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Zuerich, Oct. 17, 2013

STSM at INRA, Avignon, Sept. 29 – Oct. 12 2013Dear Dr. Fulvio Ducci,
Dear members of the STSM selection committee,

I was happy to learn, that my STSM was approved. In the first two weeks of October 2013, I was in the lab of Dr. Sylvie Oddou-Muratorio at INRA, Avignon to work on the project **“Adaptive genetic variation in European beech at ecologically marginal and central sites”**. The aim of my stay was to run first analyses to understand differentiation in European beech at ecological marginal and central sites as well as along other environmental gradients. This goal was successfully reached with the help of Sylvie and her team. I am grateful for this STSM as it contributed to the proceeding of the project and strengthened the collaborative work.

Attached are the Scientific report as well as the Host report by S. Oddou-Muratorio. Please don't hesitate to contact me if further information is needed for the approval of the reports by the scientific committee or if additional information is needed for the payment of the approved grant of EUR 1620.

Sincerely yours,



Attachments:

- Scientific report by ARP
- Host report by SOM

Adaptive genetic variation in European beech at ecologically marginal and central sites

Motivation

European beech is a dominant forest species in Europe. Its evolutionary potential in the context of climate change is of major concern, especially as it is a drought susceptible species and longer drought periods are expected. In this study, we evaluate local adaptation of European beech at contrasting environmental sites across Switzerland, including ecological marginal and central sites, to understand if microevolution based on regionally available genetic variation might contribute to the persistence of European beech.

Scientific report

Aim of the STSM

The aim of the STSM was to run an environmental association analyses in the lab of Dr. Sylvie Oddou-Muratorio. To be able to do so, I had first to clean the genotype data table. Second, the spatial genetic pattern was investigated to understand, if historical rather than environmental effects might have caused genetic patterns. Third, I calculated a number of environmental variables based on temperature, precipitation, edaphic and geographic factors, all variables which were generated by the collaborators at WSL (Project ADAPT, led by Dr. C. Heiri). Eventually, an outlier analyses was done on genotypes derived from mesic vs. dry sites as well as an environmental association analyses.

Data preparation and pre-analyses

The accuracy of the SNP genotyping done by LGC Genomics was tested based on 20 duplicated genotypes which were included as blind controls. Overall, the genotyping success was very high and only in one out of 3480 comparisons the genotypes did not match due to different allele callings. Based on the duplicated genotypes, a few more additional SNP positions could be revealed out of the raw data produced by LGC, leading to a final dataset of 174 SNPs of 54 known genes in 360 individuals with a missing rate of 1.2%. A total of 153 SNPs were polymorphic over the whole dataset. Splitting the dataset into different sampling units reduced the numbers of polymorphic markers by a maximum of three markers.

The analyses of the spatial genetic pattern of the SNP variation of the Swiss provenances indicated that no spatial pattern is available. All individuals were intermixed. Including the geographic information as a prior information into the analyses did also show no spatial aggregation of genotypes. These analyses were done with Structure (Pritchard et al. 2000) and BAPS (Corander and Marttinen 2006).

The environmental variables were partly prepared before the STSM and the data tables were finalized during the STSM. While for the first analyses the individual values of 57 climatic, edaphic and geographic measures were included in the analyses, the use of PCA to describe a local environment was discussed and first steps towards its implementation were taken.

Main analyses

The first part of the dataset includes three regions, within which a mesic and nearby ecological marginal, dry stand was sampled and genotyped. An outlier analyses was

performed using BayeScan (Foll and Gaggiotti 2008). A few SNP positions indicate to be under weak selection between dry and mesic stands. Especially one SNP reached across regions as well as within regions always the highest posterior probability, yet this probability is still below the threshold suggested by Foll and Gaggiotti (Foll and Gaggiotti 2008).

The second part of the dataset includes genotypes of 78 stands (3 individuals per stand) sampled across Switzerland. These samples were used for an environmental association study, performed in the novel software LFMM (Frichot et al. 2013). This software screens genomes for signature of local adaptation using an integrated framework based on population genetics, ecological modeling and machine learning technique. The residual population structure is included via unobserved factors. If the structure is underestimated, the false positive rate might increase. Therefore, I run the program using different numbers of unobserved factors. The different runs gave very similar results, suggesting that the rate of false positives as well as false negatives was low. Overall about 16 of 152 SNP positions indicated an association to one or several environmental variables. Several of the environmental variables were linked to more than one SNP position. While the water retention capacity of the soil was linked to several SNPs, most of the other edaphic factors had no effect.

Outlook

In the next steps, the effect of additional as well as compound environmental variables based on PCA will be investigated. Then the SNP positions under selection will be investigated to understand their function, their link to other SNP positions in the dataset as well as the general knowledge on the importance of the gene as such. Finally, a publication will be written and the results will be integrated into the WG2 of the MaP-FGR.

Added value of the STSM to the project

This study is a joint project between S. Oddou-Muratorio, G.G. Vendramin, C. Heiri and me. While most of the exchange on the project is per eMail, it was of high importance to meet in person and work in close collaboration on the first analyses. Thereby this project profited from the recent knowledge of Sylvie and her team gathered through the analyses of a similar dataset. I had the opportunity to get introduced to novel statistical approaches which deal with outlier analyses as well as environmental association analyses. We discussed on a daily bases the approaches taken and options to fine-tune the analyses by e.g. determining parameter settings. Moreover, I learned new ways on how to transform datasets, a time consuming task when working with a vast variety of programs which all have different input requirements.

During my stay, Dr. Katalin Csillery, a post-doc in the lab of Sylvie, started to analyze the dataset with additional techniques which will allow the evaluation of up-dating genotypes based on the raw output of LGC as well as a comparison of the Swiss dataset with the genetic data available on the same SNP positions on Mt Ventoux.

Furthermore, we had several discussion rounds with scientists at INRA, including François Lefèvre and Hendrick Davi, on SNP genotyping and tree physiologically important environmental variables, amongst other themes.

Finally, on the last day we had a video-conference with Beppe to discuss the results as well as the next genotyping projects.

Overall, this STSM was a high success, as the main goals were reached and analyses beyond the prior goals were performed. All of the major approaches were applied and I learned novel statistical techniques. During the lively discussions and exchanges, also on the ongoing projects of Sylvie and her team, we were able to fructify each other's work and benefited from each other's experiences and skills. Last but not least, I believe that such STSM are very important to strength not only the scientific but also the personal relationships among project partners, additional goals which were very well achieved.

Reference list

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Dr FULVIO DUCCI

COST MC Chair

Avignon, le 15th of October 2013

**Report on the hosting a short term scientific mission from Andrea Pluess, ETH Zurich,
at INRA, Avignon (30-09-2013 to 11-09-2013)**

Dear Dr. Fulvio Ducci,

Herewith I report the success of the 2 weeks scientific mission (STSM) of Dr Andrea Pluess, ETH Zurich in our group, INRA Avignon. As detailed in the scientific report of A Pluess, this mission allowed us to : 1/ analyze the new SNP data set produced by Andre Pluess in 78 natural Swiss populations, 2/ discuss these results in regards of previous results obtained in French populations on Mont Ventoux and 3/plan a future collaborative genotyping project at the European scale.

We thank the COST Action MaP-FGR for funding this mission.
With kind regards,

Sylvie Oddou-Muratorio

A handwritten signature in blue ink, appearing to read 'S. Oddou-Muratorio', with a long horizontal line extending from the bottom left.