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Protecting the durability of major resistance genes to plant viruses with quantitative resistance

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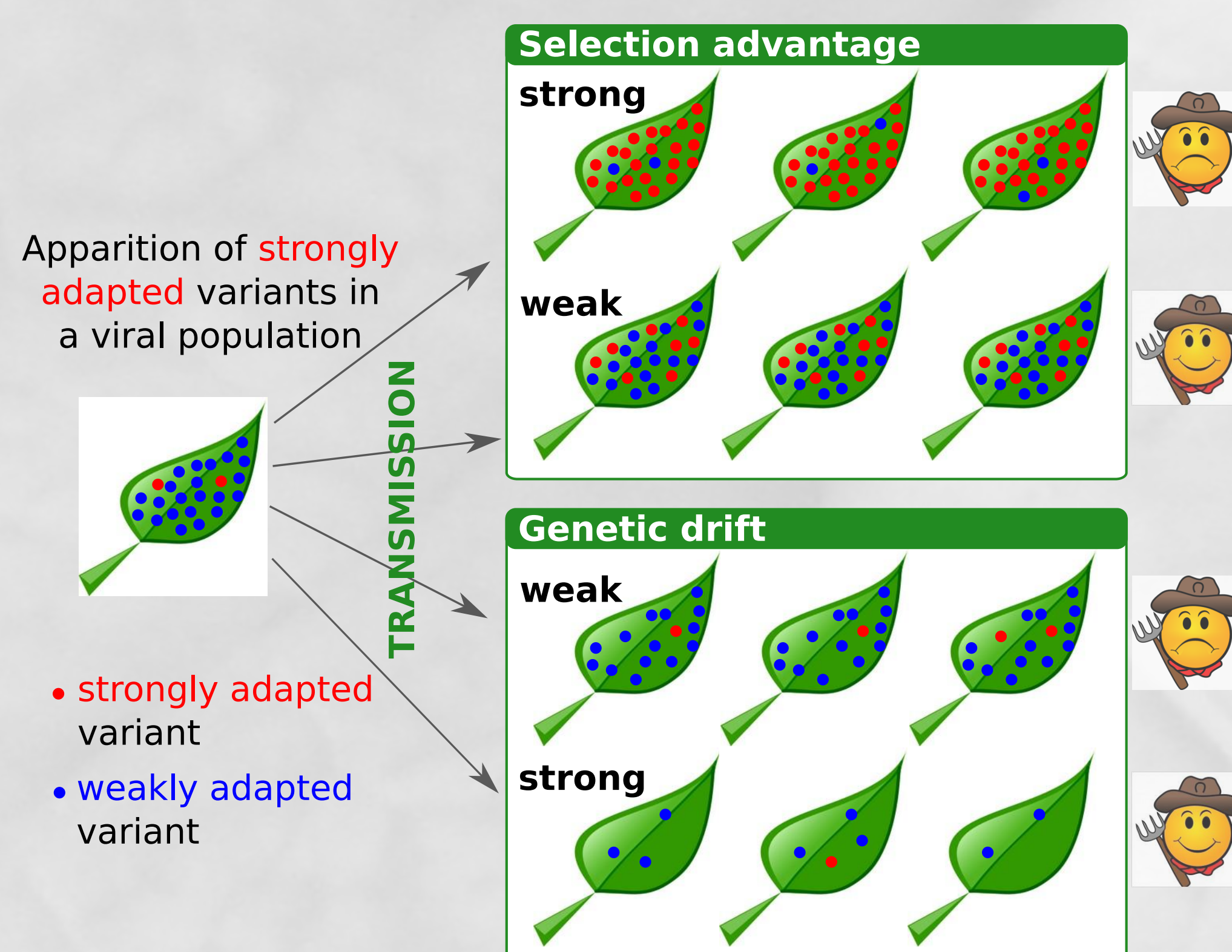
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1. Introduction & definitions

The deployment of virus-resistant plants often leads to the emergence of **resistance-breaking** (RB) mutants that suppress the yield benefit provided by the resistance.

