

Finanzierung: BBSRC grant

163 - Exploration of the small RNA landscape in *Petunia hybrida* infected with latent viruses and a pospiviroid using high throughput sequencing

Chofong G. N.¹ **Ralf Horres**², **Katja R. Richert-Pöggeler**¹

¹Julius Kühn-Institut, Messeweg 11-12, 38104 Braunschweig, Germany

²GenXPro GmbH, Frankfurt HRB76425, Frankfurt am Main, Germany

The words “latent”, “cryptic” or “symptomless” describe viruses that inflict no phenotypic alteration on their host. Moreover, for the genera *Caulimovirus*, *Badnavirus*, *Petuvirus* and *Solendovirus* endogenous sequences are reported. These integrated sequences may change from dormant to infectious under certain environmental conditions and genotypes.

The petuvirus *Petunia vein clearing virus* (PVCV) infects *Petunia* ssp. with complete or portion of its dsDNA integrated into petunia chromosomes. In a natural environmental setting this might be in co-existence with exogenous viruses and viroids. As a rule the plant tends to deploy machinery against these. In an arms race the infectious entities exploit the host RNAi machinery generating viroid-derived small interfering (vd-si)RNAs, viral suppressor (vsi)RNAs that inhibit expression of host defense genes by mimicking microRNAs. Here, we seek to understand the interaction among a latent carlavirus, pospiviroid, ePVCV and petunia through RNA-omics, microscopy and molecular biology approaches.

Preliminary siRNA sequencing data for the mixed infected *P. hybrida* mapped to five pararetroviruses references related to *petunia* and to plants with good matches of up to 60% for *Solanaceae*.

Ongoing analysis will help to contribute to the knowledge of the collection of vsiRNAs for better reconstruction of the virome, shed light on the mechanism of vsiRNA action on host mRNA, contribute to the understanding of benefits for the host during symbiosis with EPRV, latent virus and viroid (if any) that could have impact on plants. These will be seminal in designing strategies for plant resistance using RNA interference in both horticultural and agricultural crop plants.

We thank M. Wassenegger for viroid analysis in *S. jasminoides*, C. Maaß for photography of *S. jasminoides* and Philipp Schwartz Initiative of the Alexander von Humboldt Foundation for the financial support.

164 - Untersuchung der Translationsinitiation von Zuckerrübe infizierenden Poleroviren

Investigation of translation initiation of sugar beet infecting poleroviruses

Lukas Rollwage¹, **Roxana Hossain**¹, **Niels Wynant**², **Mark Varrelmann**

¹Institut für Zuckerrübenforschung, Holtenser Landstraße 77, 37077 Göttingen, Germany

²SESVanderHave NV., Industriepark 15, BE-3300 Tienen, Belgium

Der Krankheitskomplex der virösen Vergilbung (engl. Virus yellows disease (VY)) in Zuckerrüben ist ein zunehmendes Problem für den europäischen Rübenanbau seit dem Verbot von Neonicotinoiden zur Saatgutbeizung im Jahr 2019. VY wird durch Blattlaus übertragbare Viren verursacht. Namentlich sind dies *Beet yellows virus* (BYV, *Closterovirus*), *Beet mosaic virus* (BtMV, *Potyvirus*), *Beet mild yellowing virus* (BMYV) und *Beet chlorosis virus* (BChV) (beide *Polerovirus*). Vor allem die von *Myzus persicae* übertragenen Mitglieder der Gattung *Polerovirus* sind aufgrund ihrer persistenten Übertragungsweise von besonderer Relevanz. Alle Zuckerrübe infizierenden Poleroviren tragen ein viral genome-linked protein (VPg) (Stevens et al. 2005), welches in seiner Funktion als mRNA-Cap-Analogon für die Translationsinitiation postuliert wird. Für Potyviren konnte mehrfach gezeigt werden, dass das VPg mit verschiedenen eukaryotischen Translations-Initiationsfaktoren (eIFs) der