Tomato - a model plant to study molecular resistance mechanisms to pathogens

M. D. Campos¹, M.R. Félix², M. Patanita¹, P. Materatski¹, C. Varanda¹

¹MED – Mediterranean Institute for Agriculture, Environment and Development, Instituto de Investigação e Formação Avançada, Universidade de Évora, Pólo da Mitra, Ap. 94, 7006-554 Évora, Portugal

²MED – Mediterranean Institute for Agriculture, Environment and Development & Departamento de Fitotecnia, Escola de Ciências e Tecnologia, Universidade de Évora, Pólo da Mitra, Ap. 94, 7006-554 Évora, Portugal

Email: mdcc@uevora.pt

Tomato (Solanum lycopersicum) is one of the most economically important vegetable throughout the world. It is one of the best studied cultivated dicotyledonous plants, often used as model system for plant research into classical genetics, cytogenetics, molecular genetics and molecular biology. Tomato cultivation has been limited by an abundance of infectious diseases, that reduce yield and affect product quality, causing symptoms including wilts, leaf spots/blights, fruit spots and rots. The diseases are mainly caused by fungi, but also by oomycetes, bacteria, viruses, viroids and nematodes. So, it is crucial to establish effective and integrated control methods (i.e. cultural practices, disease resistant varieties, use of chemicals), and understand tomato-pathogen interactions. This diversity of pathogens that affect tomato, emphasizes the importance of the tomato-pathosystem as a favourable model for studying plant-pathogen interactions, contrarily to other 'traditional' model plants as Arabidopsis. The responses of plants to biotic stresses are very complex as the multitude of interactions involves two living organisms, the plant and the pathogen. The use of the tomato as model plantpathogen system helps to accelerate the discovery and understanding of the molecular mechanisms underlying disease resistance. The identification of key functional genes in susceptible responses and the understanding of molecular basis of compatible interactions are possible with techniques that allow the study of differential gene expression in tomato plants affected by different pathogens. Although various resistance genes have been functionally identified in the resistance system, little is known about the complex molecular mechanisms involved in defense responses. Next-generation sequencing (NGS) technologies, which produce massive quantities of sequencing data, have greatly accelerated research in biological sciences and offer great opportunities to better understand the molecular networks of plant-pathogen interactions. Here we discuss on the use of functional genomics as a mean to study tomato plant immunity, with a special focus on emerging techniques that are allowing to acquire a deeper knowledge in view of plant breeding. The identification of plant regulatory components involved in protection against pathogens can therefore be of major importance for a sustainable plantdisease management, namely relying on the plant innate immune mechanisms.

This work is funded by the project "Development of a new virus-based vector to control TSWV in tomato plants" with the references ALT20-03-0145-FEDER-028266 and PTDC/ASP-PLA/28266/2017, and the project "Control of olive anthracnose through gene silencing and gene expression using a plant virus vector" with the references ALT20-03-0145-FEDER-028263 and PTDC/ASP-PLA/28263/2017, both projects co-financed by the European Union through the European Regional Development Fund, under the ALENTEJO 2020 (Regional Operational Program of the Alentejo), ALGARVE 2020 (Regional Operational Program of the Algarve) and through the Foundation for Science and Technology (FCT), in its national component. It is also funded by Portuguese National Funds through FCT under the PhD Scholarship SFRH/BD/145321/2019 attributed to M. Patanita and under the project UIDB/05183/2020.