FUNCTIONAL INSIGHTS INTO UNIVERSAL STRESS PROTEINS OF PSEUDOMONAS

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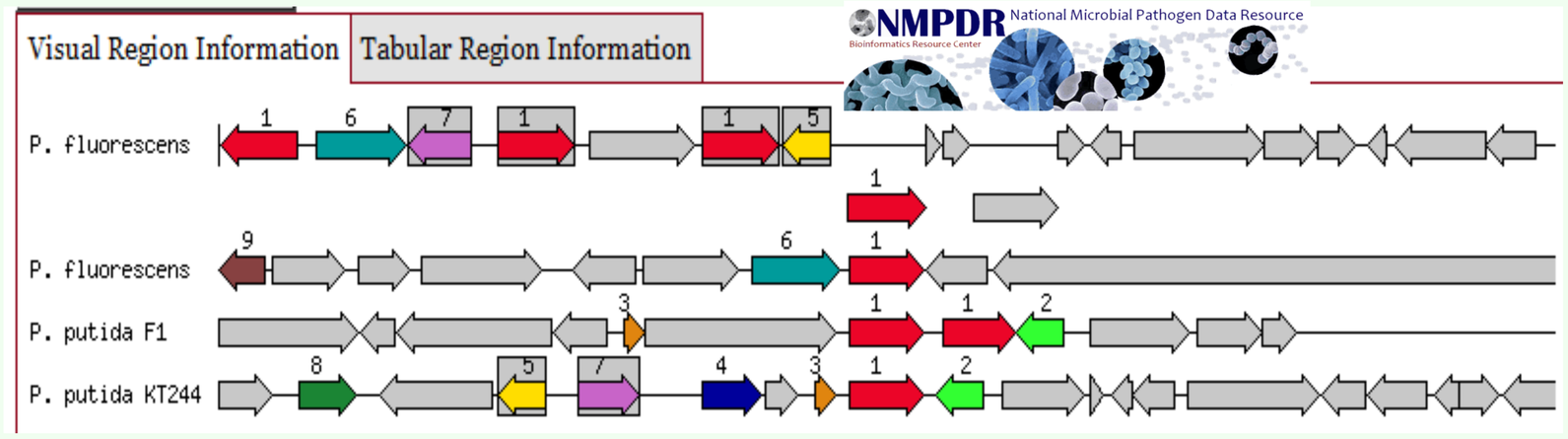
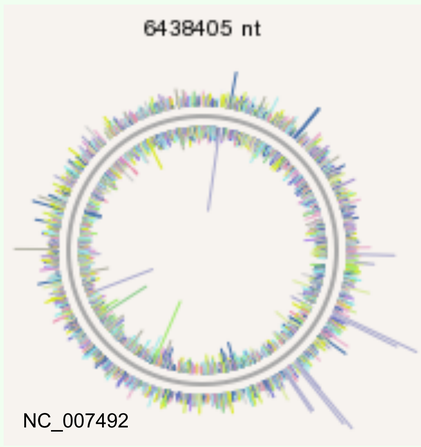
PSEUDOMONAS GENOMES AND UNIVERSAL STRESS PROTEINS

- There are at least 15 completely sequenced *Pseudomonas* genomes providing opportunities for comparative analysis of proteins containing the universal stress protein domain (Pfam00582) that is known to provide cells with the ability to respond to environmental stresses such as nutrient starvation, drought, high salinity, extreme temperatures, and exposure to toxic chemical.

EVIDENCE FOR FUNCTIONAL COUPLING OF UNIVERSAL STRESS PROTEINS IN PSEUDOMONAS FLUORESCENS Pf0-1



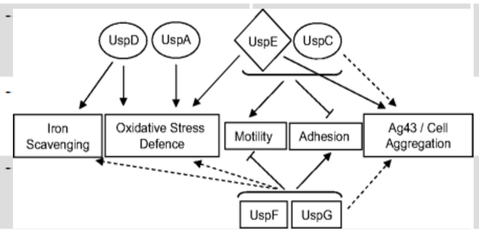


- **Using the GenomeViewer Tool of the National Microbial Pathogen Data Resource (NMPDR) we observed that:**
  - **Four of the 6 predicted universal stress proteins of the motile, soil-inhabiting, obligate aerobe *Pseudomonas fluorescens* Pf0-1 were clustered in the same genomic region as a transcriptional regulator: Crp/Fnr family (Set 7) and an enzyme: acetyltransferase (Set 5).**
  - **The transcriptional regulator is predicted to have a role in oxidative stress while the enzyme is important for cell growth and development.**
- **The physiological impact of this genomic region warrants further studies.**

