



Comparison of two *Claviceps purpurea* populations

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Claviceps purpurea (Fries) Tulasne causing ergot has a wide range of host species. The disease is serious to rye cultivation and less severe to other cereals and grasses. The fungus infects young, unfertilized ovaries of the hosts. Due to the very short time in which infection can occur, growth rate of mycelium can play an important role in the infection process. Knowledge about the genetic structure of pathogen populations is necessary to implement effective control strategies. In the study we assess the differentiation of *C. purpurea* populations using both non molecular and molecular methods. The aim of the study was to investigate whether pathogen population from rye plots in plant breeding stations differed from this obtained from rye fields.

We compared the mycelial growth rate and the genetic diversity of *C. purpurea* 45 isolates originated from rye plots with 47 isolates obtained from rye fields. Among 92 isolates significant differences in growth rate were revealed. To assess DNA polymorphism SRAP and RAPD methods were used. High genetic intra species variation was revealed. The significant genetic differentiation between two *Claviceps purpurea* populations was further supported by the result of the analysis of molecular variance (AMOVA), where both the within-population and the between-population variations were found to be highly significant, where 10.0% of the molecular variance was contributed by the differentiation between populations. The population originated from an experimental plots displayed higher genetic variation than those from a rye fields. We postulate that genetic background of the host can be more important for population variability of the fungus than strong directional selection imposed by agricultural practices. Moreover, some associations of four markers with linear mycelial growth were found on the basis of regression analysis.