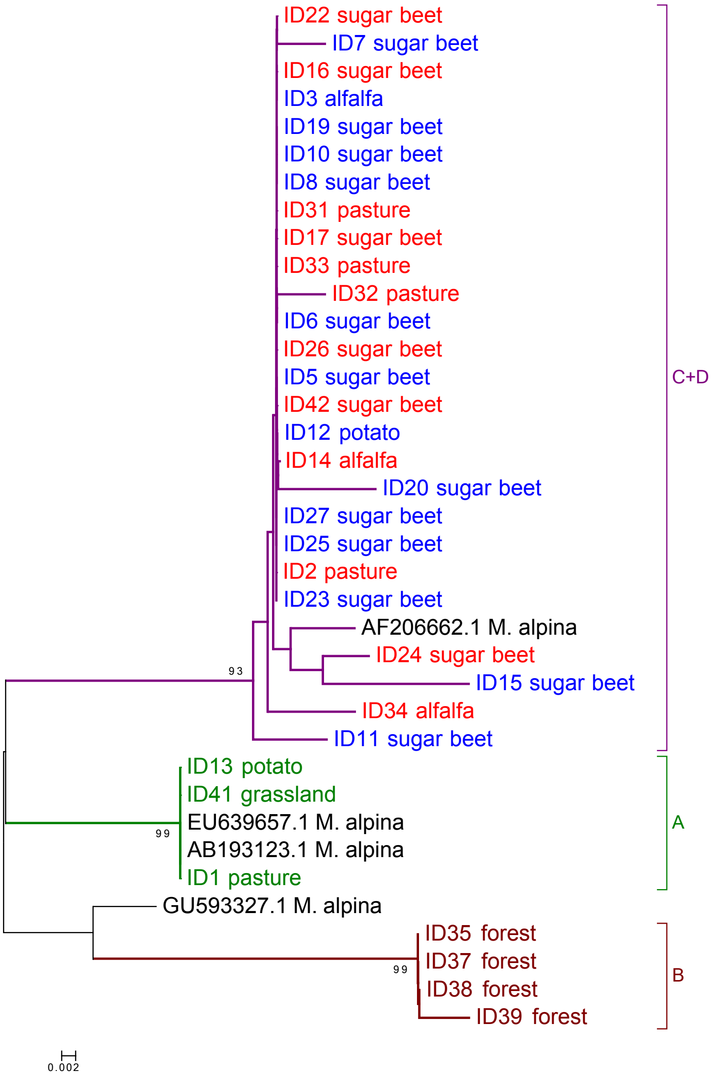

FIG S2 Neighbor-Joining tree based on GLELO amino acid sequences. The evolutionary distances were computed using the JTT matrix-based method (Jones et al., 1992); units are the number of amino acid substitutions per site. Node support above 75% is given.

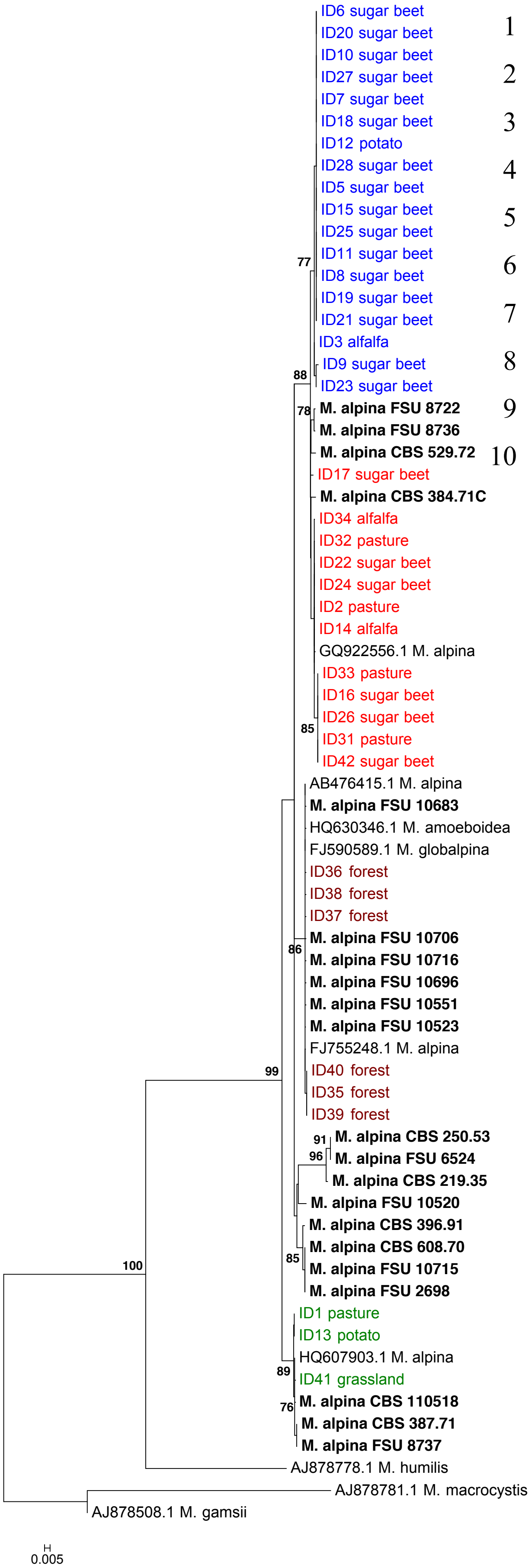

FIG S3 Neighbor-Joining tree based on ITS sequences (sequences from Wagner et al., (2013) are bold). The evolutionary distances were computed using the Tamura 3-parameter method (Tamura, 1992); units are the number of base substitutions per site. The rate variation among sites was modeled with a gamma distribution (shape parameter = 0.28). Node support above 75% is given.

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