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Molecular description of *Blumeria graminis* f. sp. *hordei* isolates

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The air-born fungus *Blumeria graminis* f. sp. *hordei* (*Bgh*) is a causal agent of barley powdery mildew. The pathogen attracts substantial attention due to its destructiveness. However, molecular diversity studies based on “house-keeping” genes do not provide sufficient resolution when applied to isolates from geographically limited regions. This study focused on developing a more efficient genotyping system capable to discriminate between closely related isolates. Whole genome sequence data were employed to design a panel of molecular markers based on microsatellites and insertion sites of transposable elements which represent an abundant part of the genome. A genotyping marker panel comprising 16 SSR, 14 SNP and 2 ISBP/RJM markers was applied on a set of 97 isolates originating from the Czech Republic, 50 Australian isolates and a collection of 11 isolates representing global *Bgh* diversity. The marker panel provided significant resolution of studied isolates, most of them showing unique genotype profiles. The analysis of phylogenetic relationship performed by neighbor-joining algorithm for 97 Czech isolates resulted in 87 separate clades and revealed high diversity of the pathogen population within a small geographical area. After supplementing with data on virulence of individual isolates, this study might open new opportunities of studying the host-pathogen relationship and patterns of the pathogen spatial distribution. This work has been supported by the Czech Ministry of Education, Youth and Sports (grant awards LD14105, LO1204).

