1. **Introduction**

During infection by a phytovirus a plant can be systemically infected or have a rapid reaction to circumcise the infection generating a lesion.

Using the Virus\_cycle\_inside\_lesion.R script (R v3.6.1) we simulated the experiment (REF) through several steps. (i) Generation of lesion from infected *N tabacum*. (ii) Multiplication from a random lesion. (iii) Generation of lesion from a single (“smallest *Ne*” modality) or 20 digital lesions (“intermediate *Ne*” modality).

This model takes account of the following postulates : (i)A few number of particle initiate a lesion,(ii) the effect of mutation is neglected as the production of virions is limited, (iii) two type of particle are considered : **virions A** which can reproduce either in *C. quinoa* and *N. tabacum* and **virions D** which can reproduce only in *C. quinoa* (and defective in *N. tabacum*), (iv) the percentage of virions **A** in a lesion determine the probability of infection in *N. tabacum* as : I = . Result for each passage is given by the mean of I for twelve random lesion.

1. **Variables**

The scripts use 10 different variables:

* **a** and **b** refers to the maximum and minimum particle able to generate a lesion.
* Simulation will pick a random number (*mm*) between **a** and **b** each time a lesion will be generated. The number (*mm*) will represent the number of particle inside the lesion. From the pool of the precedent lesion, a random particle (A or D) will be chose until to reach the value of *mm*.
* **mA**, **tA** and **mD**, **tD** refers to the lower and maximum multiplication of the virion A and B respectively.
* During the phase of multiplication in the lesion a random number between **ma** and **tA** will be pick for each A particle. Same with **md** and **tD** for the particle D.

For example if in the lesion there is 4 A particles and the multiplication rate is 10, then 40 particles A will be generated.

* **I** is the initial percentage of infectious particle in the systemic host. This attribute is directly from experimental data.
* **Np** is the number of passages in the simulation.
* **R** is the number of replicates
* **w** refers to the number of lesion used to generate the next generation of lesions (in the article we used 1 or 20).

1. **Outputs**

Infectivity.csv will gives the % of infectivity in the systemic host at each passage for each repetition.

Intra\_variance.csv will gives the intra-variance between the lineages.