
 [EE] Evening Poster | M (Multidisciplinary and Interdisciplinary) | M-TT Technology & Techniques

[M-TT36]Environmental Remote Sensing

convener: Wei Yang (Chiba University), Yuji Sakuno (Institute of Engineering, Hiroshima University), Akihiko Kondoh (千葉大学環境リモートセンシング研究センター)

Mon. May 21, 2018 5:15 PM - 6:30 PM Poster Hall (International Exhibition Hall7, Makuhari Messe)

Our human beings are encountering various environmental issues on the Earth, and it is urgent to find out the solutions. Remote sensing is currently the only feasible means to observe the Earth environment at regional/continental/global scales over long periods, and consequently detects the environmental changes occurred all over the world. This session invites presentations on theory, science, technology, and applications of remote sensing to study the Earth environment from regional to global scales. Both oral and poster presentations are sincerely welcome.

[MTT36-P01]Remote sensing for high-throughput phenotyping of forest genetic trials using UAVs

*Filippo Santini¹, Shawn Carlisle Kefauver², Jordi Voltas¹ (1. Department of Crop and Forest Sciences – AGROTECNIO Center, University of Lleida, Avda. Alcalde Rovira Roure 191, E-25198 Lleida, Spain, 2. Integrative Crop Ecophysiology Group, Department of Evolutionary Biology, Ecology and Environmental Sciences, University of Barcelona, Barcelona, Spain)

Keywords: Remote sensing, Unmanned aerial vehicles, Genetic trial, Forest species, High-throughput phenotyping, *Pinus halepensis*

The analysis of genetic differentiation in key functional traits of forest species is a fundamental step to understand the adaptive structure of populations and their potential to react to environmental changes. While traditional phenotyping techniques are costly and time-consuming to implement in forest trees, and especially so in the case of adult individuals, remote sensing data derived from cameras mounted on UAVs (unmanned aerial vehicles) provide potentially valid high-throughput information for assessing morphophysiological differences among individuals. In this work we characterise, for the first time, the extent of intra-specific genetic variation in key functional traits for a widespread conifer through UAV data. Three flights (July-2016, November-2016 and May-2017) were performed in a genetic trial located in Spain which consisted of 56 populations of the circum-Mediterranean conifer *Pinus halepensis* Mill. Ortho-mosaics of RGB (red, green, blue), multispectral (visible and near infrared wavelengths) and thermal images of the trial were obtained with centimetric spatial resolution. The images were analysed to retrieve values of canopy temperature, vegetation cover and several vegetation indices at the plot level (i.e., composed by trees belonging to the same population). Differences among populations emerged consistently across flights for vegetation cover and vegetation indices related to green biomass, indicating genetic divergence in crown architecture and density. On the other hand, differences in needle pigments were found only in May-17 and were probably related to contrasting phenology of needle emergence and development among populations. This finding, coupled with the absence of genetic divergence in photosynthetic efficiency-related indices across flights, points to a negligible genetic differentiation in the photosynthetic machinery of *P. halepensis*. Differences in canopy temperature were significant in July-16 (peak summer), being indicative of variation in stomatal conductance among populations under drought stress. Volume over bark, taken as an estimation of above-ground growth, was positively correlated with green biomass and negatively correlated with canopy temperature at the population level, indicating a significant influence of canopy properties and stomatal conductance on growth in *P. halepensis*. This work is the first attempt to apply high-

throughput phenotyping techniques in forest genetics based on aerial images. Our results suggest that remote sensing data derived from UAV is a promising tool to assess genetic differentiation in phenotypic traits, potentially improving our ability to bridge genomics and phenomics in forest tree species.