

Pseudomonas bohemica sp. nov, a novel bacterium with a great genomic potential of produce novel drugs

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Novel antimicrobials and antifungals are needed to overcome problems that they implicate, such as resistances developed against them and their associated toxicity. Bark beetles establish symbiosis with several microbial strains which play different roles within the beetle holobiont. They protect the bark beetle holobiont by producing substances which inhibit the growth of bark beetle antagonists¹, and therefore, those strains can be of great interest in pharmaceutical industry. We isolated several strain from *Ips acuminatus*, finding a novel *Pseudomonas* species, *P. bohemica* capable to inhibit different microorganisms and, once that its genome has been sequenced and mined, it shows a high potential to produce antimicrobials, antifungals, antitumorals and others kinds of drugs in potential, which could be undescribed yet.

MATERIALS AND METHODS:

Bacterial associates were obtained from *Ips acuminatus* adults collected from their tree hosts in different locations within the Czech Republic. Our isolates were tested against different microorganisms. Total DNA of the strain with greater capability to inhibit the tested microorganisms was obtained and their genome sequence was obtained in an Illumina MiSeq. Automatic annotation of the genome was performed with RAST² and the 16S rRNA sequence was obtained and compared with those of type strains of bacterial species using EzBiocloud on-line server for species identification. The SEED Viewer³ and AntiSmash⁴ were used in order to find the gene clusters potentially implicated in the synthesis of bioactive secondary metabolites.



Figure 1: Bark beetle used as a source of bacterial isolations: *Ips acuminatus*

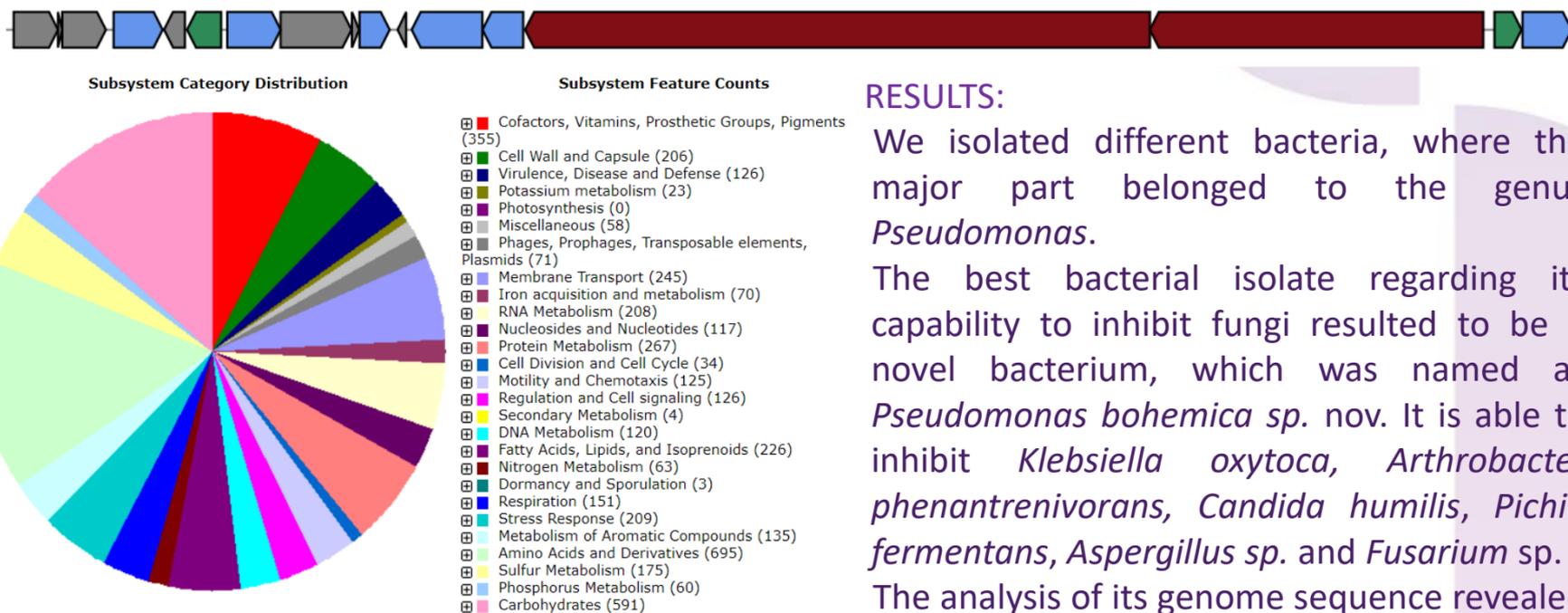


Figure 2: Image of the bacterial genome obtained from The SEED Viewer

CONCLUSION:

Bark beetles constitute a fascinating niche to find novel and interesting microorganisms such as *Pseudomonas bohemica* sp. nov., which represents a promising bacterium for finding novel substances with potential clinical applications.

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RESULTS:

We isolated different bacteria, where the major part belonged to the genus *Pseudomonas*.

The best bacterial isolate regarding its capability to inhibit fungi resulted to be a novel bacterium, which was named as *Pseudomonas bohemica* sp. nov. It is able to inhibit *Klebsiella oxytoca*, *Arthrobacter phenantrenivorans*, *Candida humilis*, *Pichia fermentans*, *Aspergillus* sp. and *Fusarium* sp.

The analysis of its genome sequence revealed several gene clusters related with others implicated in the biosynthesis of secondary metabolites with antimicrobial, antifungal, antitumoral, antiviral and anti parasitic activity among others. However, the low similitude between our clusters and those described point that they could produce different derivatives and, taking into account that we found several clusters that are not related with others described, *Pseudomonas bohemica* represent an interesting bacteria to find novel bioactive substances⁵.

1. García-Fraile, «Roles of Bacteria in the Bark Beetle Holobiont – How Do They Shape This Forest Pest?»
2. Aziz et al., «The RAST Server».
3. Overbeek et al., «The SEED and the Rapid Annotation of microbial genomes using Subsystems Technology (RAST)».
4. Weber et al., «antiSMASH 3.0—a comprehensive resource for the genome mining of biosynthetic gene clusters».
5. Saati Santamaría et al., «Discovery of Phloeophagus Beetles as a Source of *Pseudomonas* Strains That Produce Potentially New Bioactive Substances and Description of *Pseudomonas Bohemica* Sp. Nov.»