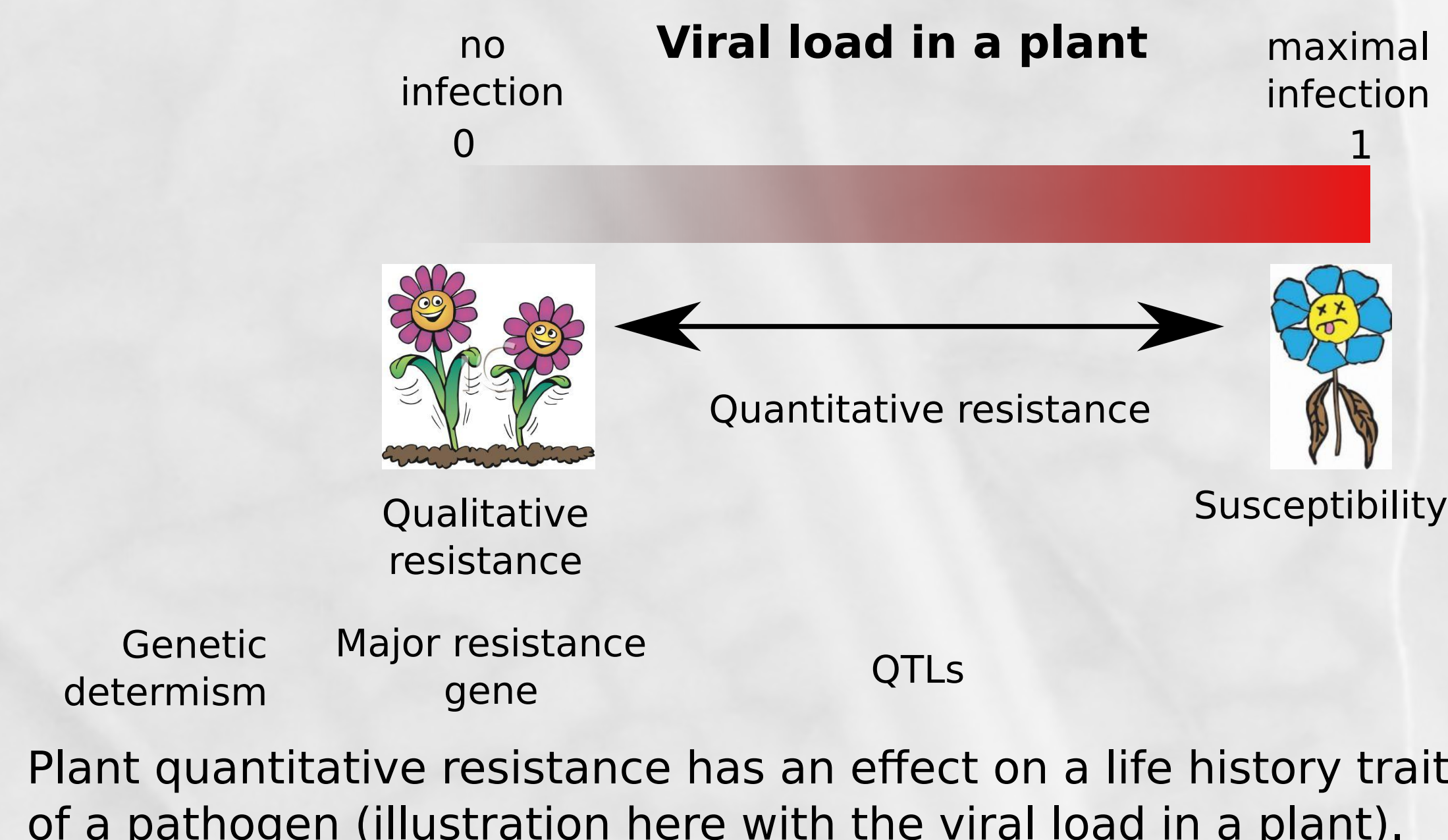
Combining **qualitative** and **quantitative** resistance can **increase the sustainability** of the **qualitative resistance** (Palloix *et al.* 2009, New Phytol, Brun *et al.* 2010, New Phytol).

