

10th International Conference



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ABSTRACT BOOK



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EMERGING APPROACHES

S8_OP46: Isolation and characterization of a *Sphingomonas* strain able to degrade the pleuromutilin antibiotic tiamulin

S8_OP47: Genome analysis of *Lactocaseibacillus paracasei* SRX10: An Indigenous Strain for Use as a Multi-Functional Adjunct Culture in Cheese Production.-

S8_OP48: Tracking viral infection temporal dynamics after microbial resuscitation following seasonally y soil rewetting using viromics and stable isotope metagenomics

S8_OP49: Intergenerational memory of single cell division times in a growing microcolony

S8_OP50: Bacteriophage selection alters antibiotic resistance in *Vibrio alginolyticus*

S8_OP51 (FT): Evaluation of meat spoilage markers for the development of on-package freshness sensors

S8_OP52 (FT): An interactive online stochastic quantitative microbiology tool for risk-based decision support in the Food Industry applied to *Bacillus cereus* in milk

FOOD-NUTRITION

S9_OP53: Microbial inactivation: Setting the basis for a risk-based design in food processing

S9_OP54: Combination of spectral and NGS data for the microbiological quality assessment of shellfish

S9_OP55: Vineyard-mediated factors are still operative in spontaneous and commercial fermentations shaping the vinification microbiome and affecting the antioxidant and anticancer properties of wines

S9_OP56: Where Greek cheeses belong within the global cheese microbial map: a comparative integrative analysis of cheeses' microbial signatures

S9_OP57: Monitoring the survival of probiotic bacteria during the shelf life of a novel Greek sheep traditional yogurt and following subsequent *in vitro* digestion

S9_OP58 (FT): Microbial electrostimulation and electrocution using low intensity electric fields – A novel approach for selective control of microbial growth *in vitro* and in food matrices

S9_OP59 (FT): *Listeria monocytogenes* colony growth dynamics after exposure to acidic conditions and disinfectants

S9_OP60 (FT): Short-term effects of fruit juice enriched with probiotics on glycemic responses : A randomized controlled clinical trial in healthy adults



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EMERGING APPROACHES

S8_OP46

ISOLATION AND CHARACTERIZATION OF A SPHINGOMONAS STRAIN ABLE TO DEGRADE THE PLEUROMUTILIN ANTIBIOTIC TIAMULIN.

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Tiamulin (TIA) is a veterinary antibiotic commonly used in livestock farming which is persistent in the animal digestive system and downstream receiving environments, it is ecotoxicologically relevant, and its environmental dispersal entails high-risk for antibiotic resistance development according to our previous work 1,2. Little is known regarding its biodegradation potential in soil where it can end up upon manuring. Antibio-phagy is a desirable microbial trait which could be exploited in bioaugmentation strategies for the reduction of antibiotics pressure in environmental settings. Aiming to develop such a strategy, a *Sphingomonas* strain able to degrade TIA was isolated from soil exhibiting accelerated biodegradation through liquid enrichment in minimal media where the antibiotic was the sole carbon/nitrogen source. The capacity of the strain to degrade TIA was characterized at a range of antibiotic concentrations, pHs, and temperatures, while genomic, transcriptomic and metabolomic analysis were performed in an attempt to further characterize the genetic background of the strain relative to its biodegradation capacity and elucidate the TIA metabolic pathway. The isolate completely degraded TIA at concentrations up to 100 mg l⁻¹ within 3 days, with pH and temperature optima of 6.5-7.5 and 25 °C respectively. Phylogenomics analysis indicated a novel species (83.87 % average nucleotide identity with *Sphingomonas laterariae*, ≤ 95 %), which we coined *candidatus Sphingomonas perruchonii*. Transcriptomics showed the enhanced (log₂ fold-change value of ≥ 6)

upregulation of several oxidoreductases, transporters, and hydrolases, a lyase, a transcription regulator, and secondary metabolites biosynthetic genes under the TIA treatment compared with succinate as carbon source, while a Bcr/CflA family resistance gene (efflux pump coding, homologous to bicyclomycin, chloramphenicol, florphenicol, and tetracycline resistance genes) was also significantly upregulated. Most of the highly upregulated genes under TIA lacked homologues in other sphingomonads according to pangenome analysis. Metabolomics identified five metabolites, although only one of them, a dioxygenated derivative of TIA was formed in significantly higher amounts in the presence of the bacterium and its formation pattern was conducive with TIA degradation. The current study is the first to report a TIA-degrading isolate with the potential for use in the bioaugmentation of contaminated manures.

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References

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2. Katsivelou, E. et al. (2023). *Sci. Total Environ.* doi: 10.1016/j.scitotenv.2023.164817