

POPULATION GENOMICS AND GENE FUNCTIONAL ANALYSES REVEAL THE GENETIC BASIS OF CLIMATE ADAPTATION IN WOODLAND STRAWBERRY

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ABSTRACT

Understanding the genetic basis of climate adaptation on the warming globe is an urgent question from ecological, agricultural and forestry perspectives. In perennial plants, which live for many years and pass all four seasons as adult plants, correct timing of developmental phases including reproductive development, growth cessation and dormancy determines their ability to cope with climate. Woodland strawberry, the member of the most economically important family of perennial fruit and berry crops, the Rosaceae, is an ideal model to explore perennial climate adaptation: it has strong environmental responses, available molecular tools and wide geographical distribution in Europe. We have gathered a unique collection of over 200 woodland strawberry accessions covering the full geographical distribution of the species in Europe and sequenced their genomes. Population structure clearly separates European woodland strawberry to eastern and western groups that are growing in different climatic zones. Clear latitudinal and longitudinal clines are found in the photoperiodic and temperature regulation of flowering and vegetative development demonstrating the local adaptation of woodland strawberry populations. Fixation index analysis reveals the allelic differentiation of flowering time genes along east-west and north-south axes, and some of these genes have been targets of natural selection. Furthermore, gene ontology (GO) categories associated with the regulation of cell cycle are highly differentiated between populations from northern Norway and southern Finland, and phenotypic analyses reveal that faster developmental rate partially explains early flowering in the northern populations. To understand the genetic and molecular basis of adaptation in more detail, we are carrying out QTL mapping, gene expression analyses using RNAseq and Nanostring assays, and functional studies using CRISPR-Cas9 gene editing. Our research in crop's wild relative will speed up existing and future breeding programs in the Rosaceae and open new avenues to understand climatic adaptation in perennials. The latest results will be discussed.