FA1203: Sustainable management of *Ambrosia artemisiifolia* in Europe (SMARTER)

STSM Report – Dijon 2015

# Inferences from $Q_{ST}$ - $F_{ST}$ comparisons: adaptive divergence for various plant traits in ragweed populations along a biological control gradient

23rd July – 4th August, by Yan SUN

## STSM details

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## Host details

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## Purpose of the STSM

The main purpose of this STSM is to analyse microsatellite data and quantitative trait data, which were obtained from my previous postdoc project at University of California, Berkeley on “Herbivores as drivers of evolutionary change? A case study of common ragweed and potential insect biological control agents”. The postdoc project is using ragweed as a model system to study rapid evolutionary changes in response to a gradient in intensity and exposure history to specialist herbivores, i.e. biological control insects, in China, and in response to distinct abiotic and biotic differences in a new environment (Chinese populations vs. US populations). Besides learning how to handle all data properly, I also discussed with Dr. Le Corre for future collaboration with the COST SMARTER Task Force Genetics and especially with its coordinators. I will be involved in a phylogenetic study of genetic variation in ragweed from worldwide, Chinese, European, Australian and North American populations.

This STSM also directly contribute to the scientific objectives of COST SMARTER, especially of WG1. The STSM will contribute to a better understanding of the expected impact of biological control agents. Moreover, this STSM strongly benefit to my postdoc project on common ragweed at UC Berkeley, USA (Jan 2014 – June 2015), and also my planned postdoc in Germany started from next year. There will be many mutual benefits between my postdoc project and the EU COST Action SMARTER in contributing and speeding-up the achievement of developing long-term and cost-effective management options for common ragweed.

## 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:

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| Friday 24th July | meet at INRA Dijon with Dr. Le Corre, discussed the analysis tools and make a study schedule. Using the microsatellite data (10 populations with 9 markers) from Dr. Le Corre to learn: i) using 'PeakScaner' to sort out the genotype from nine markers; ii) using R with package 'MsatAllele' to visualize and bin of scored microsatellite fragment sizes, and to produce a population genetic input files; iii) using 'Micro-checker' to find the microsatellite null alleles and scoring errors, and to find out if there is any more potential alleles which were missed from 'PeakScaner' analysis. |
| Monday 27th July | continuing data analysis learning: i) using 'Structure' for multi-locus (nine markers) genotype data to investigate population structure; ii) using the '.f'results file generated by program 'Structure' in 'Structure Harvester' to assess and visualize likelihood values across multiple values of *K* and hundreds of iterations for easier detection of the number of genetic groups that best fit the data (optimal cluster number) by implementing the Evanno method; iii) using the output data reformatted by 'Structure Harvester' into a downstream program 'Clumpp' to minimize the variance across all the iterations of the selected *K* value and to result a dataset of mean individual inferred ancestry for all iterations; iv) using R to plot the output data from 'Clumpp' to visualize the structure of each populations. |
| Tuesday 28th July | continuing data analysis learning: i) using R with package 'adegenet' to run a PCA finding the principal locus and to calculate $F_{IS}$ and $H_S$; ii) using R with package 'HierFstat'to calculate $F_{ST}$; iii) using software 'Fstat' and 'genepop web' to also calculate $F_{ST}$. |
| Wednesday 29th July | continuing data analysis learning: i) Using trait data from publication (Chun et al 2011) in R with package 'lme4' – mixed effect model to calculate $Q_{ST}$; ii) using R with package 'QstFstcomp' to compare the $Q_{ST}$ and $F_{ST}$; iii) discussed with Dr. Le Corre that how to combine the mixed effects model into the $Q_{ST}$-$F_{ST}$ comparison R package 'QstFstcomp'; iv) visit the greenhouse of INRA Dijon and there ragweed projects that conduced in INRA, discussed with a PhD student of Dr. Le Corre, Lucie Meyer, for her expertise and experiences for microsatellite analysis for ragweed. |
| Thursday 30th July | continuing data analysis learning: i) $Q_{CT}$-$F_{CT}$ comparison by using R; ii) $Q_{SC}$-$F_{SC}$ comparison by using R; iii) using the data from my postdoc project to fit in $Q_{ST}$-$F_{ST}$, $Q_{CT}$-$F_{CT}$ and $Q_{SC}$-$F_{SC}$ comparison by using R. |
| Friday 31st July | mainly for locating and making up the deficiencies to fill learning gaps; and also trying to analysis my own data. |
| Monday 1st August | discussion with Dr. Le Corre for my future postdoc project "Herbivores as drivers of demographic and evolutionary change in invasive alien |

plants under present and future climate conditions” in Germany and potential collaboration: i) we also discussed with Dr. Christophe Délye for some technic details, i.e. the best way and time to sample the populations, the best way to extract DNA from samples which can be used for poor-seq, NGS, RADseq; ii) the potential project for a phylogeny study of worldwide ragweed populations, I have DNA for 10 Chinese populations and will start contacting some Chinese colleagues for seeds materials to hopefully get 20 Chinese populations; iii) test more primers with my Chinese and US populations in Dr. Le Corre’s lab to help her select better primers and also to help me get better microsatellite data.

## Description of the main results obtained:

In total, I have learned six programs and five R packages to analysis microsatellite data and qualitative traits data with published data, and at the end tried successfully with part of my own data. By the end of October, I expect to finish all my analysis.

## Foreseen publications/articles resulting from the STSM

Two publications with regard to biological control herbivores as drivers of evolutionary change of ragweed populations in the introduced range.

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

Cf. attached email from Dr. Le Corre, INRA, Dijon, France.

I greatly acknowledge the warm-hearted, most helpful and efficient support by my host researcher Dr. Le Corre and also nice discussion with Ms. Lucie Meyre and Dr. Christophe Délye. Your commitment was cru