



Epidemiological interactions between strains of the plum pox virus

Combining a mathematical model with field data

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Multiple viral infections in plants

- Diversity of plant pathogens
- Several viruses or strains infecting a single host

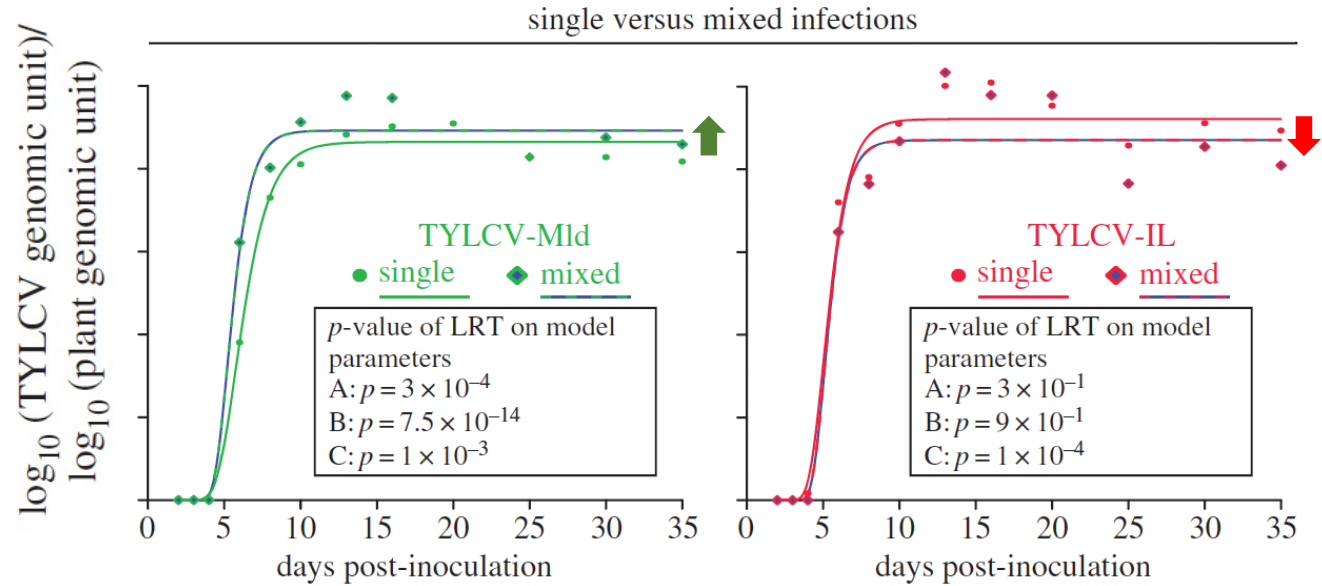
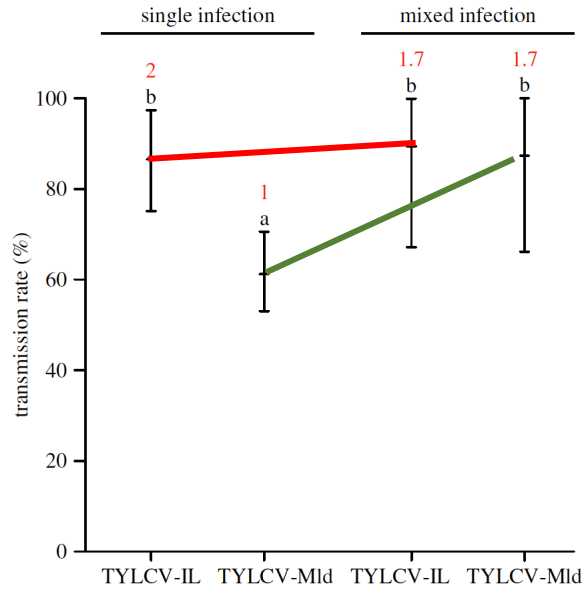
Host species ¹	N ²	Multiple infections ³																											
		Single infections					AMV+										BMV+				CMV+								
		AMV	BWYV	CMV	TSWV	WMV	B	C	T	W	B+C	B+T	C+T	T+W	B+C+T	B+T+W	C	T	C+T	C+T+W	B+T	B+W							
<i>Amaranthus</i> spp.	87	1	5	31	3	4	1																						
<i>C. bursa-pastoris</i> (L.) Medicus	5	0	0	0	1	0	No multiple infection																						
<i>Chenopodium album</i> L.	69	4	0	3	1	1																					1		
<i>Cirsium arvense</i> (L.) Scop.	42	8	8	20	1	3					4					1													
<i>Convolvulus arvensis</i> L.	113	10	6	7	0	0	5																						
<i>Conyza</i> sp.	121	5	10	7	5	1	1 1 1							1															
<i>Datura stramonium</i> L.	26	4	2	2	0	3	2		1																				
<i>Diplotaxis eruroides</i> (L.) DC.	164	15	11	44	11	2	1 2						1	3		1		2											
<i>Lactuca serriola</i> L.	66	1	1	13	1	1																		1					
<i>Lamium amplexicaule</i> L.	35	2	2	5	2	0					1					1													
<i>Malva sylvestris</i> L.	4	0	0	1	0	0																							
<i>Medicago sativa</i> L.	90	38	4	9	5	5	2 3		1							1													
<i>Papaver rhoeas</i> L.	61	1	0	0	3	0																							
<i>Plantago</i> sp.	61	7	6	7	4	0					1					3					1								
<i>Portulaca oleracea</i> L.	7	0	0	5	0	0																							
<i>Silybum marianum</i> (L.) Gaertner	29	1	2	1	1	0																							
<i>Solanum nigrum</i> L.	24	0	0	4	0	0																							
<i>Sonchus oleraceus</i> L.	51	3	1	4	3	2					1					1													
<i>Taraxacum</i> sp.	15	0	0	10	0	0																							
<i>Trifolium pratense</i> L.	37	1	0	2	1	1																				1			
<i>Xanthium strumarium</i> Moretti.	8	1	0	1	1	1																				1			