Quantitative resistance decreases the fixation rate of RB mutants (Quenouille *et al.* 2012, Mol Plant Pathol). Two possible mechanisms :
(i) **decrease in selection advantage**
(ii) **increase in genetic drift**.



Qualitative resistance : total resistance to the virus conferred by a major resistance gene.

Quantitative resistance : partial resistance to the virus conferred by Quantitative Trait Loci (QTLs).



Objective : To analyze the **effect of quantitative resistance**, in terms of genetic drift and selection, on the **sustainability of qualitative resistance** by coupling experimental and modeling approaches.

2. Materials & methods

Plants :

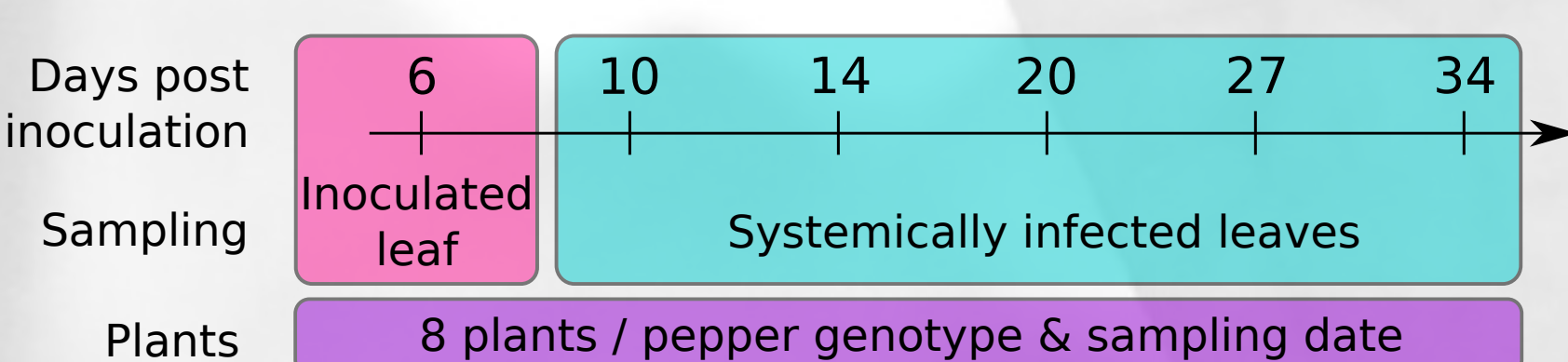
16 pepper genotypes :
(i) carrying a major resistance gene (*pvr2*³) and several combinations of QTLs,
(ii) with contrasted resistance-breakdown frequency f_{RB} (proportion of plants infected when inoculated with an unadapted virus variant), and number of primary infection foci N_{FP} .

Virus inoculum :

Mixture of 5 RB *Potato virus Y* (PVY) variants carrying distinct mutations, conferring weak to strong adaptation to the qualitative resistance.

Virus variant	Adaptation to <i>pvr2</i> ³	Proportion in inoculum
G	weak	1/5
N	weak	1/5
K	strong	1/5
GK	strong	1/5
KN	strong	1/5

Sampling :



Laboratory analyses :

Double antibody sandwich enzyme-linked immunosorbent assay (DAS-ELISA) to quantify the global virus load in plants.

