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Development of a high-throughput computational pipeline to identify new chemical management strategies for sugar beet pathogens.

Fungal and viral diseases cause significant economic losses to U.S. sugar beet farmers. Despite extensive efforts to breed more resilient sugar beet varieties, pathogens like *Cercospora beticola*, *Rhizoctonia solani*, *Fusarium oxysporum*, and beet curly top virus remain problematic, owing in part to evolutionary shifts in virulent populations as a response to the selective pressures imposed by different agronomic practices (e.g., application of fungicides). The persistence of these harmful agents underscores the need for new management strategies. Here we describe a computational pipeline that leverages advances in machine learning, protein structure modeling, and high-throughput drug discovery to identify compounds that can reduce fungal and viral infections in a field setting. This framework implements small molecule docking protocols to screen diverse chemical libraries *in silico*, specifically targeting the molecular interactions and functional activities that contribute to pathogenesis and disease progression. Our approach is highly adaptable to different biological contexts and complementary to existing defense mechanisms within a host plant. By this methodology, we found several compounds that may function as putative inhibitors of secreted *Cercospora* effector proteins. Experiments to validate the specificity of these chemicals and characterize their effectiveness in combatting Cercospora leaf spot disease are ongoing.