Malpica et al. 2006 Plos One
5 viruses tested in 21 weed species
16/21 species with multiple infections

Multiple viral infections in plants

- Diversity of plant pathogens
- Several viruses or strains infecting a single host
- Interactions between viruses
 - Often characterized in the lab
 - Epidemiological consequences ?

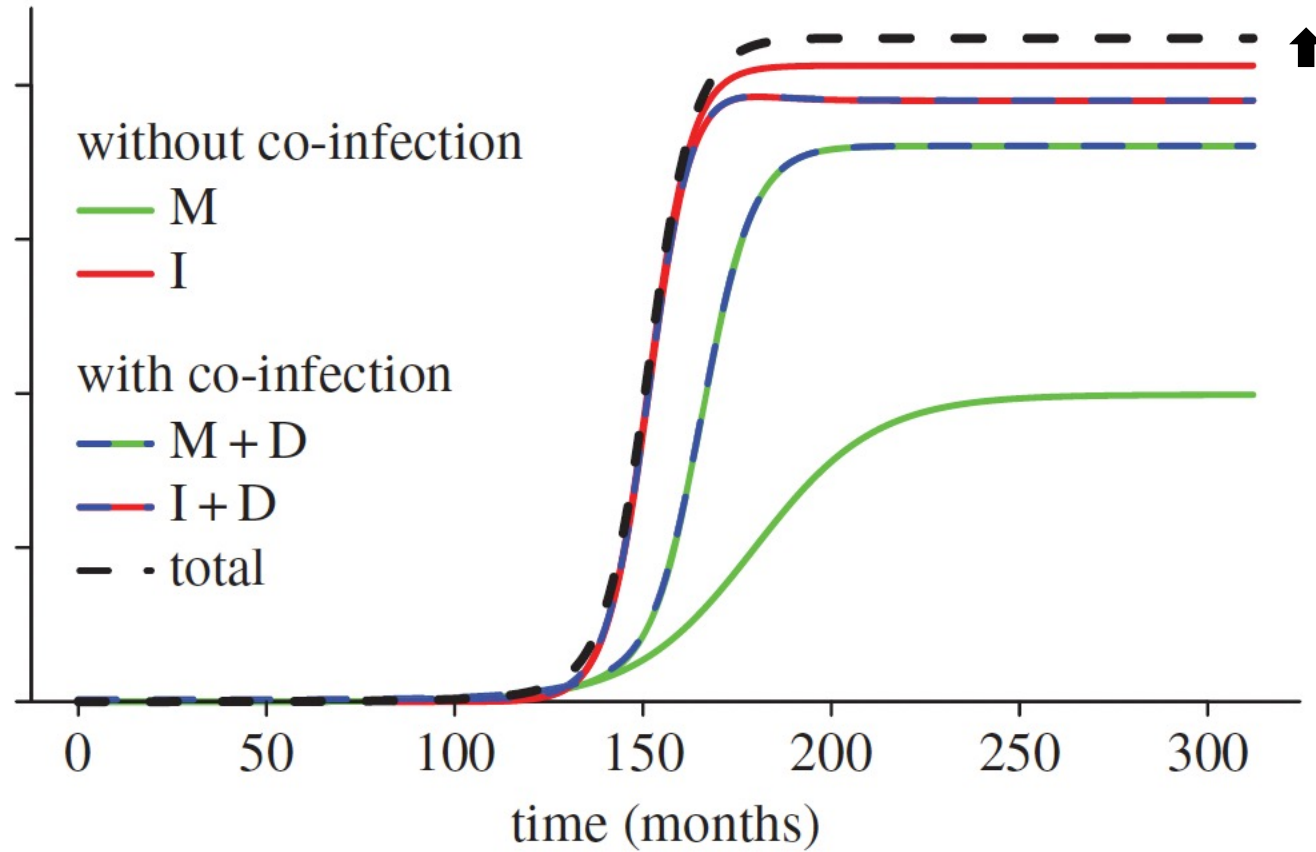
TYLCV-Mld was introduced before TYLCV-IL in La Réunion.



