ABSTRACT

BSBMV belongs to the unassigned genus *Benyvirus* in the family *Benyviridae*. Compared to *Beet necrotic yellow vein virus* (BNYVV) it possesses a similar vector, particle morphology and host range. The genome organization is comparable to BNYVV as well; however, a fifth RNA that has been detected in some BNYVV isolates is missing in BSBMV. Worldwide distribution in sugar beet differ significantly. BNYVV is found in all main sugar beet growing areas whereas BSBMV is restricted to the US. Remarkable differences can be observed in symptom formation; BSBMV more often is found to systemically colonize as well sugar beet leaves and causes mosaic symptoms. Formation of rhizomania like symptoms by BSBMV is still unclear. Moreover, BSBMV is not controlled by BNYVV resistance genes like *Rz1* in sugar beet. In the US, both viruses occur in mixed infections but information about interaction between species is limited. The objective of this study is to establish the experimental system for studying the molecular causes for the biological differences, characterize the colonization strategy as well as the interaction of both *Benyvirus* species in sugar beet. To achieve this, an infectious cDNA clone for agrobacterium mediated inoculation was constructed, similar to that one already available for BNYVV (Delbianco et al., 2013; unpublished results). The recombinant virus produced symptoms compared to the wild-type virus and could be successfully transmitted by *Polymyxa betae*. First experiments to generate artificial reassortants were performed in the experimental host *Nicotiana benthamiana*. Virus symptoms occurred delayed and were much milder than from parental virus. Further experiments will study the colonization of sugar beet in dependence of the anti BNYVV resistance traits.

References: