STUDY OF THE GENOMIC DIVERSITY OF VERTICILLIUM SP. CAPABLE OF COLONIZING SUNFLOWER. HOW KNOWLEDGE OF PATHOGEN GENETIC STRUCTURE CAN BE COMBINED WITH CLASSICAL BREEDING APPROACHES TO GUIDE IT

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ABSTRACT

Plant disease management approaches are mainly represented by resistance genes and agrochemicals that are used repeatedly until their efficacy is overcome by the targeted pathogen. Despite no sexual cycle observed, comparative genomics show extensive chromosomal rearrangements and lineage-specific genomic regions that increase *V. dahliae* evolutionary potential. Yet, the complex relationship between spatial pattern of disease, plant genetics, crop practices and the evolutionary dynamics of *Verticillium* population remains poorly studied. The objective of this study was to investigate how uniform is the genetic make-up of the pathogen presents within a field. A spatial analysis was performed on a field with sunflower disease history to generate regions of high or low disease prevalence. Two sunflower genotypes were sampled 45 times in predefined areas according to the disease prevalence map previously established: i) a Symptomatic (S) and ii) an Asymptomatic (AS). Qualitative PCR were carried out to: i) point out the presence of *Verticillium* in stems (VdFE1/VdFE2 primers pair), and ii) to determine the defoliating and race profiles of the strains studied (Ave1F/Ave1R and D_NDf/D_NDr primers pairs used as markers for increased virulence and defined on tomato and cotton). Results showed i) a full colonization of S genotype by *Verticillium dahliae* and 75% of AS genotype colonized by undetermined *Verticillium* sp.; and ii) the exclusive presence of *Verticillium dahliae* strains that do not carry Ave1 gene. Deeper investigation of genomic diversity of *Verticillium dahliae* will be presented to better determine *V. dahliae* strains profile capable of colonizing sunflower.

Key Words : Verticillium, host-pathogen interaction, agrosystem, disease prevalence, cultivar specificity