TYLCV-IL transmits better than TYLCV-Mld but TYLCV-Mld beneficiates from co-infection

TYLCV-IL accumulates better in single infection than TYLCV-Mld but not in mixed infection

Epidemiological consequences of the interactions between both TYLCV strains ?



- Both strains co-exist at equilibrium
- Larger disease prevalence when both strains co-exist

Insights from combining data and epidemiological model

Detecting virus interactions from field data

- Screening of pathogen occurrence in the field
- Statistical independence between infection events
(Vaumourin et al. 2014 Front. Cell. Infect.)

$$p(A \cap B) = p(A)p(B)$$

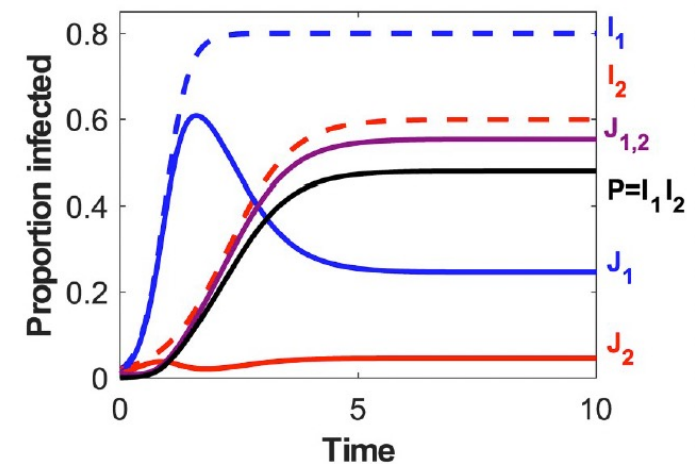
- Using epidemiological model
(Hamelin et al. 2019 Plos Biol.)

- **H0**

- **Chronic infection**
- **No virus-induced mortality**
- **System at the endemic equilibrium**
- **No interaction between pathogens**

- Statistical independence is not met under H0

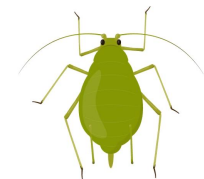
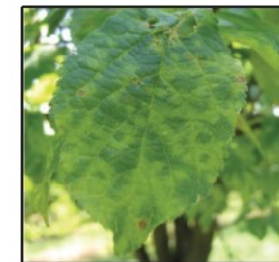
$$p(A \cap B|H0) > p(A)p(B)$$



Multiple PPV infection

- Perennial plants
 - Hard to use in experiments
 - Common multiple virus infections
- Sharka disease on *Prunus* trees
- Mainly three plum pox virus strains in Europe
 - PPV-M
 - PPV-D
 - PPV-Rec

Rimbaud et al. 2015
Annu. Rev. Phytopathol.



Question

- What are the epidemiological consequences of interactions between PPV strains in multiple infections ?
- How do interactions between PPV strains change over a tree lifespan ?

