

Multiple infections and the evolution of the rice yellow mottle virus (RYMV)

The impact of multiple infections on the evolutionary trajectories of pathogen populations and their consequences for epidemiological outcome



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Introduction

Pathogens actually share host plants with a myriad of other microbes, some of them being pathogenic. Multiple infections, or 'co-infection', occur when a single host plant is infected by various pathogen species, or genotypes. This is known to affect symptom expression and/or pathogen multiplication in various pathosystems. However, the population-scale consequences, in terms of epidemiology and evolution, remain poorly explored in spite of their importance for the control of crop diseases (1).



Brader et al (2017) Annu Rev Phytopath

Background

West Africa has experienced a large surge in rice consumption over the last decades. To face this growing demand, areas cultivated with rice have been increasing drastically and rice cultivation is intensifying. New epidemic risks are associated with these agricultural changes.

Major rice diseases in West Africa include the rice yellow mottle disease, due to the virus RYMV, and Bacterial Leaf Streak (BLS), due to Xanthomonas oryzae pv oryzicola (Xoc). These two diseases co-exist in western Burkina Faso, with on average 14.5% of studied fields presenting the two types of symptoms (co-occurrence in 25x25m fields; 2). In a peculiar disease hotspot the frequency of co-occurrence can reach more than 70%, and RYMV-*Xoc* co-infection represents up to 37.5% of rice plants (3).

Experimentally, RYMV-Xoc co-infection leads to lower viral loads but stronger bacterial symptoms, compared to the mono-infection condition (3).

Both the virus and the bacteria present high levels of genetic diversity in southwestern Burkina Faso : at least 28 MultiLocus Genotypes (MLG) of *Xoc* found at the regional scale; four different genetic groups of RYMV evidenced in a single irrigated perimeter (4).

Sampling sites



10 fields x 2 sites x 2 years Sites and fields chosen for the local high virus and bacteria co-occurrence Stratified random sampling in 16 auadrats per field

RYMV-Xo co-infection levels











Fields sampled only in 2022

Objectives

1) Evaluate the outcome of **RYMV-RYMV** mixed infections in experimental settings

Greenhouse experiments were performed in 2023, the molecular analyses biology will be completed at the beginning of the training



→ A total of 86 samples, not detected as co-infected when observing symptoms, had both pathogens (RYMV and Xo) in molecular detection

RVMV symptoms	BOLD KTIVIV and	BIS symptoms	No symptom
KINIV Symptoms	BLS symptoms	DES Symptoms	No symptom
(<i>N</i> = 907)	(<i>N</i> = 37)	(<i>N</i> = 424)	(<i>N</i> = 325)

RYMV genetic and pathogenic diversity



2) Setting up experimental evolution to evaluate the impact of multiple infection on evolutionary outcome

In greenhouses, the trainee will set up an experiment to evaluate the hypothesis of an impact of multiple infection on RYMV evolution





Oxford Nanopore Technology (ONT) sequencing will be used to deep sequence obtained RYMV genomes

Related Literature

1. Tollenaere C et al. 2016. Evolutionary and Epidemiological Implications of Multiple Infection Plants. in Trends Plant Science, doi:10.1016/j.tplants.2015.10.014

2. Barro M. et al. 2021. Spatiotemporal Survey of Multiple Rice Diseases in Irrigated Areas Compared to Rainfed Lowlands in the Western Burkina Faso. *Plant Disease*, doi:10.1094/PDIS-03-21-0579-RE

3. Tollenaere C et al. 2017. Virus-Bacteria Rice Co-Infection in Africa: Field Estimation, Reciprocal Effects, Molecular Mechanisms, and Evolutionary Implications. Frontiers in Plant Science, doi:10.3389/fpls7.00645

4. Billard et al. Dynamics of the rice yellow mottle disease in western Burkina Faso: epidemic monitoring, spatio-temporal variation of viral diversity and pathogenicity in a disease hotspot. *bioRxiv*, doi: 10.1101/2023.03.27.534376

Dynamics of RYMV genetic diversity in a 5 years survey



Estimation of viral load in mono-infection by different RYMV isolates

