**INTRODUCTION**

Wildfires exert strong ecological and evolutionary forces on ecosystems altering plant traits, soil characteristics, and community composition (Certini 2005; Hurteau & Brooks 2011; Hutto et al. 2016). With increasing fire severity (i.e. impact of fire on ecosystem, *sensu* Keeley 2009), forests experience deeper and longer term disruption including changes in soil pH and nutrient availability, species turnover, increase in standing dead wood, and soil erosion (Certini 2005; Peay et al. 2009; Kipfer et al. 2011; Pan et al. 2013). Regular fire intervals occur in all ecosystems with many species adapting to this kind of regular disturbance. Coniferous forests have developed adaptations to periodic fires such as regeneration post-fire or serotinous seed release (Stevens-Rumann & Morgan 2019). However, ongoing climate change and a long-term policy of fire suppression has led to an increase in the occurrence of highly destructive wildfires which has negative effects on these forests.

In addition to a direct impact on soil and vegetation, wildfires strongly alter above- and below-ground microbial communities important for forest health and resilience (Dahlberg et al., 2001; Baar et al. 2002; Glassman et al. 2016; Huang et al. 2016). Temperate forest trees form associations on their roots with ectomycorrhizal (EM) fungi which profoundly affect seedling establishment, nutrient and water availability, and resilience to abiotic and biotic stress (Smith & Read 2008; Patternson et al. 2019). Ponderosa pine forests, the most widely distributed pine species in the western United States, is well adapted to periodic low- to medium severity surface wildfires, but increasingly are unable to recolonize and regrow with the increasing frequency and severity of wildfires (Brown & Wu 2005; van Mantgem et al. 2009). Research into EM community resistance (i.e. the extent to which a community is displaced by disturbance) and resilience (i.e. the rate of recovery following a disturbance) can elucidate how forest ecosystems are likely to be affected in the future (Pimm 1984; Attiwill 1994; Kipfer *et al.,* 2011).

Effects of wildfires on communities of EM varies with fire intensity (i.e. energy output from fire, *sensu* Keeley 2009) and fire frequency (Peay et al. 2009; Buscardo et al. 2010; Cowan et al. 2016). Post-fire, colonization by EM is dominated by the fungal spore bank consisting of species that are disturbance adapted and poor competitors (Baar et al. 2002 Glassman et al. 2016), but increasing fire intensity and frequency can kill the spore bank slowing recolonization (Peay et al. 2009; Cowan et al. 2016). Following the intermediate disturbance hypothesis, diversity increases after fires of intermediate severity (Peay et al. 2019), but EM diversity decreases with higher intensity fires or short fire intervals (Wilkinson 1999; Dahlberg et al. 2001; Peay et al. 2009). With increasing time since fire, communities begin to resemble pre-fire communties due to dispersal of EM fungi from surrounding intact communities (Glassman et al. 2016). Unfortunately, much of the research into the effect of fire on EM communities has been conducted at relatively small spatial scales making it difficult to apply findings across forests.

The Madrean Sky Island Archipelago in southern Arizona supports diverse ecosystems unique from the Sonoran Desert surrounding them. Hosting a heterogeneous landscape spanning grasslands to coniferous forests at the summit, these biodiversity hot spots bridge the flora and fauna of the northern temperate Rocky Mts. with that of the southern subtropical Sierra Madre Mts. (DeBano & Ffolliott, 1995). The montane forests that survive at in these islands provide a unique opportunity to look at fire in similar forests with different precipitation regimes. Our goal was to determine whether similar, but distinct forests converge on similar EM communities post-fire. To answer this, we examined effects of fire on EM communities associated with Ponderosa pine in two mountain ranges in southeastern Arizona. Specifically, we asked (1) to what extent does diversity and community composition change as a function of fire in the Santa Catalina Mts. and Pinaleno Mts.? and (2) how similar are EM communities after fire?