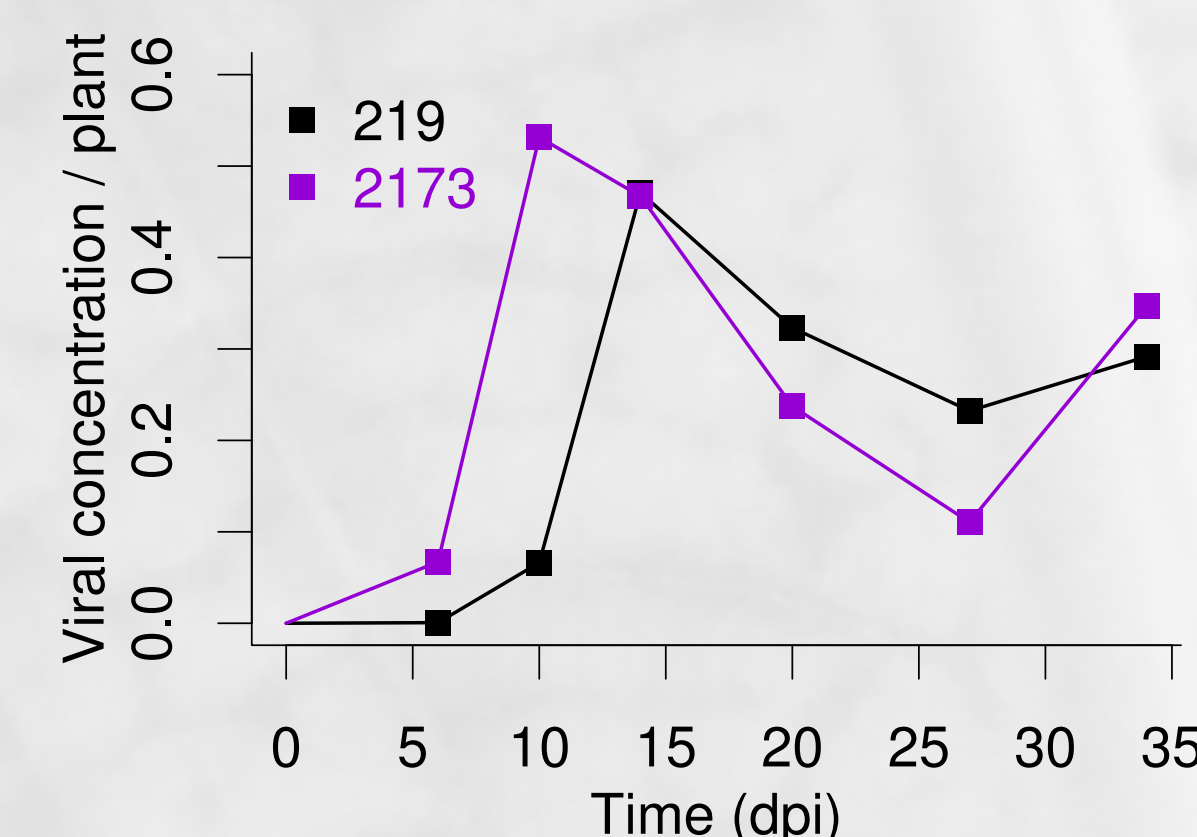
Miseq Illumina sequencing on the region of interest of the virus genome (realized in collaboration with the Genomic Platform of INRA Toulouse) to characterize virus populations.

3. Preliminary results : demo-genetic dynamics of virus variants

Focus on 2 contrasted pepper genotypes :

Relative viral concentrations per host plant at each sampling date

Slower viral multiplication in the plant **genotype DH219**, that could lead to strong genetic drift during the first days.



Frequencies of the 5 virus variants in each **plant** at each sampling date, and in the **inoculum**.

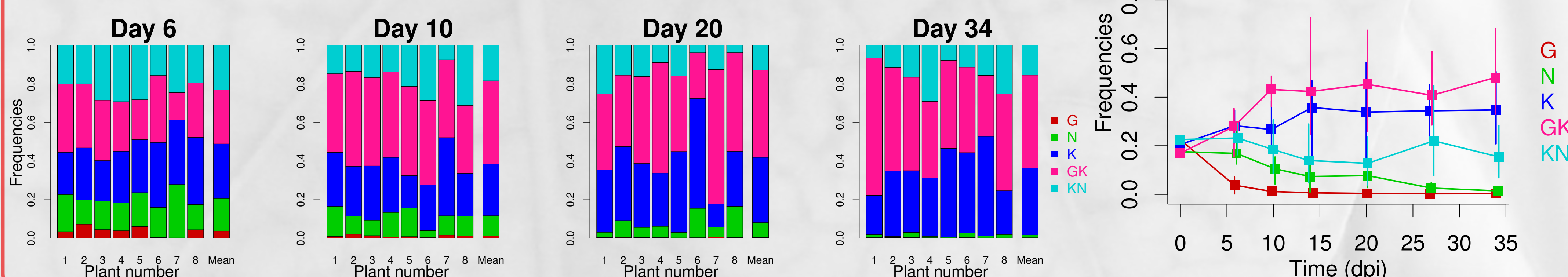
Genotype DH2173 : $f_{RB} = 51.6\%$ $N_{FP} = 11.6$

