Project Update: July 2023

We are currently halfway into the project and have successfully finished all the sampling and pre-processing of the samples, as well as preliminary analysis. A total of 29 conifer species were sampled, from which three to four samples per species were collected. A niche modelling of species distributions was conducted to identify possible unsampled populations. Once distributional ranges were corroborated, field trips were made to sample remaining populations not previously included in the study. Taxonomically ambiguous species populations were sampled and labeled based on the opinion of experts as well as local stakeholders and habitants and later confirmed through sequencing and the construction of a phylogeny.
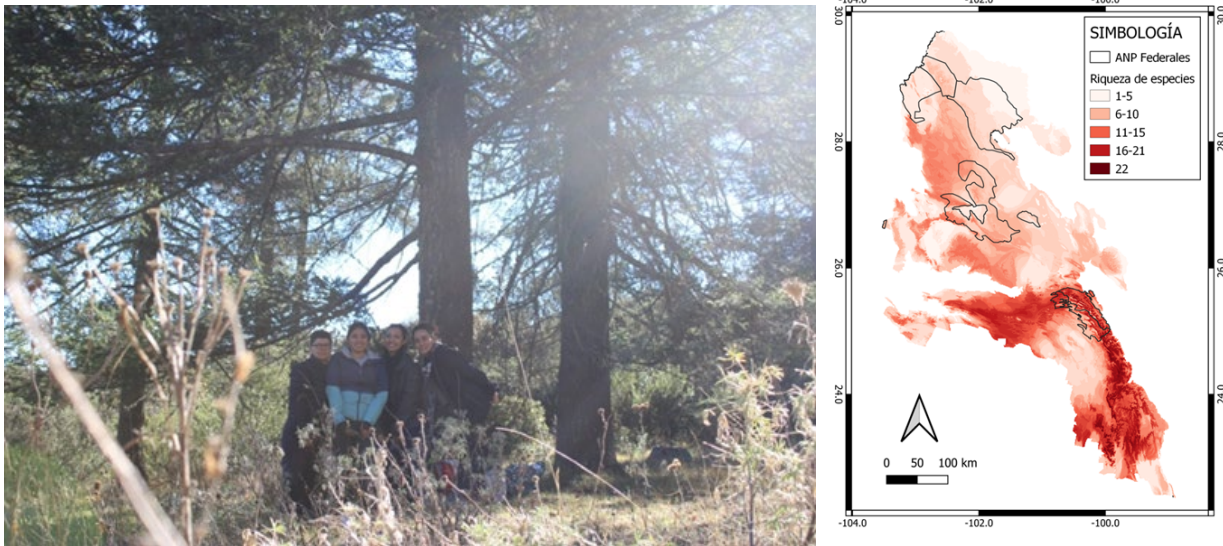

Figure 1. Project team in a sampling site "Sierra de Arteaga", January 2023. **Figure 2.** Conifer richness and Natural Protected Areas distribution.

After the conclusion of fieldwork, richness of conifer taxa was mapped along the Sierra Madre Oriental (SMO) to identify regions of high species richness, and later mapped against Natural Protected Areas (NMA) to identify gaps in protection of high priority zones. This map will be the base upon which phylogenetic diversity across the landscape will be paired up and compared against. High conifer rich areas were identified in the southern region of the SMO (Fig. 2), where the lack of NPA is an important matter of conservation concern, especially when analysed against our last project's results where we highlighted the extreme dry conditions the south of the SMO will likely face in future years.

After having extracted the DNA of all collected samples and stored in a DNA collection, two genes (*rbcL* and *trnL-trnF*) were amplified and sequenced for all species. The resulting sequences were complemented with *matK* genetic information already available in data bases and information gaps were filled by sequencing the remaining gene for those species not available and those that had unreliable distribution information. A single-gene Bayesian based phylogeny was built based on the concatenation of all gene sequences (Fig. 3).

