



FA1203: Sustainable management of *Ambrosia artemisiifolia* in Europe (SMARTER)
STSM Report – Dijon 2015

SCIENTIFIC REPORT

Test of potential EST-& SSR markers on different populations of common ragweed of Armenia

25th July – 25th August by Alla Aleksanyan

STSM details COST STSM Reference Number: COST-STSM-FA1203-27152

Applicant details:

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Host details

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Purpose of the STSM

The main purpose of this STSM is at first to learn how to analyze genotyping and secondly, to utilize the lab facilities of the French group for selecting own EST-SSR-markers, in order to characterize the genetic variation in common ragweed in Armenia. This STSM also directly contribute to the scientific objectives of COST SMARTER, especially of Task Force Genetics.

The STSM will contribute to a better understanding of the population genetic structure of *Ambrosia artemisiifolia* in Europe

Description of the work carried out during the STSM and of the future collaboration

The STSM was hosted in INRA Dijon, UMR Agroecology, Dijon, France:

During the stay, I engage in two main activities.

- To test and screen a large set of candidate SSR markers, retaining only those that give good PCR amplification on DNAs extracted from *Ambrosia artemisiifolia* plants representative of the populations occurring in Armenia. The candidate SSR markers tested were those developed at INRA Dijon by Dr Valérie Le Corre and collaborators. These candidate markers are of three kinds: genomic SSRs developed from next-e 454 sequencing, genomic SSRs developed from next-generation Illumina sequencing and coding-sequence SSRs, also called EST-SSR. The latter ones were developed by the

bioinformatics analysis of EST resources available in Genbank. The first activity was carried out during the first two weeks.

- Analyzing genotyping data for European populations of *Ambrosia artemisiifolia*, and study their genetic structure. Genotyping was performed by a dedicated INRA facility. We selected 17 markers based on genotyping data already available at INRA Dijon for populations from France and other parts of Europe: polymorphic markers with reliable PCR amplification and few null alleles were chosen. Population genetics analyses included the estimation of classical parameters such as genetic diversity and genetic differentiation and the estimation of population structure using a Bayesian clustering method.

Description of the main results obtained:

In total, I have learned seven programs and five R packages to analyze microsatellite data and qualitative traits data with published and unpublished data. I have also learned main techniques for genetic analysis in laboratory, the methods of analysis of microsatellite genotyping data.

The results of these studies will be useful for SMARTER and are very important for Armenia, and will provide new opportunities for comparative collaborative research in future between Armenia and other projects and groups.

Future collaboration with the host institution:

Future collaboration will include publishing of few joint articles, continuing genetic analysis and genotyping of different populations of common ragweed from Armenia and neighboring countries. And some other joint experiments between France and Armenia.

Foreseen publications/articles resulting from the STSM

The present STSM has contributed to the development of scientific publication that is to be submitted in due time to peer-reviewed scientific journals. But for finishing current article we should continue contribution and joint research with host institution. At the same time the population genetic results about the population diversity of the Armenian-selected populations getting from STSM will be source of a first paper about genetics of common ragweed in Armenia.

Confirmation by the host institution of the successful execution of the STSM

A letter of confirmation (sent by email to Maurizio Vurro) by the host institution is attached to the present document (Appendix 1).

Acknowledgements

I am very grateful to Valérie LE CORRE and all staff of her laboratory for hosting and supporting me at the INRA Dijon for this short-term scientific mission, for the fruitful work and discussions, and for a very pleasant stay in Bourgogne.

Alla Aleksanyan
Yerevan, Armenia
22.09.2015

Dear Dr Maurizio Vurro,

I am writing to confirm, that, thanks to COST-STSM-FA1203-27152, Dr Alla Aleksanyan has been visiting our laboratory, “UMR Agroecology” at INRA Dijon, France for one month in August 2015. During her stay she worked mainly with me. Her objectives were to learn laboratory methods for analyzing the genetic diversity of *Ambrosia artemisiifolia* populations using microsatellite markers and to learn using appropriate softwares for analysing genotyping data.

During her stay, Alla Aleksanyan had the opportunity to test the PCR amplification of several microsatellite markers newly developed in our lab, on plant material she collected from several Armenian populations of *Ambrosia artemisiifolia*. Then she could learn using several softwares and R packages enabling to: extract genotype data from chromatograms, estimate standard population genetics parameters and investigate population structure using a Bayesian clustering approach. She could train on some microsatellite datasets previously obtained in my laboratory for several European populations of *Ambrosia artemisiifolia*.

At the end of the stay, we could discuss about future collaborations and considered analyzing further the genetics of *Ambrosia* populations from yet little studied areas, such as Armenia and neighbouring countries. The STSM awarded to Dr Alla Aleksanyan has allowed effectively starting a collaboration project which will allow studying the genetic diversity and colonization origin of populations of *Ambrosia artemisiifolia* from the Caucasus region, an area not studied yet.

Best regards,

Valérie Le Corre