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Abstract

Abiotic stresses, such as excessive salinity or nutrient deficiency, which often result in substantial yield losses, constitute significant challenges to global agriculture. These stresses are particularly detrimental in regions facing poverty, food insecurity and water scarcity. Improving the resilience of crops of high economic and nutritional value such as tomato (*Solanum lycopersicum* L.) to abiotic stresses could offer significant benefits, both economically and in terms of public health. The aim of this thesis is to identify the genetic components of abiotic stress tolerance in tomatoes and to explore the potential of genomic prediction to improve these traits.

In the first chapter, we looked at the genetic architecture of nitrogen deficiency tolerance. We used a comprehensive methodology that integrates QTL mapping with multiparental population, genome-wide association study (GWAS) using a diversity panel, and RNA-seq to identify candidate genes related to nitrogen metabolism. The next two chapters are devoted to the study of salt stress tolerance. We first studied several traits associated with sodium accumulation in various plant organs and developmental stages in a GWAS panel, which enabled us to identify QTLs and a key candidate gene involved in sodium transport within the plant. In addition, we have also studied the impact of salt stress on the root metabolome, characterising metabolites differentially regulated by salt stress and identifying biomarkers of salinity tolerance. QTLs and candidate genes linked to these target metabolites have been identified. In the following two chapters, we engaged GWAS and genomic prediction in multi-environmental analyses using a diversity panel grown under a range of environmental conditions. We have identified interaction QTLs - whose allelic effects vary according to environmental conditions - and compared different GWAS methodologies. Then we have evaluated the effectiveness of various genomic prediction models for improving tolerance to abiotic stress.

Our results revealed several candidate genes that require further experimental validation to elucidate their functional roles and potential applicability in breeding programmes. Preliminary results from genomic prediction models highlight the interest of using these approaches to predict tolerance to abiotic stresses, although further validation in breeding populations is required.

Keywords: Tomato, Genome-Wide Association Studies (GWAS), Genomic Prediction, Abiotic Stress, Salt Stress, Nitrogen Deficiency

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