The resulting phylogeny was used to conduct the corresponding analyses to obtain phylogenetic diversity and evolutionary distinctiveness indices. Evolutionary distinctiveness results were then paired up with global (Red List of Endangered species, IUCN) and local (NOM-059 Mexican list of protected species) risk assessments to identify conservation concerns in the form of EDGE (Evolutionary Distinct and Globally Endangered) and EDLE (Evolutionary Distinct and Locally Endangered) species shown in Table 1, where the five most evolutionary distinct species are highlighted in green, followed by the highest five rated EDGE species in orange and lastly the five highest EDLE species highlighted in yellow. Our preliminary results show the importance of the use of local risk assessments for local conservation prioritisations and management decisions, as well as the urge to fill risk assessment gaps as the total lack of them for some taxa might put species in vulnerability when identifying conservation priorities.
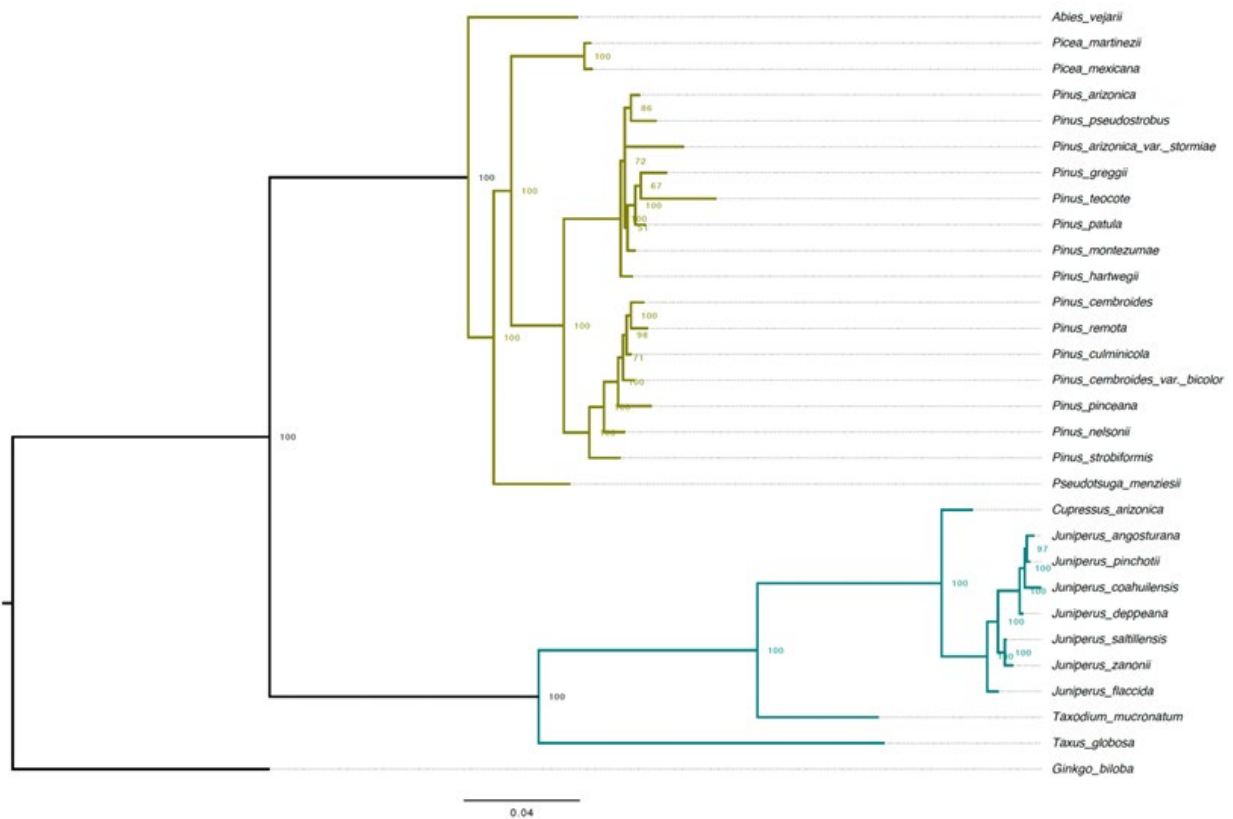

Figure 3. Bayesian phylogeny includes all conifer species in the Sierra Madre Oriental Mountain range.

Table 1. Evolutionary distinctiveness indices for conifer species within the Sierra Madre Oriental

Species	Evolutionary Distinctiveness (ED)	EDGE	EDLE
Taxus globosa	0.129510856	0.5861933	0.1287161
Taxodium mucronatum	0.059828062	0.0587998	0.0587998
Abies vejarii	0.041671493	0.0477581	0.1101413
Juniperus coahuilensis	0.036925302	0.036953	0.036953
Pinus teocote	0.036708138	0.0367436	0.0367436
Cupressus arizonica	0.036641532	0.0366793	0.0366793
Juniperus angosturana	0.034115038	0.1028607	0.0342392
Juniperus zanonii	0.032827124	0.0328271	0.0392313
Juniperus pinchotii	0.032721822	0.032891	0.032891
Juniperus flaccida	0.032013248	0.0322047	0.0322047
Juniperus deppeana	0.031800114	0.0319981	0.0319981
Pseudotsuga menziesii	0.030695025	0.0309265	0.0371648
Juniperus saltillensis	0.030337281	0.4942948	0.0305794
Pinus arizonica var. stormiae	0.028812303	0.0977198	0.0290982
Pinus pinceana	0.020326606	0.0208159	0.4845314
Picea mexicana	0.020003424	0.4842146	0.4842146
Pinus greggii	0.019629177	0.0887537	0.0201322
Picea martinezii	0.019610796	0.4838296	0.4838296
Pinus pseudostrobus	0.018272079	0.0188003	0.0188003
Pinus strobiformis	0.01773116	0.0182689	0.0182689
Pinus remota	0.016207391	0.0167706	0.0230089
Pinus nelsonii	0.015048484	0.479345	0.479345
Pinus cembroides	0.015035426	0.0156167	0.0156167
Pinus cembroides var. bicolor	0.013285045	0.0138907	0.020129
Pinus patula	0.013035714	0.0136446	0.0136446
Pinus arizonica	0.012550704	0.0131657	0.0131657
Pinus hartwegii	0.012363643	0.012981	0.012981
Pinus culminicola	0.011355133	0.4756998	0.4756998
Pinus montezumae	0.011339344	0.0119687	0.0119687

We are currently working in the construction of the phylogenetic diversity maps for conifers in the SMO and the further interpretation of results, as well as working with stakeholders to plan and strategise how we will use the results of this project to build a proposal for new natural protected areas to be considered.