**METHODS**

We conducted this study in the Santa Catalina Mountains and the Pinaleno Mountains of southern Arizona, USA. The ranges are located at approximately the same latitude and are separated by approximately 150 km (Figure 1; Table 1) (Shreve 1919). They have similar orientations, are composed predominantly of gneiss and granite, and have similar plant communities (Shreve 1919; Shreve 1922). The ranges only differ in their annual average precipitation and soil characteristics (Table 1 and 2). Prior to 1900, wildfires in both the Santa Catalina Mts. and the Pinaleno Mts. were more frequent and less intense with fire intervals being about every 4 to 6 years (Grissino-Mayer et al. 1995; Swetnam 2005; Iniguez *et al.*, 2008). From 1900, fire suppression and grazing severely reduced the number and frequency of wildfires increasing the length of fire intervals (Grissino-Mayer et al. 1995; Swetnam 2005).

Portions of the Santa Catalina Mts. and Pinaleno Mts. experienced severe wildfires between 2002 and 2004. The 2002 Bullock fire and 2003 Aspen fire burned 123.7 km2 and 343.0 km2, respectively, in the Santa Catalina Mts. (Iniguez *et al.*, 2008). In the Pinaleno Mts., the 2004 Nuttall-Gibson complex burned 120.3 km2 in the northern and southern portions of the range (USDA Forest Service, 2013).

**Site selection**

In each range we selected burned areas that had experienced a low- to intermediate severity fires in the Bullock, Aspen, or Nuttall-Gibson complex events of 2002-2004. To designate burned areas we used visual cues (e.g., presence of burn scares on trees, charcoal layer within soil horizon) and cross-referenced our observations with burn maps from Monitoring Trends in Burn Severity (MTBS) (accessed online, 2017). We identified two burned and two unburned areas in each range, which were sampled in 2014 (Santa Catalina Mts., unburned) and 2016 (Santa Catalina Mts., burned; Pinaleno Mts., burned and unburned) (Table 1). We sampled six trees per site in 2014 (a total of 12 trees), but reduced our sampling to five trees/site (10 trees per burn status per range) in 2016 because species accumulation curves indicated that five trees would be sufficient to capture local species richness in this region (Bowman and Arnold, 2018).

**Collection of roots**

We collected three root cores (5 cm diameter; 15 cm depth) in three positions at the canopy dripline of each tree (uphill, parallel, and downhill of the tree) (Santa Catalina Mts.: 66 root cores; Pinaleno Mts.: 60 root cores). We removed the litter layer prior to coring. We transported cores in plastic bags in a cooler to the lab and stored them at -20°C before processing.

**Collection of soil for chemical analyses**

We collected soil cores from three trees per site (total 24 soil cores, 12 per range) and stored samples at 4°C for processing within 72 hrs after collection. Each sample was sieved over a 2 mm mesh and dried at room temperature for 72 hrs. Motzz Laboratories (Phoenix, AZ, USA: http://www.motzzlaboratory.com/) performed chemical analyses.

**Sample processing for EM fungi**

We gently cleaned roots with tap water over a 2 mm sieve and then used a dissecting microscope to select root tips with evidence of EM fungal colonization. In some sites *P. ponderosa* occurred in mixed stands with Douglas Fir (*Pseudotsuga menziesii*) and/or oak (*Quercus* sp.) (Table 1). We verified that roots were from *P. ponderosa* as described in Bowman and Arnold (2018).

We sorted EM root tips from *P. ponderosa* to morphotypes based on physical characteristics of the EM mantle (Agerer, 1995). The number of live root tips per morphotype was recorded for each root core. One or two representatives of each morphotype per core were chosen for DNA extraction. We stored all other root tips in cetyltrimethyl ammonium bromide (CTAB) at -80 °C. The remaining root samples were air dried for 5-7 days, and their dry weight was recorded.

