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Rhizomania, caused by the *Beet necrotic yellow vein virus* and vectored by *Polymyxa betae*, is one of the most damageable diseases of sugar beet. Since the widespread use of resistant cultivars, multiple *Rz1* resistance-breaking events have been reported worldwide. Understanding the dynamic of the emergence of resistance-breaking isolates and their ability to spread is of the uttermost importance.

A field-based strategy was set up to follow the evolution of the disease in the epidemic foci of Pithiviers, in France. With the help of high-throughput PCR-based methods, the wide diversity of the BNYVV populations with high infectious potentials in soils was evidenced, with the presence of mixed viral infections (BNYVV A-, B- and P-pathotype) and the emergence of BNYVV reassortants. Variations according to the sugar beet genotype as well as to the spatial dispersion of the virus strongly suggest micro-evolution of the virus over a single season, as well as the fact that the host plant resistance is able to shape the viral population. The data accumulated over four years provide insights for a sustainable management of the sugar beet resistance. A model for the virus epidemic is proposed.

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Within-host micro-evolution and reassortment of BNYVV

Yann Galein

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## The epidemiology of rhizomania in the Pithiviers region of France

### Diversity, micro-evolution and interaction with cultivars at the field scale

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JUIN 2013

Thèse présentée en vue de l'obtention  
du grade de docteur en sciences agronomiques  
et ingénierie biologique

Faculté d'ingénierie biologique,  
agronomique et environnementale

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