### **Soil Bacteria Protecting People and The Earth**

### **ABSTRACT:**

In spring 2022, two soil bacterium isolates were identified. The Gram + isolate was found to be an antibiotic producer. The Gram – isolate was found to be an environmental specimen that produced enzymes to break down waste. The isolation of these strains was done using microbiology techniques. Isolates were genetically tested using PCR, imaged using gel electrophoresis, and genome analysis were completed. The findings were compared to a database called BLAST and further information was gathered. Both discoveries support the hypothesis of the more diverse our garden soil is the better opportunities to discover beneficial microbial life. These discoveries can be used in all facets of life such as medicine and bioremediation.

### **INTRODUCTION:**

- Tiny Earth Project: Collect and biochemically test a local soil sample to identify specific bacterium for antibiotic activity. Samples are entered into a global database. It is hoped that future antibiotics and bioremediatory potential can be discovered and utilized from these microbes.
- **Every bacteria has very specific metabolic attributes. Being** able harness components of those attributes-might help us solve current and future antibiotic resistance and

environmental concerns.





Fig. 1 Soil Sample AKBB: W122°13'39.19",N47°45'2.47" **MATERIALS and METHODS:** 

Soil Sample YV: 47.6497939, -122.0422764

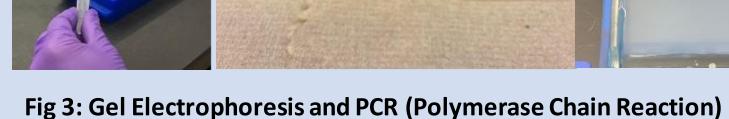


Fig 2. Process of selecting isolates

- Serial Dilutions and Plating Microbes/master plates
- **Picking interesting bacteria -> zone of inhibition**
- **Gram staining**
- Microscopy
- **PCR-BLAST**

**Biochemical tests:** 

- TSI; Urease
- Citrate; MOI
- Motility



- Selective and Differential media: EMB, XLD, MacConkey, Starch









_	<b>Biochemical tests</b>	AKB-Hydrocarbon d	egrader	YV- Antibiotic pro
	Gram Stain	Gram negative		Gram positive
h	Endospore Stain	None (vegetative)		Endospore produ
-	Triple Sugar Iron (TSI)	Negative for fermen	tation	Positive for fermentation
	Citrate	Positive (uses sodium citrate as carbon source)		Negative
	Motility	Positive (motile)		Positive (motile)
	Urease	Negative for producing NH3 and CO2 from urea		Negative for prod NH3 and CO2 fron
	MIO + Kovax	Negative for indole production	in di indi	Negative for indo production
	Oxidase	Positive (Aerobe)		Positive (Aerobe)
	Catalase	Positive (makes catalase enzyme)		Negative
	P. kagi ATC P. kagi ATC P. kagi ATC P. paychards Pseudomonast sp. GM33 Pseudomonast sp. GM33 Pseudomonast sp. GM48 Pseudomonast sp. GM74 Pseudomonast sp. GM74 Pseudomonast sp. GM78 Pseudomonast sp. GM78 Proved CCUG 53114 Pseudomonast sp. GM78 Premekel COUG 53115 Premekel COUG 5315 Premekel COU	6 17489T 17516T P 105460T C \$3590T 4641 T T C 25886 MG 2223T rophile DSM 17535T rophile DSM 17535T rophile DSM 17535T ropenses CECT 7677T C 4973T P restroiens LMG 2336T P entroiens LMG 2336T P entroiens LMG 2336T P / jessenii subgroup T T C 700688T T T SM30 21318T DSM 16007T SM30	92 99 8 99 8 96 8 99 8 99 8 99 8 99 8 99 8 99 8 99 8 99 8 99 8 99 8 99 8 99 8 99 8 99 8 99 8 9 9 8 9 8 9 8 9 8 9 8 9 8 9 8 9 8 9 8 9 8 9 8 9 8 9 8 8 9 8 9 8 9 8 9 8 8 9 8 8 9 8 8 9 8 8 9 8 8 8 9 8 8 8 9 8 8 8 9 8 8 8 9 8 8 8 9 8 8 8 8 8 8 8 8 8 8 8 8 8	3. paranthracis Mn5 <sup>T</sup> (MACGO 3. anthracis ATCC 14578 <sup>T</sup> (ABJ pacificus EB422 <sup>T</sup> (MAOI0000 tropicus N24 <sup>T</sup> (MACF000000 albus N35-10-2 <sup>T</sup> (MACI00000 mobilis 0711P9-1 <sup>T</sup> (MAOC000 wiedmannii FSL W8-0169 <sup>T</sup> (LC luti TD41 <sup>T</sup> (MACE0000000) toyonensis BCT-7112 <sup>T</sup> (NC_02 cereus ATCC 14579 <sup>T</sup> (NC_04 thuringiensis ATCC 10792 <sup>T</sup> (NZ oroteolyticus TD42 <sup>T</sup> (MACD0000 paramycoides NH24A2 <sup>T</sup> (MACE00000 paramycoides NH24A2 <sup>T</sup> (MACE00000 paramycoides DSM 2048 <sup>T</sup> (NZ_CM00000 eudomycoides DSM 12442 <sup>T</sup> (N_ 8. bingmayongensis' FJAT-13831 cytotoxicus NVH 391-98 <sup>T</sup> (NC_02 manliponensis' BL4-6 (JOTN0000 subtilis ATCC 6051 <sup>T</sup> (CP00332

