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M. M. Alguacil, E. Lumini, A. Roldán, J. R. Salinas-García, P. Bonafonte, and V. Bianciotto. 2008. The impact of tillage practices on arbuscular mycorrhizal fungal diversity in subtropical crops. *Ecological Applications* 18:527-536.

Appendix A. Color-coded version of Fig. 1 showing the tillage system groups.

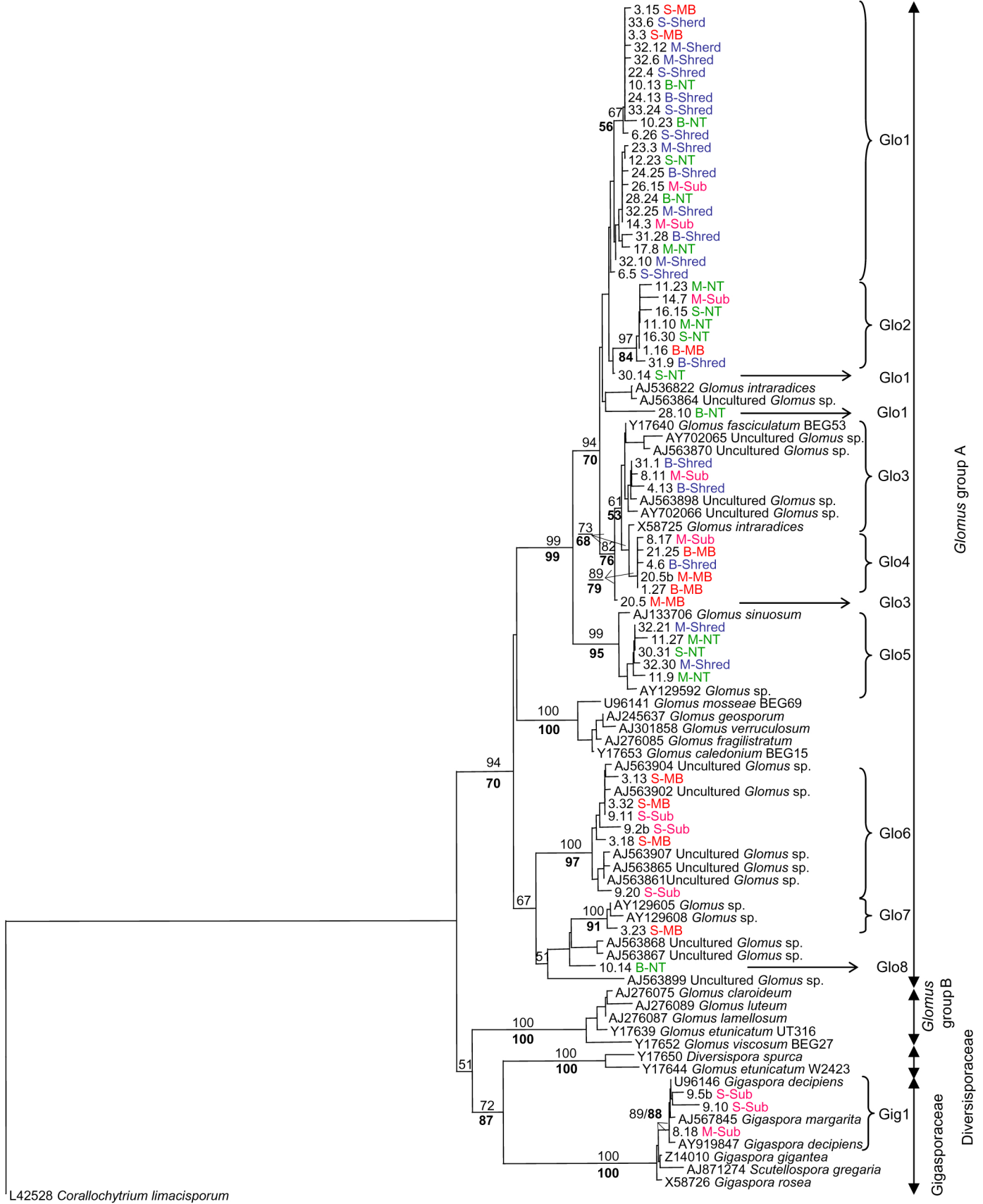


FIG. A1. Neighbor-joining (NJ) phylogenetic tree showing arbuscular mycorrhizal (AM) fungal sequences isolated from roots of maize, bean, and sorghum crop roots under different tillage systems and reference sequences from GeneBank. Numbers above the branches indicate the bootstrap values (above 50%, 100 replicates) of the NJ analysis; numbers below the branches indicate the bootstrap values of the maximum parsimony analysis. Clone identifiers relate to the tillage system and crop species; abbreviations are: MB, moldboard (red letters); Shred, shred-bedding (blue letters); Sub, subsoil-bedding (pink letters); NT, no tillage (green letters); S, sorghum; M, maize; and B, bean. Group identifiers (for example, Glo1) are the AM fungal sequences types found in our study. *Corallochytrium limacisporum* (Cavalier-Smith and Allsopp 1996) was used as the outgroup.

#### LITERATURE CITED

Cavalier-Smith, T., and M. T. E. P. Allsopp. 1996. *Corallochytrium*, an enigmatic non-flagellate protozoan related to choanoflagellates. *European Journal of Protistology* 32:306–310.