**DNA extraction, PCR, and sequencing of root tips for EM fungi**

We extracted total genomic DNA from root tips immediately after sorting as described in Bowman and Arnold (2018). Briefly, we extracted DNA with 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) and adjacent D1- D2 region of the nuclear ribosomal large subunit (LSU) was PCR-amplified using primers ITS1F and LR3. We did not use primer ITS4B because Ascomycota were prevalent in preliminary surveys (Bowman & Arnold, 2018).

We visualized PCR products with SYBR green following electrophoresis on a 1% agarose gel in 1% Tris base, acetic acid, and EDTA (TAE) buffer. We cleaned samples that amplified with ExoSAP-IT (Affymetrix, Santa Clara, California, USA). Bidirectional Sanger sequencing was performed by the University of Arizona Genetics Core with the Applied Biosystems Big Dye Chemistry Terminator v. 3.1 cycle sequencing kit. We assembled sequences, scored bases, and assigned quality scores with *phred* and *phrap* in Mesquite v. 2.01+ (Maddison and Maddison, 2011; Ewing and Green, 1998; Ewing et al., 1998). We manually edited assembled sequences in Sequencher v. 4.10.1 (GeneCodes Corporation). Sequences were classified to family or genus with UNITE and NCBI to ensure that amplified DNA was from EM species rather than soil fungi or root endophytes. All sequences have been deposited to GenBank (Appendix #).

We isolated 9,844 EM root tips from 132 root cores. Of these, 514 root tips were selected for sequencing. A total of 442 (86%) were sequenced successfully. We assembled operational taxonomic units (OTUs) in the web-based Mobyle SNAP Workbench with the sanger\_otu\_clustering\_workflow (Monacell and Carbone, 2014; U’Ren et al., 2014). The assembly pipeline used removed chimeric sequences (Edgar et al., 2011); automatically trimmed small subunit ribosomal DNA (SSUrDNA), large subunit DNA (LSUrDNA), and 5.8S sequences; and removed any sequences lacking either the ITS1 or ITS2 region. Sequences were clustered into OTUs at 97% similarity, resulting in a total of 116 OTUs (Izzo et al., 2005; Smith et al., 2007). Overall, 54 OTUs (47%) were singletons and 20 (17%) were doubletons.

**Statistical analyses**

*Species richness and diversity*

Diversity was analyzed with Fisher’s alpha, which is robust to variable sample sizes and is used for communities that generally follow a logarithmic series distribution, as is common in microbial communities . Diversity and species richness were calculated per tree with the ‘vegan’ package in R (Table 3) (Oksanen, 2018). Data were assessed for normality and heterogeneity of variance prior to analysis (data not shown). Species richness and diversity were normally distributed. We removed outliers from the Fisher’s alpha analysis if the species richness was equal to the community abundance as this falsely inflated the Fisher’s alpha value (Table 3). We assessed differences between burned and unburned sites within each range for species richness and Fisher’s alpha using a t-test. All analyses were carried out using R (R Core Team, 2018).

*Community composition*

We analyzed the community composition of EM communities based on fire history, both within each range and across both ranges, with an analysis of similarity (ANOSIM) and assessed patterns visually using non-metric multidimensional scaling (NMDS). To assess community differences, we used two similarity indices: Jaccard (a presence/absence measure) and Morisitia-Horn (an abundance measure) (Magurran 2004). We checked data for normality and equal variance prior to ANOSIM (data not shown). The datasets that failed to meet the assumptions required for ANOSIM were analyzed with a permutation multivariate analysis of variance (PERMANOVA).

*Taxonomy*

We assigned taxonomy to sequences with the NCBI and the UNITE databases (UNITE community). We assessed the taxonomic composition of communities with a chi-square analysis at the class level and genus level as a function of fire history within each range. Rare genera (those with fewer than four occurrences across all sites) were removed prior to analysis. Additionally, we used indicator species analysis to assess whether particular taxonomic groups were more prevalent within unburned or burned sites. The analysis was implemented using the ‘indicspecies’ package in R (De Cáceres & Legendre, 2009).

