Contribution to phenomics for quantitative disease resistance in a germplasm collection of capsicum spp.: a multivariate analysis by self-organizing map

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Large-scale phenotyping of genetic resources for agronomic traits is useful to structure collections, identify valuable progenitors, and define core-collections for association studies. Plant diseases are one of the main threats for crop production, and resistant genitors are constantly needed for breeding. Many traits such as partial resistance to *Phytophthora capsici* in pepper (*Capsicum* spp.) exhibit a continuous range of responses evolving over time, and large collections are difficult to reliably assess for quantitative traits. To phenotype a pepper collection of 1186 lines for *P. capsici* resistance, we measured 6 variables along a 21 day-time-course post inoculation. By a Self-Organizing Map multivariate analysis, an undemanding clustering method that locates lines and weights variables on a precise map, we defined 10 clusters of distinct resistance levels. The most resistant one gathers 7.5% of the collection, including 6 well-known genitors, confirming the relative rarity of resistance. Other clusters highlight distinction between early and late resistances. Resistant lines originate mostly from *C. annuum*, and a majority of *C. pubescens* lines were resistant. Our results reveal that resistance phenotype is highly frequent in Asia, a secondary centre of diversification of pepper. We are now constructing a trait-specific core-collection and achieving an association study by sequencing strategic positions on a locus of interest to detect candidate SNPs.