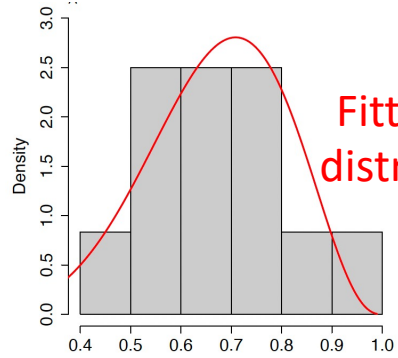
A survey of multiple PPV infections in Serbia

- No sharka management in Serbia : endemic equilibrium
- Plum trees
- Estimation of the fraction of infected trees in each visited orchard (N = 91)
- Leave sampling of three infected trees per orchards
- PPV strains identified in the lab

All multiple infections were found in the collected samples

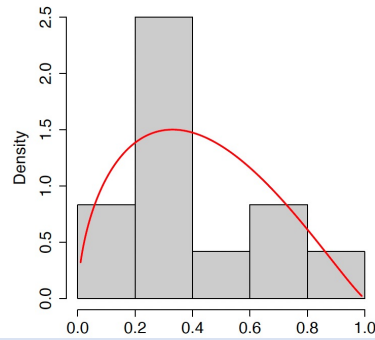
A multi-strain epidemiological model

- Density probability of parameters
- Epidemiological model with age structure



Fitted Beta distributions

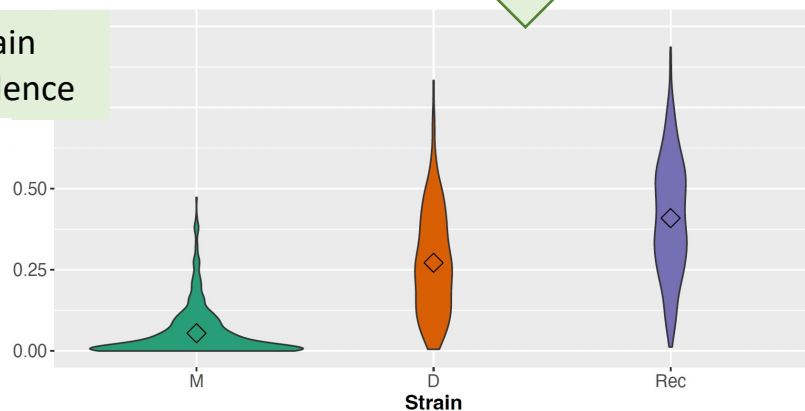
Frequency of infected trees



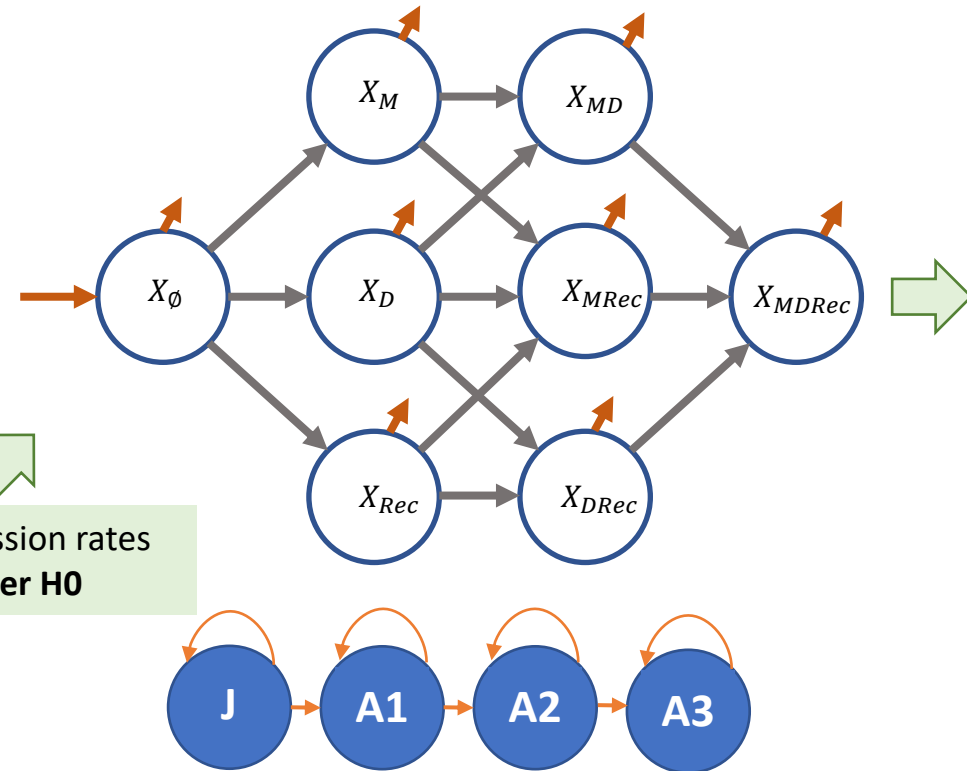
Frequency of infection type in the samples