**RESULTS**

Species richness and Fisher’s alpha did not vary based on fire history (Fig. 2A and 2B, respectively). Average Fisher’s alpha across all sites was 15.0 (± 7.9) with unburned sites having 13.2 (± 7.5) and burned sites having 17.3 (± 8.0) .

*Community composition*

Community composition in unburned differed from burned sites in both ranges (Fig. 2C and 2D). EM communities in sites without recent burn history (unburned sites, Fig. 3A) showed only a slight overlap, whereas sites with a recent fire history (burned sites, Fig. 3C) in both ranges are completely distinct with no overlap in community composition.

*Taxonomy*

We found that EM taxonomy differed between unburned and burned sites (Fig. 3B & 3D). The most abundant genera were *Cenococcum*, *Russula*, *Tomentella*, and *Lactariu*. Burned sites within the Santa Catalina Mts. were characterized by a species of questionable EM status, *Sistotrema* (Table 4). In the Pinaleno Mts., unburned sites were characterized by a species of *Lactarius*, an EM genus, and *Phialocephala*, a dark septate endophyte (DSE) (Table 4).

**DISCUSSION**

In this study, we aimed to determine whether 1) EM community diversity and composition would differ in unburned and burned sites 15 years post-fire and 2) if similar patterns would be observed in geographically distinct, but environmentally similar forests. We found no difference in species richness or diversity based on fire history, but community composition and taxonomy differed in FA sites compared to paired FU sites. Overall, we found similar patterns in both ranges. These findings demonstrate that even in geographically distinct forests hosting unique EM communities, EM species diversity and community composition respond similarly to fire.

Whereas EM communities across both ranges differed between burned and unburned sites, EM communities in the Santa Catalina Mts. and Pinaleno Mts. showed no similarity in burned sites (Fig. 4B) compared to a higher level of similarity in unburned sites (Fig. 4A). Although care was taken to ensure that both environment and fire conditions across sites were similar, some differences were still evident (Supplementary figure S1 and S2). Despite these environmental differences, the contrast between unburned and burned sites suggests that disturbance has a stronger effect than environment in shaping EM communities. Alternatively, these community differences could indicate that changes in community composition are governed by non-disturbance processes, such as historical contingency or underlying species pool. Our observation that the taxonomic composition of EM communities within the two ranges showed contrasting patterns supports the latter hypothesis.

When fire intensity is intermediate, EM communities assessed immediately post-fire show an increase in both diversity and species richness compared to pre-fire status (Stendell *et al.* 1999; Baar *et al.* 2002). The slightly higher species richness and diversity we found in burned compared to FU sites could indicate these sites are continuing recovery to pre-fire conditions. The differences in community structure, though, suggest that these communities have yet to return to a pre-fire state. A study in which recovery of sites post-fire was assessed found that approximately 15 years was sufficient for EM community recovery to near pre-fire diversity status (Treseder *et al.* 2004), although other studies have indicated that substantially longer is required for communities to fully stabilize post-fire (Visser 1995). As fire severity, community composition, and environment all can impact recovery of EM it is difficult to discern what is important here (Stendell *et al*. 1999; Dahlberg *et al.* 2001; Baar *et al.* 2002; Glassman *et al.* 2016).

Visual indicators and fire severity maps indicate that our burned sites probably underwent a low- to intermediate-intensity fire, which would have lower temperatures and low level penetration of soil horizons. Low level disturbances can leave the EM spore bank and portions of the hyphal community intact decreasing recovery time (Dahlberg *et al.* 2001; Baar *et al.* 2002; Glassman *et al.*2016). Although the spore community was not assessed here, dormant spore communities serve as the initial inoculum post-fire (Dahlberg *et al.* 2001; Baar *et al.* 2002; Glassman *et al.*2016). Common genera associated with the spore bank are *Rhizopogon,* *Wilcoxina*, and *Tomentella* among others (Baar *et al.* 2002). Although *Rhizopogon* and *Tomentella* were present in burned sites, these genera were also in unburned sites and overall relative abundance was very low possibly supporting the recovery of burned sites to pre-fire conditions.

