# Transposon Mutagenesis of Stenotrophomonas Maltophilia Oak Ridge strain 02 Team Members: Gabriella Hosack, Haley Gianfrancesco, Hanna Gilligan, Dionne Trammell Advisor: Dr. Jonathan Caguiat

#### Abstract

A multi-metal resistant strain of *Stenotrophomonas maltophilia* OR02 (S. maltophilia 02) was isolated from a metal contaminated site in Oak Ridge, TN. An EZ-Tn5 transposome was introduced into S. *maltophilia* 02. Approximately 880 transformants were replica plated onto plates containing copper sulfate, sodium selenite, mercuric chloride, sodium arsenite, and M-9 minimal salts medium to see if the transposon interrupted genes required for selenite resistance, arsenite resistance, mercury resistance, chromate resistance or growth on minimal media. 13 mutants were discovered. Of the 13 mutants discovered, 5 failed to grow on minimal media, 1 failed to grow on selenite, 1 failed grow on copper, 1 failed to grow on zinc, and 5 failed to grow on 2 or more metals. The transposon contains a kanamycin resistance genes and an *R6Ky* replication origin. The genomic DNA from the mutants was purified, digested, ligated and transformed into *E. coli*. These transformants will contain new plasmids consisting of the transposon flanked by the interrupted genes. We expect DNA sequencing to identify genes involved in oxidative stress response, metal efflux, metal transformation (reduction and oxidation) and sequestration.

#### Introduction

The Y-12 plant at Oakridge, Tennessee played a vital role in the production of nuclear weapons processing uranium during World War II to make atomic bombs. During the Cold War in the 1950s, the Y-12 plant focused on processing lithium to make hydrogen bombs. In this process, a large quantity of elemental mercury was used of which 330 tons of mercury was lost to the environment contaminating the nearby East Fork Poplar Creek (EFPC) at the Y-12 plant<sup>1,2</sup>.

Stenotrophomonas maltophilia ORO2 (S. maltophilia O2) is a gram negative bacterium, isolated from East Fork Poplar Creek and is resistant to metal salts of mercury, cadmium, copper, zinc gold and selenium<sup>3</sup>. Our goal is to study the metal resistance genes that are involved in the resistance mechanisms. For this purpose transposon mutagenesis of S. *maltophilia* O2 was used to identify genes that encode resistance to selenite and gold and that allow it to grow in M-9 minimal medium. Some of these interrupted genes were identified using a gene rescue technique.

#### **Materials and Methods**

Transposon Mutagenesis<sup>4</sup>

-Transposon – DNA segments which transfers itself from one part of the genome to another part of that genome.

-EZ-Tn5 transposome from Epicentre Biotechnologies was introduced into S. maltophilia 02 by electroporation - (Figure 1).

-Cells were spread onto kanamycin plates (Figure 3).

-Colonies that grew should have transposon inserts.

-The colonies were replica plated and screened for metal sensitivity. -Confirmed mutants are recorded in Table 1.

#### **Gene Rescue**

•The digested DNA was ligated with T4 DNA ligase which circularized the digested DNA strands.

•The ligated DNA was transformed into *E. coli* and spread on kanamycin plates.

•Only circularized DNA fragments containing the transposon will grow. •DNA was purified from the selenite, and other metal sensitive colonies. •The purified DNA was partially digested using *BfuC* I



### **Figure 2: Replica Plating**



LB Kanamycin

Zinc

## **Mutagenesis Results**

Mu	Cr	Zn	Au	Cu	Se	<b>M-9</b>	LB-Kan	Mutant
No Plas	+	+	-	+	I	+	+	CD36
No Plas	+	+	Ŧ	+	-	+	+	CD42
Anthra	+	+	÷	+	+	-	+	CF14
T	+	-	+	+	+	+	+	CG55
No Plas	+	+	÷	+	+	-	+	CH38
Senso	+	+	_	+	+	+	+	CJ22
Shikir	+	+	+	+	+	-	+	CJ47
Sei	-	+	-	I	I	+	+	CK56
Outer M	+	+	+	+	-	+	+	CK65
Amir	+	+	+	+	+	-	+	CL29
No Plas	+	+	+	-	+	+	+	CL53
Amir	_	+	+	-	-	+	+	CL68
No Plas	+	+	÷	+	Ŧ	-	+	CM28

LB-Kan = LB + Kanamycin, M-9 = minimal medium + casamino acids, Se = 10 mMSe(IV), Cu = 2 mM Cu(II),  $Au = 25 \mu M Au(III)$ , Zn = 1 mM Zn(II), Cr = 0.2 mM = 1000 mCr(IV), + = growth, - = no growth



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#### Conclusion

- The selenite-sensitive mutant, CK65, contained mutations in an outer membrane protein, OmpA, which may be involved in efflux.
- The gold sensitive mutant, CK56, contained a mutation in a gene for a Sensor Kinase protein.
- •The mutant, CF14, failed to grow on minimal medium and contained a mutation in gene for anthranilate synthase, which is important for tryptophan biosynthesis.
- •Not all sequencing reactions were successful.

#### **Summary of Mutants**

Mutant Types	Number
2 or More Metals	5
Selenite	1
Zinc	1
Copper	1
Minimal Medium	5

#### **Future Work**

•Obtain sequence data for other mutants •Obtain the complete sequence for outer membrane protein •Use complementation experiments to show that the mutated gene can restore resistance

## **Sequencing and BLAST Analysis**

#### **CF14**

		Construction of the second second second	strain FDAARGOS 4851512 Number of M	<ul> <li>Introduction of the second se Second second s</li></ul>	complete ger	nome		
ange 1	: 3539908	to 3540401 Gen	Bank Graphics	Vex	t Match 🔺 Previ	ious Match		
Score		Expect	Identities	Gaps	Strand			
797 bi	ts(431)	0.0	473/494(96%)	0/494(0%)	Plus/Plus			
uery	1		AACCCGTCGCCGTACATGI			60		
bjct	3539908		AACCCGTCGCCGTACATG			3539967		
uery	61		CCGGAAATCCTGGTGCGCC			120		
bjct	3539968		CCGGAAATCCTGGTGCGCC			3540027		
uery	121		CGCCCGCGCGGTGCAACCG	TCGAGCAGGACCTGGCG		180		
bjct	3540028		CGCCCGCGTGGCGCCACGC			3540087		
uery	181		CCGAAGGAGCGCGCCGAGC			240		
bjct	3540088		CCGAAGGAACGCGCCGAGC			3540147		
uery	241	GATGCCGGCCGTGTCTCGAAGGCCGGCACCGTGGAAGTGGGCGAGCAGTTCGTGATCGAG						
bjct	3540148							
uery	301	CGCTACAGCCACGTCATGCACATCGTCAGCGAAGTGACCGGGCAGCTGCAGCCGGGCCTG						
bjct	3540208		GTCATGCACATCGTCAGC			3540267		
uery	361		GIGCIGCGIGCCACGIICO			420		
bjct	3540268		GTGCTGCGTGCCACGTTCC			3540327		
uery	421		GAAGTGATCCGCGAGCTGG			480		
bjct	3540328		GAAGTGATCCGCGAGCTGG			3540387		
uery	481	AGCATCGGCTAC						
bjct	3540388	AGCATCGGCTAC						

locus tag="CEQ03 16490' inference="COORDINATES: similar to AA sequence:RefSeq:NP 635853.1" note="Derived by automated computational analysis using

gene prediction method: Protein Homology." codon start=1

transl table=11 product="anthranilate synthase component I

protein id="AVK73207.1

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