Weak genetic drift on virus populations :

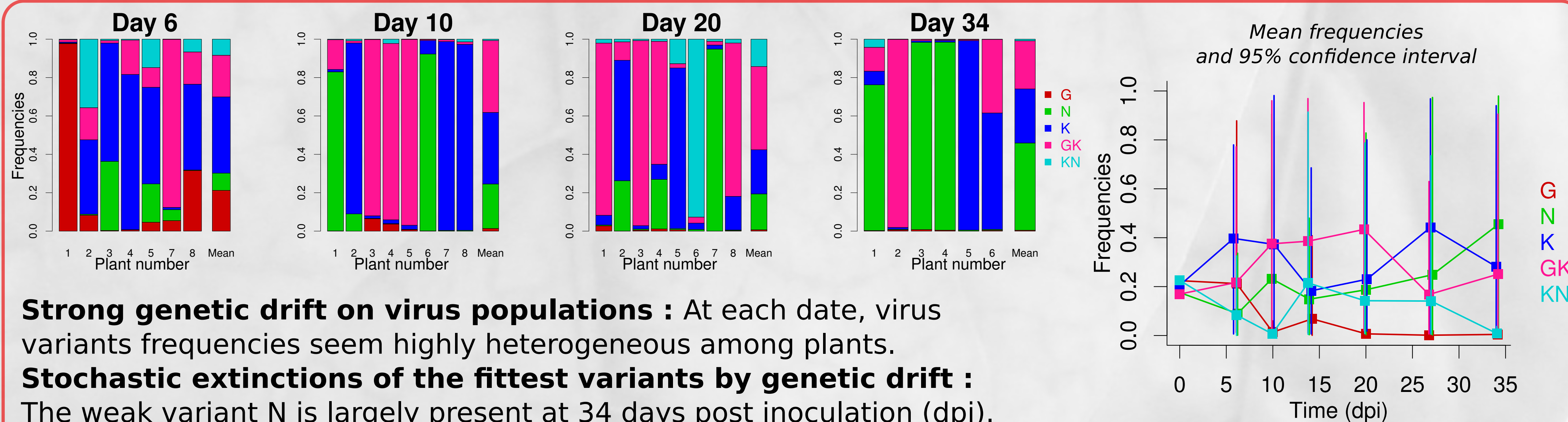
At each date, virus variants frequencies seem homogeneous among plants.

Strong selection effect on the weakest variants :

Virus variants G and N tend to disappear with time.



Genotype DH219 : $f_{RB} = 43\%$ $N_{FP} = 7$



Strong genetic drift on virus populations : At each date, virus variants frequencies seem highly heterogeneous among plants.

Stochastic extinctions of the fittest variants by genetic drift :

The weak variant N is largely present at 34 days post inoculation (dpi).

Slight selection effect : Virus variant G tends to disappear with time.

Strong bottleneck at inoculation : non-infected plants at 6 and 34 dpi.

4. Conclusion / Prospects

Identification of **contrasted patterns** in terms of **genetic drift** and **selection**.

Exploration of the links with additional parameters : a **decrease** in the **number of primary infection foci** seems associated with an **increase** in **genetic drift** and a **decrease** in the **resistance breakdown frequency**.

To estimate the effect of **genetic drift** and **selection** by fitting a **Lotka-Volterra model of competition** between virus variants to frequencies data (Fabre *et al.* 2012, PLoS Path) together with viral concentration data.

Any idea for estimating genetic drift and selection on these data ?