**Methods**

Sampling spanned fire affected and fire unaffected areas in two mountain ranges, the Santa Catalina Mountains (SCM) and the Pinaleno Mountains (PM). Both ranges are located at similar latitudes (Table 1) and have similar exposures as they both lie in a west northwest and east southeast position (Shreve 1919). PM has a maximum elevation of 3270 m.a.s.l. and SCM 2791 m.a.s.l.

The geology of both SCM and PM are similarly composed predominantly of gneiss (Shreve 1919). Climatic and geological similarities are reflected in comparable ecoclines of both ranges (ref).

Both ranges experienced severe wildfires between 2002 and 2004. The 2004 Nuttail-Gibson complex in PM burned . In SCM, two fires—the 2002 Bullock fire and the 2003 Aspen fire—burned and 343 km2, respectively.

Sampling encompassed two fire affected and two fire unaffected sites in both ranges at similar elevations. In SCM, six trees were samples per site (total 12 trees in burned sites, 12 trees in unburned sites). Based on species accumulation curves from previous studies (Bowman and Arnold, in review), we reduced sampling in PM to five trees per site (total 10 trees in burned sites, 10 trees in unburned sites). Roots were collected by soil coring. Three root cores (5 cm diameter; 15 cm depth) were collected at the canopy dripline from each sampled tree corresponding to uphill, parallel, and downhill of the tree (SCM: 72 root cores; PM: 60 root cores). The litter layer was removed prior to coring and roots were transported in plastic bags in a cooler back to the lab. Roots were stored at -20°C before processing.

Roots were gently cleaned with tap water over a 2 mm sieve. Root tips with evidence of EM fungal colonization were examined under a dissecting microscope. When cores were obtained from mixed forests (pine-oak woodlands and pine-Douglas fir forests; Table I), we used morphological and genetic evaluations to confirm the species identity of roots. *Quercus* roots were identified on the basis of morphological differences from roots of *Pinus* and were discarded. However, roots of *Pseudotsuga menziesii* are similar in appearance to those of *P. ponderosa*. Therefore, we amplified the plastid trnL region from all EM root tips collected in sites where *P. menziesii* was present and digested the PCR product using the restriction enzyme Rsal (Thermo Fisher Scientific, Waltham, Massachusetts, USA). We then used electrophoresis with a 1% agarose gel to discern host species based on banding patterns. DNA extracted from *P. ponderosa* leaves was used as a positive control.

We sorted EM root tips from *P. ponderosa* to morphotypes based on physical characteristics of the EM mantle. The number of live root tips per morphotype was recorded for each soil core. One or two representative tips of each morphotype per core were chosen haphazardly for DNA extraction. All other root tips were stored in cetyltrimethyl ammonium bromide (CTAB) at -80 °C. The remaining root samples were then air dried for 5-7 days, and their dry weight was recorded.

Total genomic DNA was extracted from root tips immediately after sorting using the RedExtract-N-Amp plant PCR kit (Sigma-Aldrich, St. Louis, Missouri, USA) following the manufacturer’s instructions. The internal transcribed spacer region (ITSrDNA, including ITS1, ITS2, and 5.8S rDNA) was PCR-amplified using primers ITS1F and LR3. We used primers ITS5 and LR3 for samples that failed to amplify during the initial PCR (Corrales et al., 2015). We did not use primer ITS4B because of the prevalence of ectomycorrhizal Ascomycota in preliminary surveys. We later separated sequences from EM fungi vs. other root-associated fungi for analyses (see below).

Soil cores were collected from three trees per site (total 24 soil cores, 12 per range) and sent to Motzz Laboratories for complete soil analyses.