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Abstracts

Tree diversity and use in agricultural and livestock landscapes in the Colombian Caribbean región

Milton Rivera Rojas[1], Sonia Camargo Roa[2], Jaime Andres Arias Rojas[1], Darwin Fabian Lombo[1], Jose Edwin Mojica[1]
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Bs-T is one of the most intervened ecosystems due to the increase of extensive livestock and agriculture. Livestock is used to occupy the territory based on integration of invasive plants, mainly grasses. Because of the lack of documentation about the uses of the tree species in Colombia, farmers, guided by organizations, have been working on sustainable livestock, promoting the incorporation of native trees into the production systems. Due to the lack of information on the uses of the native trees in the Caribbean Region, a non-probabilistic sampling was used to obtain primary information, which was focused on three consultation groups. The "Expert" group, consisting of professionals, scientists, among others, who after being surveyed, referred to the second group called "knowledgeable", consisting of technical assistants and some professionals. The last group, "producers", was named after the "knowledgeable", consisting of farmers. Moreover, tree species, their uses and used parts of the plant, were variables included in the above survey. The information was tabulated, getting the descriptive statistical analysis and recognizing diversity into the landscapes of the region; 294 tree species were reported which belong to 53 families. According to the species uses, 18 categories were reported; within construction (152), fence posts (132), firewood (110), among others. Furthermore, the main environmental values that were mentioned are; water protection (72), soil protection (85), thermal comfort on livestock (79) and fauna feeding (150). Finally, medicinal uses (143), cultural symbols (28), ornamental uses (71) and domestic uses (107) were the main uses mentioned in sociocultural perspectives.

Willows beyond wetlands: uses of *Salix* L. species for ecosystem services

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Species of *Salix* characterized by ecological resilience are predisposed for use in conservation and environmental projects in many climatic zones. The economic importance of *Salix* is increasing and emerging in a wide array of practical applications to restore ecosystems and to provide various ecosystem services. These uses include bioengineering, phytoremediation, and biomass production for fuel and lumber. Willow plantation systems offer promise for carbon sequestration, water quality improvement, soil enrichment, biodiversity conservation, and production of specialty products for crafts. Most recently, the importance of Salix to support a broad range of wildlife became important. It was reported that willow stands support a high density of breeding bird communities and willow thickets provide stopover sites for about sixty bird species, the highest number for all studied habitats. Numerous invertebrate herbivores from aphids to caterpillars feed upon willows, which support a large food-web of higher trophic level organisms. There is evidence for a rich insect fauna (up to 450 species) associated with willows. *Salix* is listed as number two on a list of host plants after oaks supporting 456 Lepidoptera species. Willows are becoming very important for sustaining fruit and berry pollinating insects as they are the earliest nectar and pollen sources for bees. They provide for a diverse pollinator group and ensure full pollination services to the surrounding plant communities – an important service considering the problem related to the bee colony collapse in North America. Current investigation generates specific knowledge about the overall insect values of various species of *Salix*.

D2a: APPLIED GENETICS FOR FOREST MANAGEMENT AND CONSERVATION

Identifying the United States tree species and populations most vulnerable to genetic degradation

Kevin Potter[1]. Maria Escanferla[2], Barbara Crane[3], Robert Jetton[4], John Hastings[5], William Hargrove[6], Gary Man[7]
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A variety of threats, most importantly insect and disease infestation and climate change, will increase the likelihood that forest tree species could experience species-level genetic degradation or population-level extirpation during the next century. Scientists and managers from throughout the U.S. Forest Service therefore developed a framework for forest tree and population conservation priority-setting assessments. This Project CAPTURE (Conservation Assessment and Prioritization of Forest Trees Under Risk of Extirpation) framework is data-driven and guided by expert opinion, and allows for the quantitative grouping of species into vulnerability classes that may require different management and conservation strategies. We have applied this framework twice to categorize and prioritize North American tree species for gene conservation, monitoring, management and restoration: once for insect and disease threats (419 tree species) and once for climate change exposure (339 species). These categorizations are based on risk factors relating to each species' (1) exposure to the threats, (2) sensitivity to the threats, and (3) capacity to adapt to the threats. We used K-means clustering to group species into classes based on these vulnerability dimensions. The most vulnerable classes encompass the species that will require immediate conservation intervention. Other groups of species will require different management approaches. We have further assessed populations within highly vulnerable species to prioritize them for *ex situ* seed collection. These assessment tools are flexible and designed for repeated application with the availability of new information. They also are valuable for determining which species and populations to target for pro-active gene conservation and management actions.