Strain prevalence



Transmission rates under H0



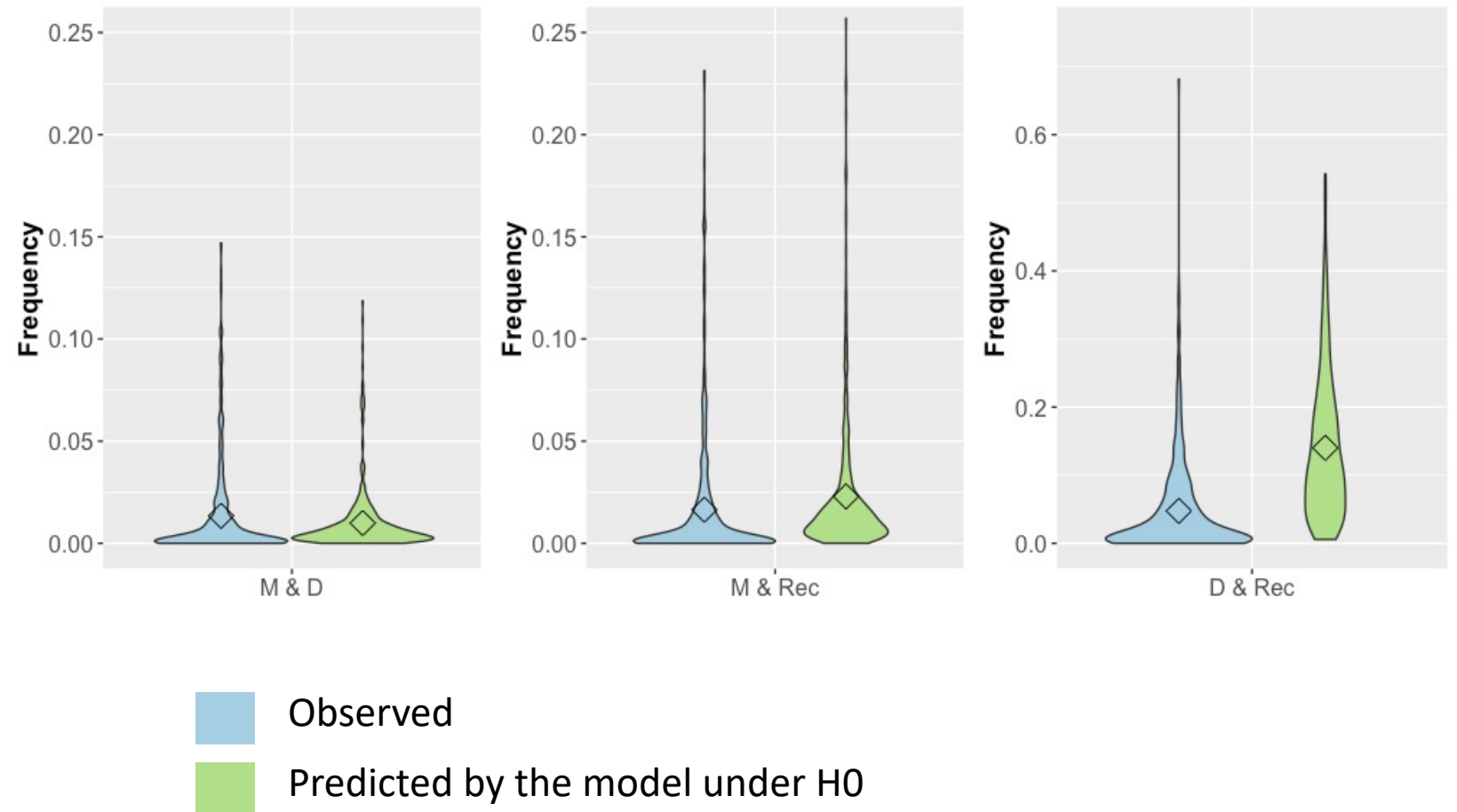
Expected distribution of multiple-infection frequencies under H0