Fig 5: Phylogenetic trees of AKB and YV bacteria

The NCBI identified AKB#11A as~ Pseudomonas reinekei Domain: Bacteria Phylum: Proteobacteria Class: Gamma proteobacteria **Order:** Pseudomonadales **Family:** Pseudomonas daceae **Genus:** Pseudomonas **Species:** reinekei (strain: PgBe 182)

The NCBI identified YV#7 as~ Bacillus mobilis Domain: Bacteria Phylum: Firmicutes **Class:** bacilli Order: caryophanales Family: Bacillaceae Genus: Bacillus Species: mobilis

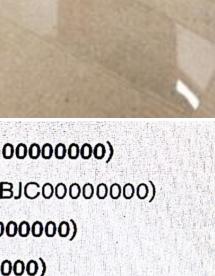
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### **DISCUSSION:**

- Antibiotics are important tools to treat and combat a large variety of microbial infections. Unfortunately, many infectious bacteria and microbes have developed resistance to the antibiotics that are currently used. It is important to discover and develop new antibiotics to combat emerging microbial resistances.
- Hydrocarbons are naturally occurring, organic compounds found in fossil fuels. Fossil fuel combustion is the major cause of greenhouse gases. Petroleum biproduct remediation is vital to combat global warming and environmental pollution. More research needed to further identify specific metabolites for the bacteria.

### **CONCLUSION:**

- The entire process using microbiological lab protocols to discover our soil bacterial strains was fascinating!
- **Pseudomonas reineke is a mesophilic bacteria capable of** degrading chloroaromatics, chlorosalicylates and some resin acids. Its ability to break hydrocarbon makes it an especially interesting bacteria to further research. P. reineke's lipase enzymes are of particular interest to scientists working to remediate petroleum/plastic contamination in the environment.
- **Bacillus mobilis** is a highly motile member of the **Bacillus** *cereus* group. *Bacilli* are found in soil and work in symphony with mycorrhiza to facilitate plant growth in heavy metal contaminated soil. *Bacilli* use biotransformation and bioaccumulation to help plants increase nitrogen, phosphorus and potassium uptake. *Bacilli* strains have also been identified that aid in the bioremediation of aquatic ecosystems by breaking down nitrogen and phosphorus. Along with these bioremediatory capabilities, *Bacillus* species are capable of the production of structurally diverse, secondary metabolites that exhibit wide spectrum antibiotic activity.

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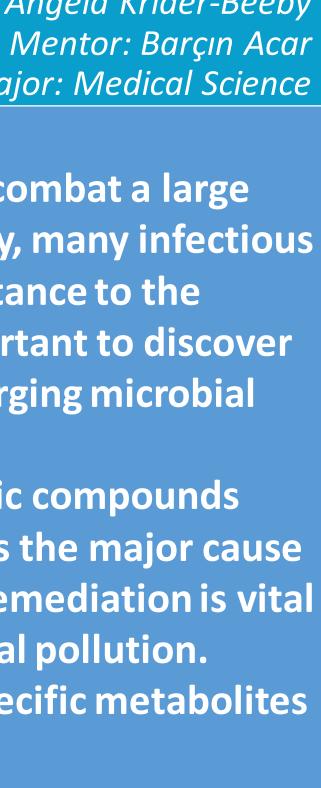
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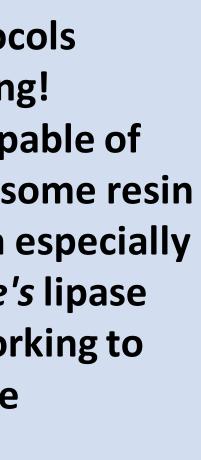
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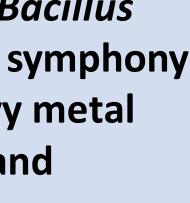
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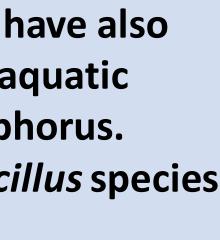
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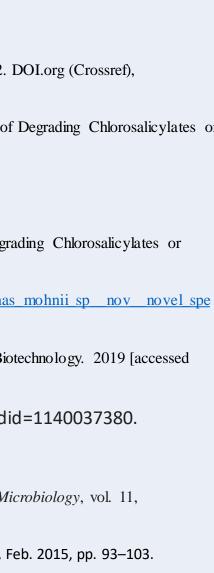












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