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Functional analysis of agrobacterium virulence genes

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Citation

Niu, X. (2013, June 25). *Functional analysis of agrobacterium virulence genes*. Retrieved from <https://hdl.handle.net/1887/21014>

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Title: Functional analysis of agrobacterium virulence genes

Issue Date: 2013-06-25

Stellingen – Propositions

Behorende bij het proefschrift – Belonging to the thesis

Functional analysis of *Agrobacterium* virulence genes

Xiaolei Niu

1 No single *Saccharomyces cerevisiae* F-box protein by itself can replace the function of VirF.

This thesis

2 VIP1 and VirE2 are not degraded after expression of VirF in the yeast *Saccharomyces cerevisiae*.

This thesis

3 Expression of VirF in the model organism *Saccharomyces cerevisiae* does not affect transcription under standard growth conditions.

This thesis

4 VirE3 strongly affects the host transcriptional machinery when expressed in *Arabidopsis thaliana*, but not in *Saccharomyces cerevisiae*.

This thesis

5 The inability of *Agrobacterium* strains lacking VirF to transform *Nicotiana glauca* is probably due to the absence of a *N. glauca* gene homologous to the *Arabidopsis* VBF gene.

Hooykaas PJ, et al (1984) Plasmid 11(3):195-205.

Melchers LS, et al. (1990) Plant Mol Biol 14(2):249-259.

Zaltsman A, et al. (2010) Cell Host Microbe 7(3):197-209.

Zaltsman A, et al. (2013) Proc Natl Acad Sci U S A 110(1):169-174.

6 Transcriptome and proteome studies of *N. glauca* will provide more insight in the function of VirF than similar studies in model organisms such as *Saccharomyces cerevisiae* and *Arabidopsis thaliana*.

Hooykaas PJ, et al (1984) Plasmid 11(3):195-205.

Melchers LS, et al. (1990) Plant Mol Biol 14(2):249-259.

7 Without evidence for VirF-dependent ubiquitination of VIP1 and of VIP1 stabilization in the presence of the proteasome inhibitor MG132, the claim that a SCF^{VirF} complex directs VIP1 degradation in yeast and plant needs to be considered as preliminary.

Magori S, et al (2011) Sci Signal 18; 4(195)

Zaltsman A, et al (2010) Cell Host Microbe. 7(3):197-209

Lacroix B, et al (2008) Proc Natl Acad Sci U S A. 105:15429-15434

Tzfira T, et al (2004) Nature 431(7004):87-92.

8 Omics technologies nowadays provide massive amount of data, but even with these powerful tools, the determination of the biological function of a gene still needs as much work as before the omics revolution.

Ambrosio AB, et al (2013) BMC Genomics. 2013.

9 When you can not reproduce results from others, do not only question your own results, but also their results, even when published in prestigious journals such as nature, science and cell.

10 Biology is not as exact as mathematics: the threshold in genome-wide transcriptional analysis is always arbitrary.

11 It is better to perform several projects at the same time if you can handle it.