Results

- Overall

Less co-infections involving PPV-Rec than expected under H0

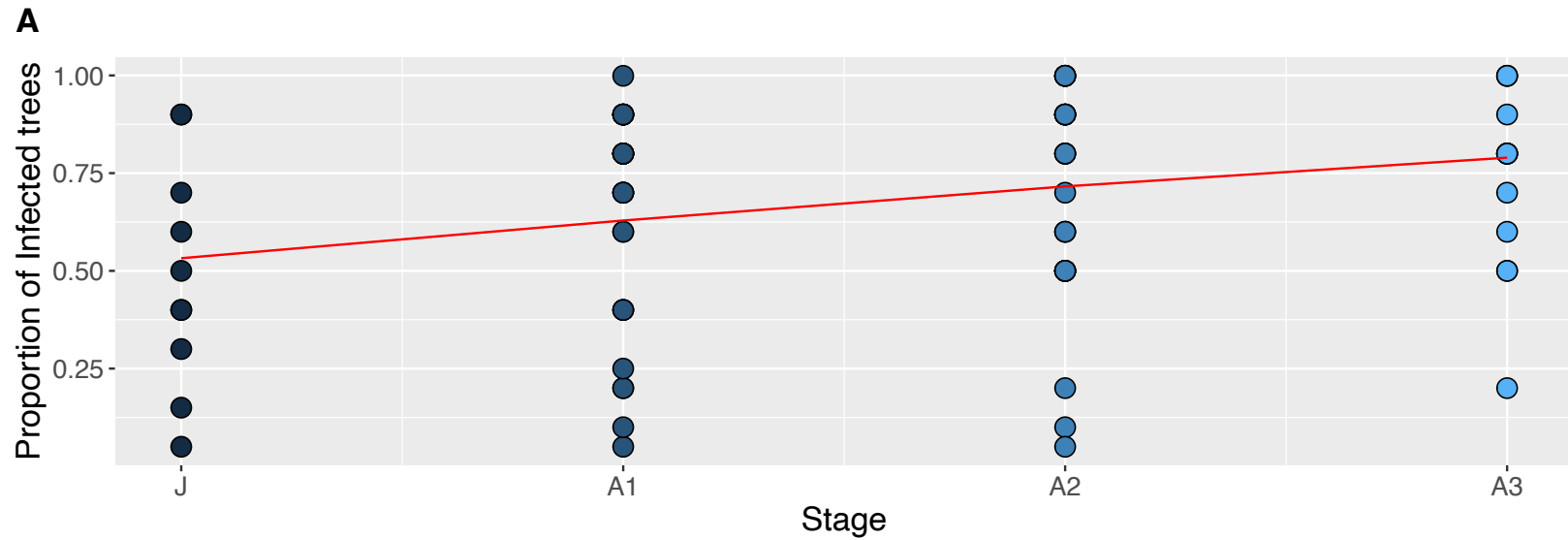
Probability distribution of the frequencies of co-infections



