Ethylene signaling, stress tolerence and fruit maturation

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The plant hormone Ethylene is involved in many plant developmental processes, as well as in biotic or abiotic stress responses (Fig.1). Ethylene is a key player in controlling the ripening of climacteric fruits such as tomato whose ripening is characterized by an increase in respiration and the induction of autocatalytic ethylene production. Most of the ripening traits like colour change, aroma biosynthesis and enhanced softening are regulated by ethylene (Liu et al., 2015). From the applied side, ethylene regulates fruit sensory attributes and hence, the control of the ethylene responses constitutes an important economical and agronomical challenge. Components of ethylene signaling are now well deciphered, and the diversity and complexity of plant responses to the hormone contrast with the linear ethylene transduction pathway that seems to operate in all plant tissues and organs. Ethylene Response Factors (ERF) are encoded by a large multigene family and, being the last known actors of the ethylene transduction pathway, they are good candidate to explain the diversity of ethylene responses (Pirrello et al., 2012). Indeed, they have been shown to mediate processes as diverse as biotic and abiotic stresses as well as seed germination and fruit ripening. By focusing on the ERF family of transcription factors, the GBF lab aims to gain more insight on the genetic and molecular mechanisms underlying ethylene action during fleshy fruit ripening.

Figure 1: *Ethylene is involved biotic or abiotic stress but also in developmental process*

Using TomExpress (http://gbf.toulouse.inra.fr/tomexpress), the new bioinformatics platform developed by the GBF group, we performed a comprehensive mining of the expression patterns of all members of the ERF gene family in wild type and tomato ripening mutants (*rin, nor, nr*), thus leading to the identification of ripening-associated ERFs. This finding point out to the prominent role of a subset of selected ERFs as putative mediators of ethylene-dependent ripening (Liu et al., 2016).

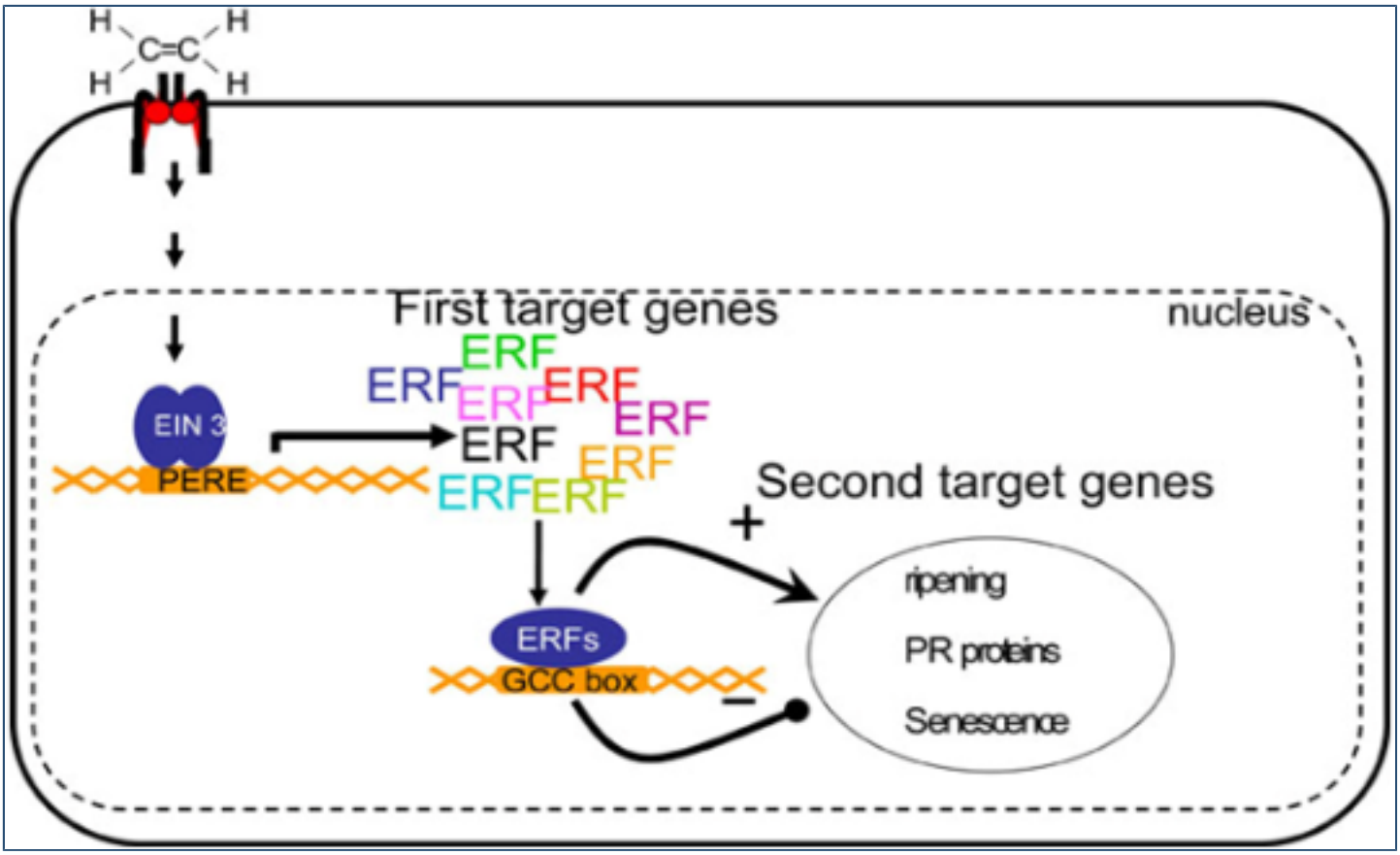

Figure 2: *ERFs are the last actors of ethylene transduction pathway. ERFs diversity (more than 60 on Arabidopsis plant model) may explain the diversity of response to ethylene.*

The outcome of our studies highlights the complex network of interconnections involving ERF genes and the master regulators such as RIN, NR and NOR during fruit maturation and ripening (Liu et al., 2014, 2016). Overall, the studies shed new light on the role of specific members of the ERF family. For instance, reverse genetics approaches uncovered the role of Sl-ERF.B3 in the transcriptional network controlling the ripening process and provides a means to uncouple some of the main ripening-associated processes (Liu et al., 2016). Since ERF is a huge family with diverse and likely redundant functions, different strategies are implemented to seek for their physiological significance including over-expression, CRISPR/Cas-9 and CRES-T. Because an increasing number of data supports the importance of the posttranslational regulation of ERFs, our group is currently developing new resources and tools to investigate the role of these ethylene mediators at the protein level. The identification

of direct target genes of the ripening-associated ERFs is becoming a major challenge towards deciphering the gene regulatory networks involved in the control of the ripening process and therefore providing new clues for improving fruit quality traits.

Publications related to the topic.

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