# Phenotypic Diversity of *Erwinia amylovora* in Bulgaria

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Z. Naturforsch. **62c**, 857–868 (2007); received March 1/June 6, 2007

Fifty-one strains of *Erwinia amylovora* isolated from nine host plants in Bulgaria were characterized phenotypically and identified by the API 20E and BIOLOG system. The identification was confirmed by PCR amplification of a specific region of the plasmid pEA29 and the genome *ams* region. The phenotypic diversity of the strains was studied on the basis of their API 20E and BIOLOG metabolic profiles, as well as of their SDS-PAGE protein profile. Metabolic diversity among the strains was established, but no connection with the origin of the strains was revealed. The Bulgarian strains showed API 20E metabolic profiles not found in previous studies of *E. amylovora*. The strains formed a homogenous group on the basis of their protein profiles. All the strains were sensitive to the antibiotics streptomycin, tetracycline and oxytetracycline. This study was an initial step towards an investigation of the diversity and evolution in the Bulgarian population of *E. amylovora,* and it was the first characterization of *E. amylovora* strains isolated from different host plants in the period 1995–2005 in Bulgaria.

*Key words: Erwinia amylovora*, Phenotypic Diversity, PCR