The geographic origin of old Italian cypresses in North Italy revealed by nuclear SSR markers

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The Italian cypress (*Cupressus sempervirens* L.) has an important role in the characterization of Mediterranean landscape mainly for its aesthetic and ornamental function and also because it is an excellent pioneer specie for reforestation and for timber production. Since antiquity cypress has been cultivated far beyond its natural geographic range for religious and aesthetic reason. At present its geographic distribution is characterized by disjoint populations or single plants. In this study genetic variability of 600 old cypress trees belonging to 26 populations from different part of North and Central Italy and one population from Turkey has been studied using SSR markers. Nine polymorphic SSR primers couples producing a total of 104 alleles. Turkey showed 15 private alleles. The number of observed alleles in all the populations per locus varied from 8 to 22. Values of Nei' s gene diversity and Shannon information index suggesting that populations are characterized by low genetic variability probably due to the strong anthropic pressure that this species has undergone. AMOVA revealed a very strong differentiation between Turkey and all Italian populations and a good significant differentiation among Italian groups. UPGMA dendrogram shows two main clusters, one with all the North-Estern Italian populations and the second one with Tuscanians and North-Western Italian populations. The only exception is the population from Bozen. These results suggest that the artificial transfer of cypress reproductive materials highlighting the human-mediated manipulation of cypress populations in Italy and the political and commercial barriers that were present before the first world war.

Forest genetic monitoring: preliminary results of a microsatellite-based genetic study of *Fagus orientalis* (Lipsky) from iran and *Fagus sylvatica* (L.) from Germany and Ukraine

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Natural disturbances and human activities effects diversity of forests on various levels: genetic, species and ecosystems. High genetic diversity of forest trees ensures that forests can grow, adapt and evolve under environmental change, but they may face threats when such change occurs faster than the species' adaptive and evolutionary mechanisms can handle. Therefore it is necessary to implement a forest genetic monitoring (FGM) system which could to assess a forest population's capacity to survive, reproduce, and persist under rapid environmental changes on a long-term scale. Consequently two FGM plots in Germany; one in Ukraine for European beech and one in Iran for Oriental beech were established based on Konnert et al. (2011) FGM plot design. Through an intensive selection procedure in each FGM plot we sampled 250 adult trees (DBH> 15 cm) and leaves from 200 saplings in four natural regeneration subplots (50 individuals in each). Subsequent genetic analyses were based on 16 nuclear microsatellite markers. Data regarding genetic variation and genetic differentiation among four FGM plots and among adult trees and natural regeneration within the plots will be presented. First results indicate that genetic diversity was distributed evenly from adults to natural regeneration. Genetic diversity within the Iranian Oriental beech population is slightly higher than in a Central European beech populations. Continuation of FGM in future will allow us to draw conclusions about the population's evolutionary potential through comparison to the now assessed baseline data.

Application of molecular genetics in certification of forest reproductive material: testing the origin and genetic diversity of European beech (*Fagus sylvatic*a L.) seed collected by commercial nurseries in Slovenia

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Long-term success of afforestation and reforestation, especially in changing environment, depends on the origin of forest reproductive material (FRM) and its genetic variation. Paper control of FRM origin is embedded in European legislation, while use of molecular tools for verification of FRM origin and its genetic variation are not obligatory. Nevertheless, such tools may be used to improve control over the origin and genetic quality of FRM, consequently contributing to more resilient forests in the future. European beech seed collected by commercial nurseries from seven forest seed stands (FSS) were submitted for certification to Slovenian Forestry Institute (SFI) in 2016 and 2018 in accordance with the Forest reproductive material act. Verification of origin and testing of genetic diversity of the individual tree seed samples and seed lots were based on the analysis of 16 nuclear microsatellite markers. Seed origin was verified through comparison against reference samples collected by SFI from the specified FSS. Tests revealed that two seed lots from 2016 did not originate from the specified FSS, in addition to exhibiting very low levels of genetic diversity. Consequently, they were not approved for use in Slovenian forests. Significantly lower levels of genetic diversity were associated with seed samples collected from too few seed trees, highlighting the importance of collecting FRM from a sufficient number of trees – a minimum of 25 trees, at least two adult tree heights apart from one another, as required by Decree on approval issued by SFI, to maintain the genetic diversity observed in natural stands.

Interim genetic monitoring application in the presence of incidental data: theory and application

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Species demography and genetic diversity are affected by climatic oscillations and anthropogenically induced stresses. Their potential for future rapid adaptation is questioned, given the pace of environmental change. Quantifying temporal alterations (at ≥10 year intervals for genetic markers) in genetic structure and diversity (forest genetic monitoring, FGM), brings prognosis before irreparable harm befalls. As the first evaluation will only create baseline data, true comprehensive FGM will materialize at the second assessment several years later. FGM may circumvent this problem by incorporating incidental comparative data from earlier studies or from younger cohorts at the baseline study, by examining: information capacity (IC) of the marker system (depending on locus numbers, polymorphism level, gene action mode), and direction of differences in allelic richness and evenness. This approach is applied in a Mt. Olympus FGM population of Greek hybrid fir using 11 f-nSSRs in two cohorts (250 adults, 200 juvenile plants). Comparisons between this and a previous study, and between cohorts showed: (a) present IC is high indicating a better representation of the underlying genome variation, (b) genetic diversity (nA, nE, LGP, I, HE) is significantly higher in the present study, (c) genetic diversity is higher in the mature cohort as seen in other studies, but differences in some metrics are not statistically significant. Conclusions: no indication for adverse effects; a gene conservation unit can be established; the interim FGM assessment proved a valuable tool for evaluating conservation potential in the absence of more complete temproral-scale data. This work is funded by project EC-LIFE13 ENV/SI/000148.