A major concern of this study was the temporal difference in sampling (Table 1). EM communities are known to undergo community shifts over relatively short time scales (i.e. seasonal), but year-to-year within the same season there can be little to no changes within the community (Koide *et al.* 2005; O’Hanlon 2012). Additionally, temporal shifts within EM communities is stronger in extraradical hyphae and less pronounced in root colonized EM (Koide *et al.* 2005). As we sampled within the same season of different years and only sampled EM colonized roots, the temporal effect on sampling should be minimal.

The slow recovery of EM communities post fire in the Southwest has important implications for the speed and ability of forests to recover from the ever increasing threat of wildfires. Additionally, the importance of disturbance and community composition in shaping EM community recovery demonstrates the importance of protecting the unique montane forests found here.

**References:**

Baar, J., T.R. Horton, A.M. Kretzer, and T.D. Bruns. 2002. Mycorrhizal colonization of *Pinus muricate* from resistant propagules after a stand-replacing wildfire. *New Phytologist* 143: 409-418.

Bowman, E.A. and Arnold, A.E. 2018. Distributions of ectomycorrhizal and foliar endophytic fungal communities associated with *Pinus ponderosa* along a spatially constrained elevation gradient. *American Journal of Botany*, in press.

Corrales, A., A.E. Arnold, A. Ferrer, B.L. Turner, and J.W. Dalling. 2015. Variation in ectomycorrhizal fungal communities associated with *Oreomunnea mexicana* (Juglandaceae) in a Neotropical montane forest. *Mycorrhiza* 26:1–17.

Dahlberg, A., J. Schimmel, A.F.S. Taylor, and H. Johannesson. 2001. Post-fire legacy of ectomycorrhizal fungal communities in the Swedish boreal forest in relation to fire severity and logging intensity. *Biological Conservation* 100: 151-161.

De Cáceres, M. and P. Legendre.. 2009. Associations between species and groups of sites: indices and statistical inference. *Ecology* 90(12): 3566-3574.

Ewing, B. and P. Green. 1998. Base-calling of automated sequencer traces using phred. II. Error probabilities. *Genome Research* 8: 186–194.

Ewing, B., L. Hillier, M.C. Wendl, and P. Green. 1998. Base-calling of automated sequencer traces using Phred. I. Accuracy Assessment. *Genome Researchh* 8: 175–185.

Fisher, R.A., A.S. Corbet, and C.B. Williams. 1943. The relation between the number of species and the number of individuals in a random sample of an animal population. *British Ecological Society* 12: 42-58.

Glassman, S.I., C.R. Levine, A.M. DiRocco, J.J. Battles, and T.D. Bruns. 2016. Ectomycorrhizal fungal spore bank recovery and sever forest fire: some like it hot. *The ISME Journal* 10: 1228-1239.

Grissino-Mayer, H.D., C.H. Baisan, and T.W. Swetnam. 1995. Fire history in the Pinaleño Mountains of southeastern Arizona: effects of human-related disturbances. In: Debano, L.F., Ffolliott, P.F., Gottfried, G.J., Hamre, R.H., Edminster, C.B., (Tech. Coords.), Biodiversity and management of the Madrean Archipelago: The Sky Islands of Southwestern United States and Northwestern Mexico. September 19–23, 1994. Tucson, Arizona. USDA Forest Service General Technical Report RM GTR-264, Rocky Mountain Forest and Range Experiment Station, pp. 399–407. Fort Collins CO.

Iniguez, J.M., T.W. Swetnam, and S.R. Yool. 2008. Topography affected landscape fire history patterns in southern Arizona, USA. *Forest Ecology and Management* 256: 295-303.