PROTEIN-PROTEIN INTERACTIONS DOCUMENTED IN MICHIGAN MOLECULAR INTERACTIONS FOR UNIVERSAL STRESS PROTEINS OF ESCHERICHIA COLI

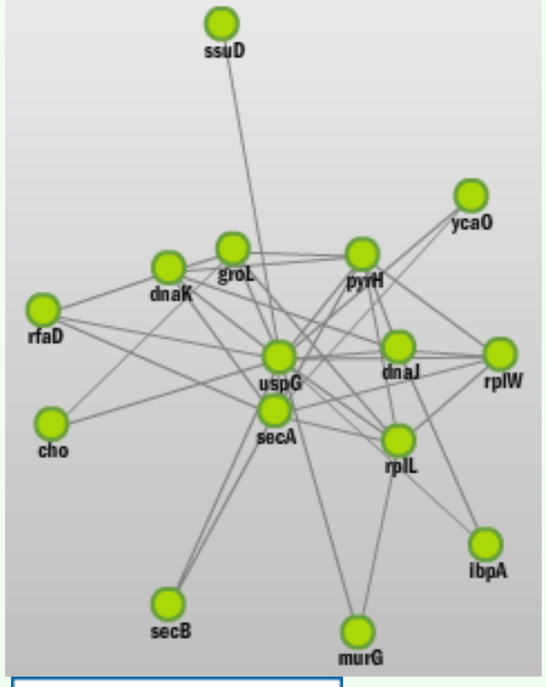
- **Multiple sequence alignments indicate that Pfl3881 and Pfl4004 of *P. fluorescens* Pf0-1 have significant sequence similarity to sequences of UspA, UspC, and UspD of *E. coli*.**
- **Since the universal stress proteins of most *Pseudomonas* species have not been characterized for function, we sought to determine known protein interactions associated with the universal stress proteins (UspA, UspB, UspC, UspD, UspE, UspF, UspG) of *E. coli*.**

Gene	Organism	Type	Other Names	Description	Cellular Components	Biological Processes	Molecular Functions	Int	Doc	Path
uspD	Escherichia coli K12	protein-coding	uspD; ECK3915; JW3894; yiiT	stress-induced protein	---	response to stress	---	-	8	-
uspF	Escherichia coli K12	protein-coding	uspF; ECK1371; JW1370; ynaF; yzzL	stress-induced protein, ATP-binding protein	-		---	-	9	-
uspC	Escherichia coli K12	protein-coding	uspC; ECK1894; JW1884; yecG	universal stress protein	-		---	-	6	-
uspG	Escherichia coli K12	protein-coding	uspG; ECK0601; JW0600; UP12; ybdQ; yzzU	universal stress protein UP12	-		---	15	12	-
uspE	Escherichia coli K12	protein-coding	uspE; ECK1329; JW1327; ydaA	stress-induced protein	---	---	---	-	13	-
uspB	Escherichia coli K12	protein-coding	uspB; ECK3479; JW3461; yhiO	predicted universal stress (ethanol tolerance) protein B	organelle inner membrane , peptidoglycan-based cell wall	response to stress , xenobiotic metabolic process	---	-	9	-
uspA	Escherichia coli K12	protein-coding	uspA; ECK3480; JW3462	universal stress global response regulator	cytoplasm	response to stress	---	-	29	-



Role of the 6 E. coli Usps in oxidative stress defense, iron metabolism, and cell surface properties. Nachin et al. 2005 (PMID: 16159758)

Gene	Source Provenance
cho	IntAct
dnaJ	DIP
dnaK	DIP
groL	DIP
ibpA	DIP
murG	IntAct
pyrH	DIP
rfaD	DIP
rplL	DIP
rplW	DIP
secA	DIP
secB	DIP
ssuD	IntAct
tuf	DIP
uspG	DIP
ycaO	DIP; IntAct



- **The only *E. coli* Usp with compiled protein interactions was UspG. The 16 protein interactions documented included interaction with N-acetylglucosaminyl transferase (murG) annotated to function in peptidoglycan biosynthetic process. Michigan Molecular Interactions (MiMI) provided an integrated view of the *E. coli* universal stress proteins including description, literature and gene ontology annotation to facilitate further studies. The NCIBI Netbowser tool was used to visualize the interactions of UspG.**

Netbrowser

FUTURE WORK

- **Integrative analysis of the universal stress proteins of *Pseudomonas* to uncover novel insights into their function in disease and extreme environmental conditions such as treatment with antibiotics and anaerobic airways in cystic fibrosis.**

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