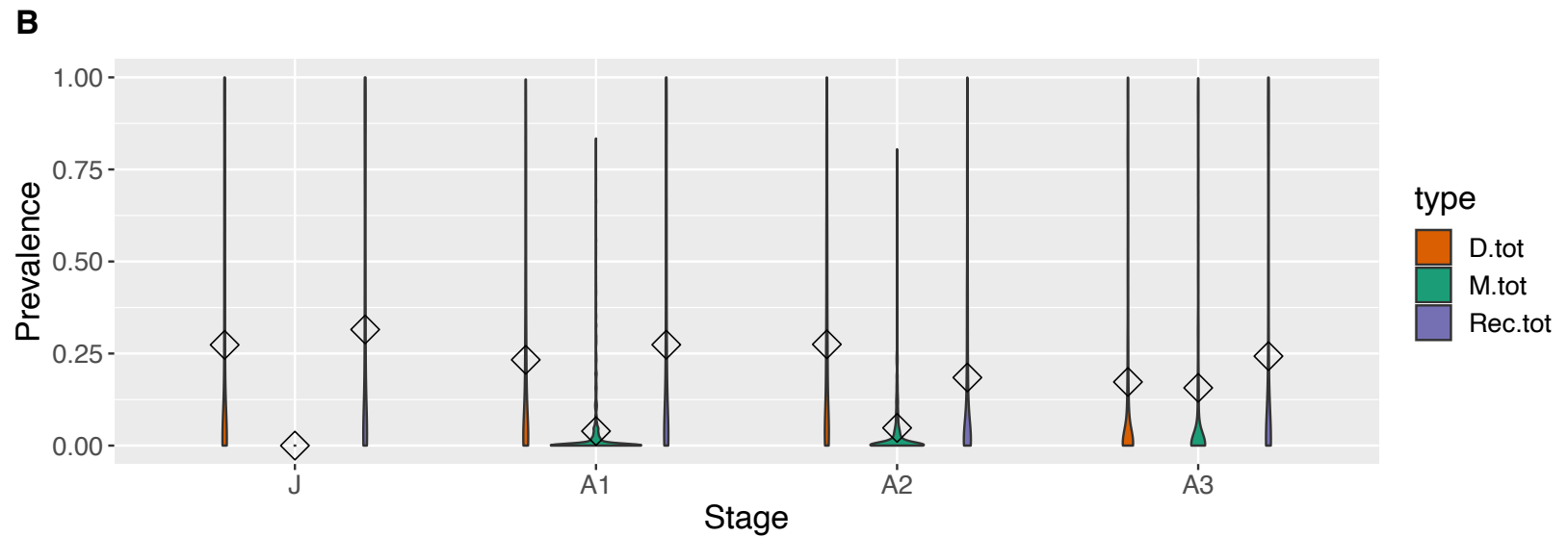
Results

- By age

Proportion of infected trees increases with age



No clear trend in strain prevalence as a function of age



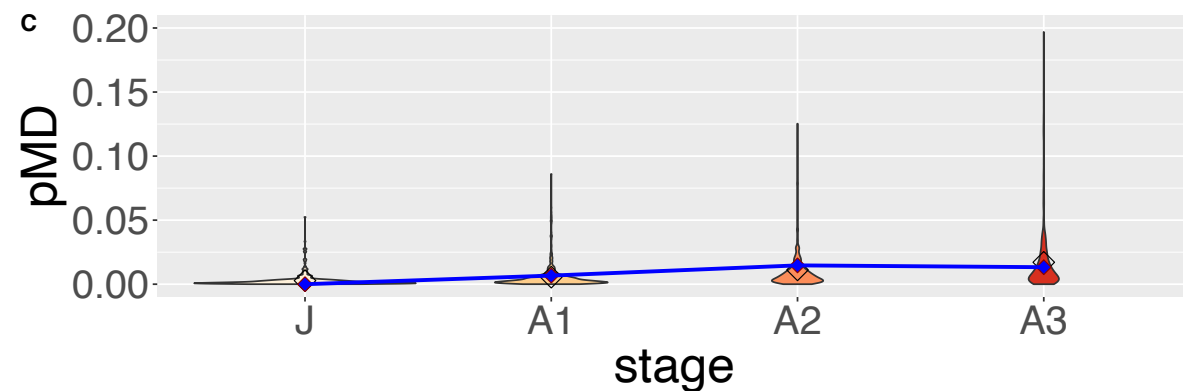
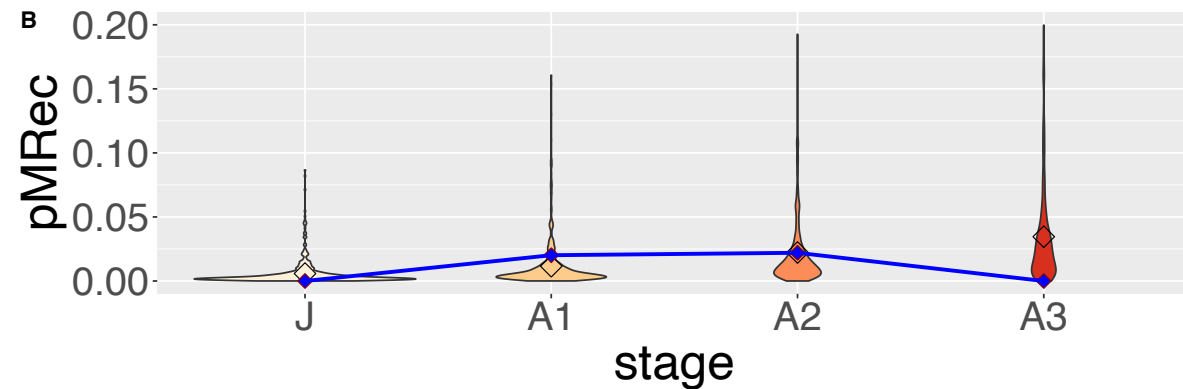
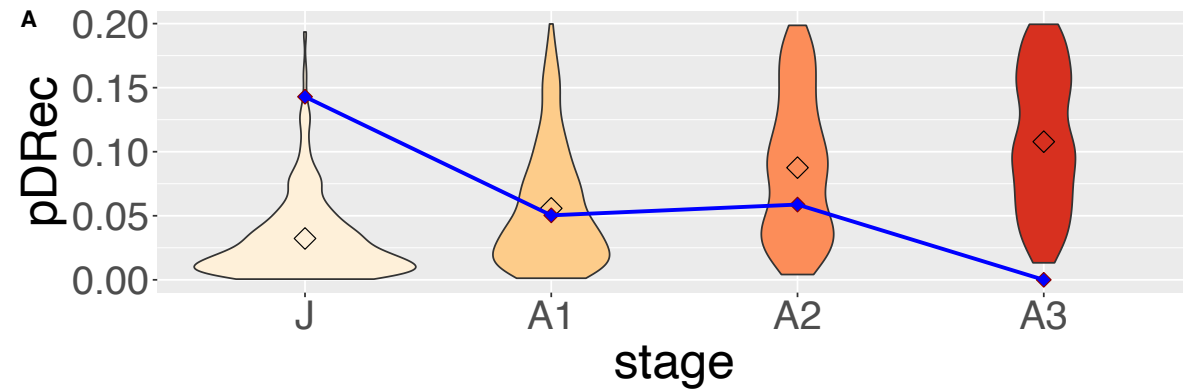
Results