Izzo, A., J. Agbowo, and T.D. Bruns. 2005. Detection of plot- level changes in ectomycorrhizal communities across years in an old- growth mixed- conifer forest. *New Phytologist* 166: 619–629.

Koide, R.T., D.L. Shumway, B. Xu, and J.N. Sharda. 2005. On temporal partitioning of a c ommunity of ectomycorrhizal fungi. *New Phytologist* 174: 420-429.

Maddison, W.P. and D.R. Maddison. 2011. Mesquite: a modular system for evolutionary analysis. Version 2.75. http://mesquiteproject.org. [Accessed July 27, 2015].

Magurran, A.E. 2004. Measuring biological diversity. Malden, MA: Blackwell Science Ltd.

Monacell, J.T., and I. Carbone. 2014. Mobyle SNAP Workbench: a web-based analysis portal for population genetics and evolutionary genomics. *Bioinformatics* 30: 1488–1490.

Monitoring Trends in Burn Severity. (2017, July - last revised). [MTBS Project Homepage, USDA Forest Service/U.S. Geological Survey]. Available online: [http://mtbs.gov/[2017](http://mtbs.gov/%5b2017), July12].

Nguyen, N.H., Z. Song, S.T. Bates, S. Branco, T. Leho, J. Menke, J.S. Schilling, P.G. Kennedy. 2015. FUNGuild: an open-annotation database for parsing fungal community datasets by ecological guild. Fungal Ecology 20, 241–248.

Oksanen, J., F.G. Blanchet, M. Friendly, R. Kindt, P. Legendre, D. McGlinn, P.R. Minchin, R.B. O'Hara, G.L. Simpson, P. Solymos, M.H.H. Stevens, E. Szoecs, and H. Wagner. 2018. vegan: Community Ecology Package. R package version 2.5-2. https://CRAN.R- project.org/package=vegan.

O’Hanlon, R. 2012. Below-ground ectomycorrhizal communities: The effect of small scale spatial and short term temporal variation. *Symbiosis* 57: 57-71.

R Core Team. 2018. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL https://www.R-project.org/

Shannon, C.E. 1948. A mathematical theory of communication. *The Bell System Technical Journal* 27: 379-423 and 623-656.

Shreve, F. 1919. A comparison of the vegetational features of two desert mountain ranges. *The Plant World* 22: 291-307.

Shreve, F. 1922. Conditions indirectly affecting vertical distribution on Desert Mountains. *Ecology* 3:169-274.

Smith, M. E., G. W. Douhan, and D. M. Rizzo. 2007. Intra- specific and intra- sporocarp ITS variation of ectomycorrhizal fungi as assessed by rDNA sequencing of sporocarps and pooled ectomycorrhizal roots from a *Quercus* woodland. Mycorrhiza 18: 15–22.

Stendell, E.R., T.R. Horton, and T.D. Bruns. 1999. Early effects of prescribed fire on the structure of the ectomycorrhizal fungus community in a Sierra Nevada ponderosa pine forest. *Mycological Research* 103: 1353-1359.

Treseder, K.K., M.C. Mack, and A. Cross. 2004. Relationships among fires, fungi, and soil dynamics in Alaskan boreal forests. *Ecological applications* 14: 1826-1838.

UNITE Community (2019): UNITE USEARCH/UTAX release for Fungi. Version 18.11.2018. UNITE Community. <https://doi.org/10.15156/BIO/786345>.

U’Ren, J.M., J.M. Riddle, J.T. Monacell, I. Carbone, J. Miadlikowska, and A.E. Arnold. 2014. Tissue storage and primer selection influence pyrosequencing-based inferences of diversity and community composition of endolichenic and endophytic fungi. *Molecular Ecology Resources* 14: 1032–1048.

USDA Forest Service. 2013. USDA Forest Service Coronado National Forest GIS Data. <<http://www.fs.usda.gov/detail/r3/landmanagement/gis/?cid=stelprdb5208076>>

Visser, S. 1995. Ectomycorrhizal fungal succession in jack pine stands following wildfire. *New Phytologist* 129: 389-401.

