Ad hoc support : Pathogen Proteins

Cloning of Phytophthora capsici effector genes to guide the development of resistant pepper varieties.

ABSTRACT

As part of the project EffeCaps, we generated 8 transcriptomes from plant tissues from two pepper genotypes that differ in their level of resistance to Phytophthora capsici, infected each with 2 isolates of P. capsici which differ in their level of aggressiveness, and at 2 times after inoculation (24 and 72 hpi). These 8 observed conditions (2 host genotypes x 2 P. capsici isolates x 2 times) were independently repeated 3 times, bringing to 24 the number of biological samples sequenced. The construction of libraries and the HiSeq 2 sequencing were performed on transcriptomics platform of URGV INRA of Evry. The sequence data were acquired in September 213. The sequencing of the 24 biological samples delivered 46 billion sequences. The first bio-analysis showed the exceptional quality of the acquired data set. It has been shown that the samples sequenced contained many more sequences from the host than from the pathogene. This data sets were compared to a library of known P. capsici effectors to identify those that were expressed in our samples. Our data revealed that 641 known P. capsici genes encoding RXLR effectors were expressed. Similarly, we identified effectors that are expressed differentially between pepper genotypes, or between isolates of P. capsici, or else, between sampling times after inoculation.

Keywords : Developing the plant of the future, Gene expression, Protein/proteomic

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PERSPECTIVES

Our sequence data set will be further studied to identify if it contains other expressed effectors, whatever the RXLR or other types, compared to those already known in the library of P. capsici effectors. The differential analysis between the different samples will be pursued to determine the effector genes significantly expressed at early step after inoculation and especially in the resistant pepper genotype whatever the tested isolate. We will further analyze the diversity of these target effector genes within the collection of P. capsici isolates maintained at INRA UR GAFL, to identify those who are under strong selective pressure. The latter will then be cloned and used to screen the pepper germplasm collection maintained at UR INRA GAFL, to identify accessions showing a hypersensitive response (HR) to the expression in planta of target effectors. The identified pepper accessions potentially bring sustainable resistance to P. capsici ; the genetic determinism of resistance will then be studied.