**Stenotrophomonas bentonitica** BII-R7\(^T\), a novel bacterial strain with bioremediation potential

I. SÁNCHEZ-CASTRO\(^1\)*, M. BAKKALI\(^2\), P. KÄMPFER\(^3\), S.P. GLAESER\(^3\), H.-J. BUSSE\(^4\), M.L. MERROUN\(^1\)

1 Departamento de Microbiología, Universidad de Granada, Granada, Spain (*correspondence: sanchezcastro@ugr.es)
2 Departamento de Genética, Universidad de Granada, Granada, Spain
3 Institut für Angewandte Mikrobiologie, Justus-Liebig-Universität Giessen, D-35392 Giessen, Germany
4 Institut für Mikrobiologie, Veterinärmedizinische Universität Wien, A-1210 Wien, Austria

*Stenotrophomonas bentonitica* BII-R7\(^T\), a Gram-stain negative, rod-shaped, aerobic bacterial strain, was isolated during a study targeting the culture-dependent microbial diversity occurring in bentonite formations from southern Spain [1]. Comparative *gyrB* and 16S rRNA gene sequence analyses showed that this isolate belongs unequivocally to the genus *Stenotrophomonas* (class Gammaproteobacteria). Members of this genus have been recently proposed for bioremediation strategies due to their versatility and particular characteristics [2]. This potential applicability was also demonstrated in our laboratory through several interaction experiments by using metals such as U and Se [3].

Based on a polyphasic approach comprising phenotypic (morphological, quinone system analysis, fatty acid profiling, etc.) and genotypic/molecular (Orthologous Average Nucleotide Identity, Original Average Nucleotide Identity, Genome-to-Genome Distance and GC percentage) we demonstrated that the isolate BII-R7\(^T\) represents a novel genospecies within this genus. Considering all analyses performed, the *Stenotrophomonas* species identified as closest to BII-R7\(^T\) were *Stenotrophomonas rhizophila* LMG 22075\(^T\), *Stenotrophomonas pavanii* DSM 25135\(^T\), *Stenotrophomonas maltophilia* DSM 50170\(^T\), *Stenotrophomonas chelatiphaga* DSM 21508\(^T\), and *Stenotrophomonas tumulicola* JCM 30961\(^T\). A comprehensive comparative analysis of BII-R7\(^T\) genome and those from *Stenotrophomonas* close species mentioned above was performed in order to evaluate their genomic potential in heavy metal bioremediation strategies as well as other biotechnological applications.