



The genetic diversity of *Rhizobium leguminosarum* bv. *viciae* in cultivated soils of the eastern Canadian prairie

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Abstract

Soil populations of *Rhizobium leguminosarum* bv. *viciae* (*Rlv*) that are infective and symbiotically effective on pea (*Pisum sativum* L.) have recently been shown to be quite widespread in agricultural soils of the eastern Canadian prairie. Here we report on studies carried out to assess the genetic diversity amongst these endemic *Rlv* strains and to attempt to determine if the endemic strains arose from previously used commercial rhizobial inoculants. Isolates of *Rlv* were collected from nodules of uninoculated pea plants from 20 sites across southern Manitoba and analyzed by plasmid profiling and PCR-RFLP of the 16S-23S rDNA internally transcribed spacer (ITS) region. Of 214 field isolates analyzed, 67 different plasmid profiles were identified, indicating a relatively high degree of variability among the isolates. Plasmid profiling of isolates from proximal nodules (near the base of the stem) and distal nodules (on lateral roots further from the root crown) from individual plants from one site suggested that the endemic strains were quite competitive relative to a commercial inoculant, occupying 78% of the proximal nodules and 96% of the distal nodules. PCR-RFLP of the 16S-23S rDNA ITS also suggested a relatively high degree of genetic variability among the field isolates. Analysis of the PCR-RFLP patterns of 15 selected isolates by UPGMA indicated two clusters of three field isolates each, with simple matching coefficients (SMCs) ≥ 0.95 . However, to group all field isolates together, the SMC has to be reduced to 0.70. Regarding the origin of the endemic *Rlv* strains, there were few occurrences of the plasmid profiles of field isolates being identical to the profiles of inoculant *Rlv* strains commonly used in the region. Likewise, the plasmid profiles of isolates from nodules of wild *Lathyrus* plants located near some of the sites were all different from those of the field isolates. However, comparison of PCR-RFLP patterns suggested an influence of some inoculant strains on the chromosomal composition of some of the field isolates with SMCs of ≥ 0.92 . Overall, plasmid profiles and PCR-RFLP patterns of the isolates from endemic *Rlv* populations from across southern Manitoba indicate a relatively high degree of genetic diversity among both plasmid and chromosomal components of endemic strains, but also suggest some influence of chromosomal information from previously used inoculant strains on the endemic soil strains.

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