**Figures**

Figure 1: Map of the Santa Catalina Mts. and sampling sites.

Figure 2: Species richness (A) and Fisher’s alpha diversity (B) as a function of both fire history and range. A. T-test, Pinaleno Mts.: T17.90=1.76, p-value=0.10; Santa Catalina Mts.: T18.68=1.81, p-value=0.09. B. T-test, Pinaleno Mts.: T7.09=1.87, p-value=0.10; Santa Catalina Mts.: T16.44=0.39, p-value=0.70. FA = fire affected, FU = fire unaffected.

Figure 3: NMDS of EM community across fire unaffected (FA) and fire unaffected (FU) sites in the Pinaleno Mts. (A) and Santa Catalina Mts (B) based on Morisita Horn similarity index. A. Pinaleno Mts., stress=0.16, ANOSIM: R=0.54, p=value=0.001; B. Santa Catalina Mts., stress=0.20, PERMANOVA: F=1.96, R2=0.09, p-value=0.02. Green = FU, black = FA; circles = Santa Catalina Mts., squares = Pinaleno Mts..

Figure 4: NMDS of EM community across fire affected (FA; A) and fire unaffected (FU; B) based on Morisita Horn similarity index . A. FA, stress=0.19, ANOSIM: R=0.33, p-value=0.001; B. FU, stress=0.15, PERMANOVA: F=3.23, R2=0.16, p=value=0.001. Green = FU, black = FA; circles = Santa Catalina Mts., squares = Pinaleno Mts..

Figure 5: Class level taxonomy of EM communities as a function of fire history. Each range assessed individually. A. Pinaleno Mts., X26=22.48, p-value<0.001; B. Santa Catalina Mts., X26=16.314, p-value=0.003. FU = fire unaffected, FA = fire affected.

Figure 6: Genus level taxonomy of EM communities as a function of fire history. Each range assessed individually. A. Pinaleno Mts., X29=37.62, p-value<0.001; B. Santa Catalina Mts., X213=34.61, p-value=0.001. FU = fire unaffected, FA = fire affected.

**Supplementary Figures:**

Figure S1: Average annual precipitation (mm) as a function of both range and fire history. ANOVA with site as a random factor, range: F1,4 = 99.21, p-value = 0.001; burn history: F1,4 = 3.59, p-value = 0.13; range:burn history: F1,4 = 7.67, p-value = 0.05. FA = fire affected; FU = fire unaffected.

Figure S2: PCA of soil characteristics as a function of both range and fire history. ANOVA with site as a random factor, range: F1,4 = 7.20, p-value = 0.06; burn history: F1,4 = 6.32, p-value = 0.07; range:burn history: F1,4 = 0.003, p-value = 0.96. FA = fire affected; FU = fire unaffected.

Figure S3 Shannon’s diversity as a function of fire history and range. T-test, Pinaleno Mts..: T18.41=1.83, p-value = 0.08; Santa Catalina Mts.: T13.48=2.06, p-value =0.06.

Figure S4: NMDS of EM community across fire affected (FA; A) and fire unaffected (FU; B) based on Jaccard similarity index. A. FA, stress=0.19, PERMANOVA: F=2.92, R2=0.14, p-value=0.001; B. FU, stress=0.13, PERMANOVA: F=2.41, R2=0.12, p=value=0.002. Black = FA, Green = FU; circles = Santa Catalina Mts., squares = Pinaleno Mts..

Figure S5: NMDS of EM community across FA and FU sites in the Pinaleno Mts. (A) and Santa Catalina Mts. (B) based on Jaccard similarity index. A. Pinaleno Mts., stress=0.15, ANOSIM: R=0.53, p=value=0.001; B. Santa Catalina Mts., stress=0.21, ANOSIM: R=0.11, p-value=0.06. Black = FA, green = FU; circles = Santa Catalina Mts., squares = Pinaleno Mts..