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Unraveling Dissemination Trajectories of Insect Vectors : Towards Enhanced Prophylaxis in Plant Health

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Introduction and Objectives
Given the tremendous crop losses caused every year by vector-borne pathogens, it is crucial to better understand epidemic processes. This study aims to contribute to this knowledge base by identifying likely dissemination trajectories of insect vectors of plant pathogens. The overarching goal is to inform the development of new surveillance and prophylactic strategies, aligning with the global imperative to reduce pesticide usage.

Materials and Methods
Two types of vectors are studied: psyllids and aphids. The approach consists in investigating probable vector flight trajectories, considering the relative importance of short and long-distance dispersal, local and distant climate, air mass movements, and historical vector abundance data. Initial analyses focus on exploring the statistical relationship between vector population dynamics and local climate using R and/or assessing air mass trajectories and connectivities with the Tropolink tool, leveraging historical vector abundance. This leads to the formulation of probable vector arrival patterns in fields, encompassing their origin, trajectory, and timing. Targeted sampling follows, allowing scenario validation through complementary analyses (e.g., population genetic and dynamics).

Results
Here we will focus on one of our models, the pathosystem psyllids-phytoplasma-apricot tree. Expected outcomes include the precise determination of the spatio-temporal scale of vectors dissemination, unveiling their origins, trajectories, and arrival timings in the fields. Factors influencing these parameters as well as their recurrence or fluctuation over time will also be determined. Results for the aphids models will also be presented and methodology compared with the psyllids model.

Discussion and Conclusion
The main prospects for this work is informing the development of new prophylactic methods in plant health. Moreover, the diversity of models studied lays the groundwork for broader generalizations of the approach, fostering discussion on the genericity of the approach and possible adaptation to other biological models of huge interest to farm animal or human health (e.g., mosquitoes, culicoids).