The Tomato-Potyvirus system, a comparative system for natural and induced resistances associated with the initiation factors 4E

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Tomato (*Solanum lycopersicum*) is one of the most cultivated vegetable in the world, but suffers from important yield losses caused by viral diseases. Therefore, the development and use of cultivars that are genetically resistant to viruses has become a critical factor of competitiveness for both breeders and producers and one of the key stakes for sustainable agriculture. In this context, generating new resistance alleles using biotechnological approaches (e.g., TILLING) appears as a powerful tool to diversify host targets to promote resistance against viruses.

Most characterized recessive resistances to potyviruses so far are natural variant of the translational initiation factor eIF4E. Those variants often encode functional eIF4E proteins but have lost the ability to interact with the viral protein VPg. In tomato, a broad-spectrum resistance to Potyvirus is associated with the natural resistance allele *pot1 - eIF4E1* from *Solanum habrochaites* PI247087. More recently null *eIF4E* alleles were obtained by TILLING but strikingly, the resistance spectrum associated with the null *eif4e1* allele is considerably narrower than the one associated with the natural resistance allele *pot1-eIF4E1*. Understanding the apparent discrepancies between those two resistances -natural and induced- could be important to help developing more efficient TILLING-based resistances to pathogens.

Therefore, we are investigating the differences between the lines harbouring those two alleles, as well as the implication of the others tomato *eIF4E* genes – *eIF4E2* or *eIFiso4E*. As a first step, genetic effects are investigated by swapping the genetic backgrounds between the natural and induced *eIF4E1* resistance alleles but also by combining KO mutations affecting several *eIF4E* genes to see whether this will impact on the plant resistance spectrum to potyviruses. Secondly, the type of mutation affecting *eIF4E1* (AA changes vs KO mutant) is also investigated and especially the incidence that a null mutation may have on the protein level accumulation of the other *eIF4E*.

Besides its applications on crop breeding, these experiments could shed new light on the Tomato/potyvirus pathosystem and redundancy among *eIF4E* genes.

Keywords: *S.lycopersicum, S.habrochaites*, eIF4E, potyvirus, TILLING