- By age

Probability of co-infection
PPV-D + PPV-Rec
decreases with tree age !

Less co-infections
involving PPV-Rec in aged
trees than expected

— Observed Predicted by the model under H0



Conclusions

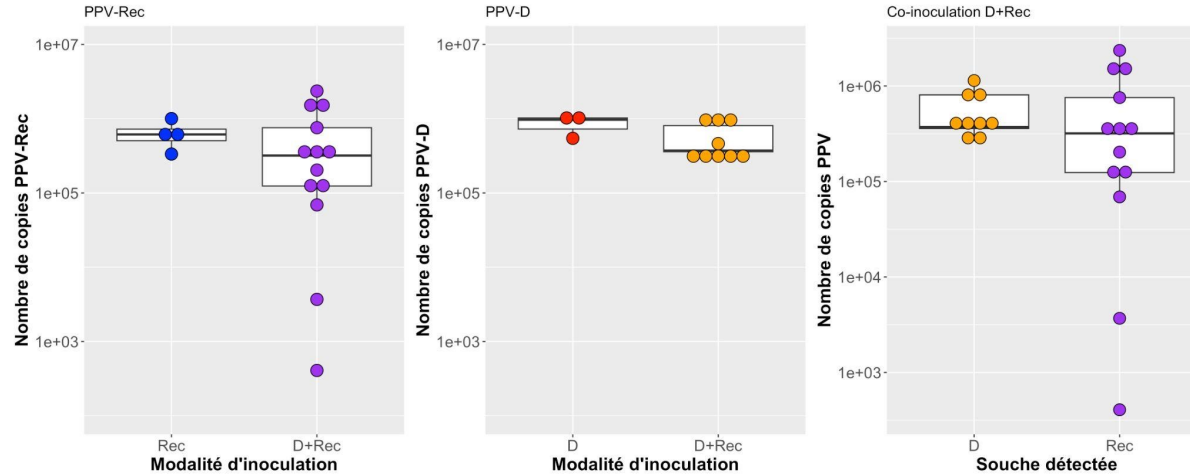
- Multiple infections involving PPV-Rec do not satisfy H0
- The age-structured model provides insights on the possible sources of discrepancies
- Possible sources of discrepancies
 - PPV-Rec is **outcompeted** over time (but PPV-Rec is a recombinant from M and D)
 - Trees develop a **resistance** to PPV-Rec when aging
 - PPV-Rec is **not at endemic equilibrium**
 - Others ?

Perspectives

- Combining field data analyses and lab experiments

Preliminary data

Amaury Beuzelin (Master 1) & Sylvie Dallot



Thank you



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