
Adaptive genomics in a natural population of *Arabidopsis thaliana*: a resurrection study in a spatially heterogeneous environment

Léa Frachon^{*1}, Cyril Libourel¹, Romain Villoutreix², Sébastien Carrère¹, Cédric Glorieux², Carine Huard-Chauveau¹, Miguel Navascuès³, Laurène Gay⁴, Renaud Vitalis³, Etienne Baron², Laurent Amsellem², Olivier Bouchez⁵, Marie Vidal⁶, Valérie Le Corre⁷, Dominique Roby¹, Joy Bergelson⁸, and Fabrice Roux^{†1}

¹Laboratoire des interactions plantes micro-organismes (LIPMO) – CNRS : UMR2594, Institut national de la recherche agronomique (INRA) : UMR441 – Chemin de Borde-Rouge - BP 27 31326 CASTANET TOLOSAN CEDEX, France

²Génétique et évolution des populations végétales (GEPV) – CNRS : UMR8198, Université Lille I - Sciences et technologies – Batiment SN2 59655 VILLENEUVE D ASCQ CEDEX, France

³Centre de biologie et gestion des populations (CBGP) – Université Montpellier II - Sciences et techniques, Institut national de la recherche agronomique (INRA) : UMR1062 – Campus international de Baillarguet - 34398 Montpellier Cedex 5, France

⁴Amélioration Génétique et Adaptation des Plantes Méditerranéennes et Tropicales (AGAP) – Montpellier SupAgro, Institut national de la recherche agronomique (INRA) : UMR1334, CIRAD-BIOS – TA A-108/03-Avenue Agropolis, 34398 Montpellier Cedex 5, France

⁵Génotype Toulouse Midi-Pyrénées [Auzeville] (GENOTOUL) – École Nationale Vétérinaire de Toulouse - ENVT, Université Paul Sabatier (UPS) - Toulouse III, Institut National Polytechnique de Toulouse - INPT, Institut National des Sciences Appliquées [INSA] - Toulouse, Inserm, Institut national de la recherche agronomique (INRA) : UMR1388 – Chemin de Borde-Rouge Auzeville, France

⁶Unité Animalerie Rongeurs (UAR) – Institut national de la recherche agronomique (INRA) : UMR1209 – France

⁷Agroécologie – Agrosup, Institut national de la recherche agronomique (INRA) : UMR1347, Université de Bourgogne – BP 86510, F-21000 Dijon, France

⁸Department of Ecology and Evolution – United States

Abstract

Rapid phenotypic evolution in natural populations has been documented in many species and can occur on a timescale of decades or even years. In few studies, genotype-by-environment interactions for fitness have even been demonstrated to occur at a very small spatial scale within a plant population. However, to our knowledge, no study specifically tested whether the microevolution rate of a plant population was dependent on a small spatial scale of ecological variation. The identity of the natural genetic variants underlying GxE interactions at a very small spatial scale is also on open question.

*Speaker

†Corresponding author: fabrice.roux@toulouse.inra.fr

Based on 195 seed families collected over eight generations in a highly polymorphic local French population of the annual selfing species *Arabidopsis thaliana*, we combined a resurrection study with an *in situ* reciprocal transplant study. Because soil variation and variation in plant – plant interactions occurs at a small scale in this population, the 195 local families have been phenotyped in six environments corresponding to a combination of three soil types and two competition treatments with the annual bluegrass *Poa annua*. In addition, the whole genome of these 195 families has been sequenced using the NGS Illumina technology. Rapid phenotypic evolution was observed for 29 traits related to survival, phenology, resource acquisition, architecture and seed dispersal. The rates of evolutionary change were however highly dependent on the phenotyping environment. Based on a Genome-Wide Association mapping approach, I will also present some results on the identification of genetic variants associated with natural variation of fitness related traits.

Keywords: Ecological genomics, Resurrection, *Arabidopsis thaliana*, GWA mapping