

IRON TRANSPORT GENE NEIGHBORS OF STRESS-RESPONSIVE MAJOR FACILITATOR IN THE GENOME OF BIOENERGY RELEVANT *RHODOPSEUDOMONAS PALUSTRIS*

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INTRODUCTION

Gene Clusters

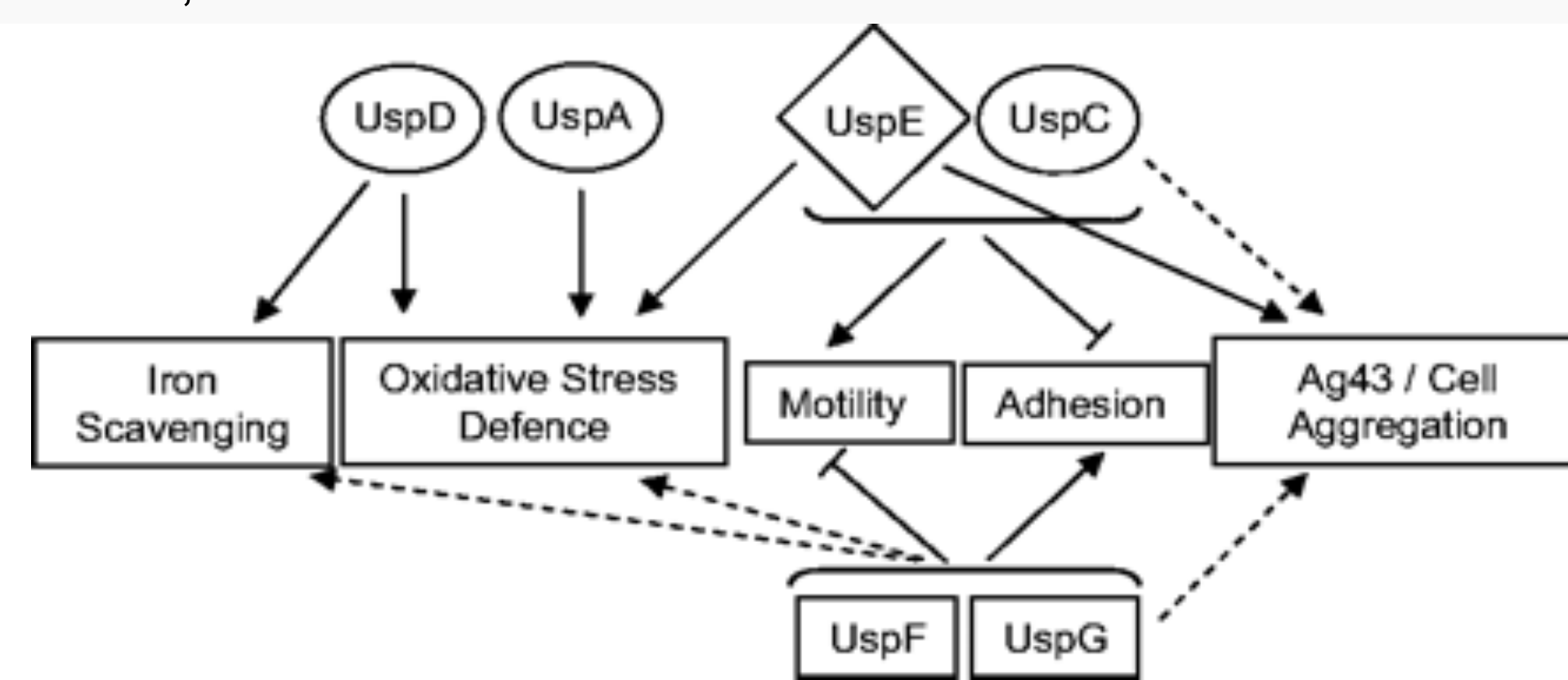
- Gene clustering properties have been used to predict gene functions based on annotation of its gene neighborhoods
- Conserved gene sets proximally arranged along the chromosome, are assumed to be dependent on each other and conserved neighbors with similar functions are preserved between several genomes
- In bacterial, gene order conservation is shaped by the relative importance of genes for cell survival and by interference from various environmental pressures imposed upon genome stability, affecting different genes and operons or putative operons

Stress Tolerant, Bioenergy-Relevant, *Rhodopseudomonas palustris*



Universal Stress Protein Domain

- The **UspA superfamily** encompasses an ancient and conserved group of proteins.
- E. coli* UspA is produced in response to environmental onslaughts: growth-arrested cells exhausted of nutrients, toxic agents, DNA damage, oxidative uncouplers, heat exposure, oxidants, metals, ethanol, and antibiotics

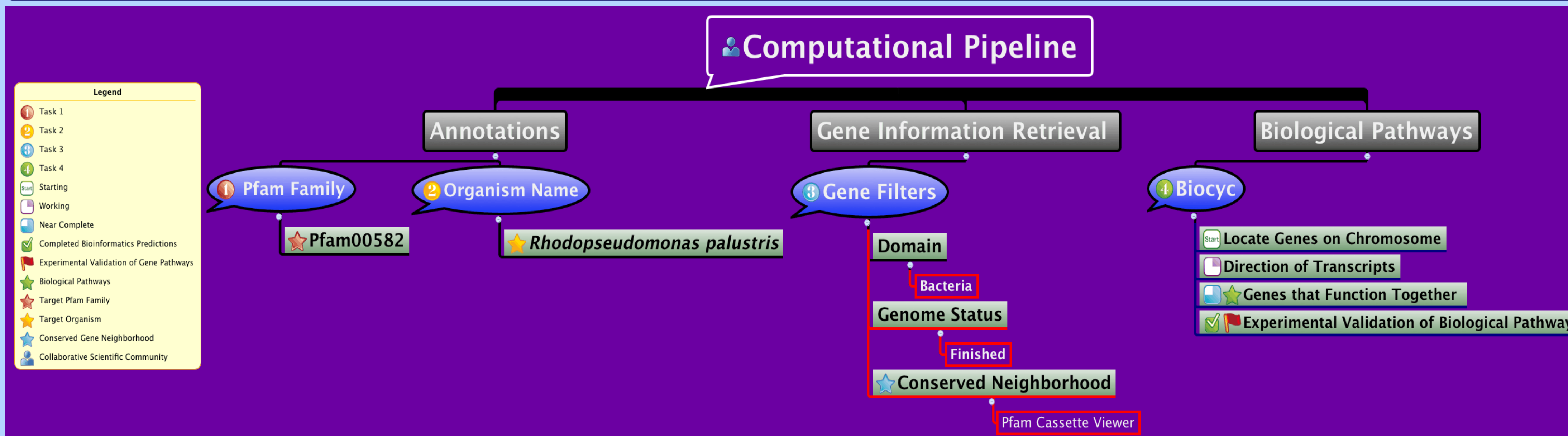


Nachin et al. 2005. PMID: 16159758

OBJECTIVE

To determine stress responsive pathways in finished genomes of *R. palustris* That contain genes that encode proteins with the Universal Stress Protein domain

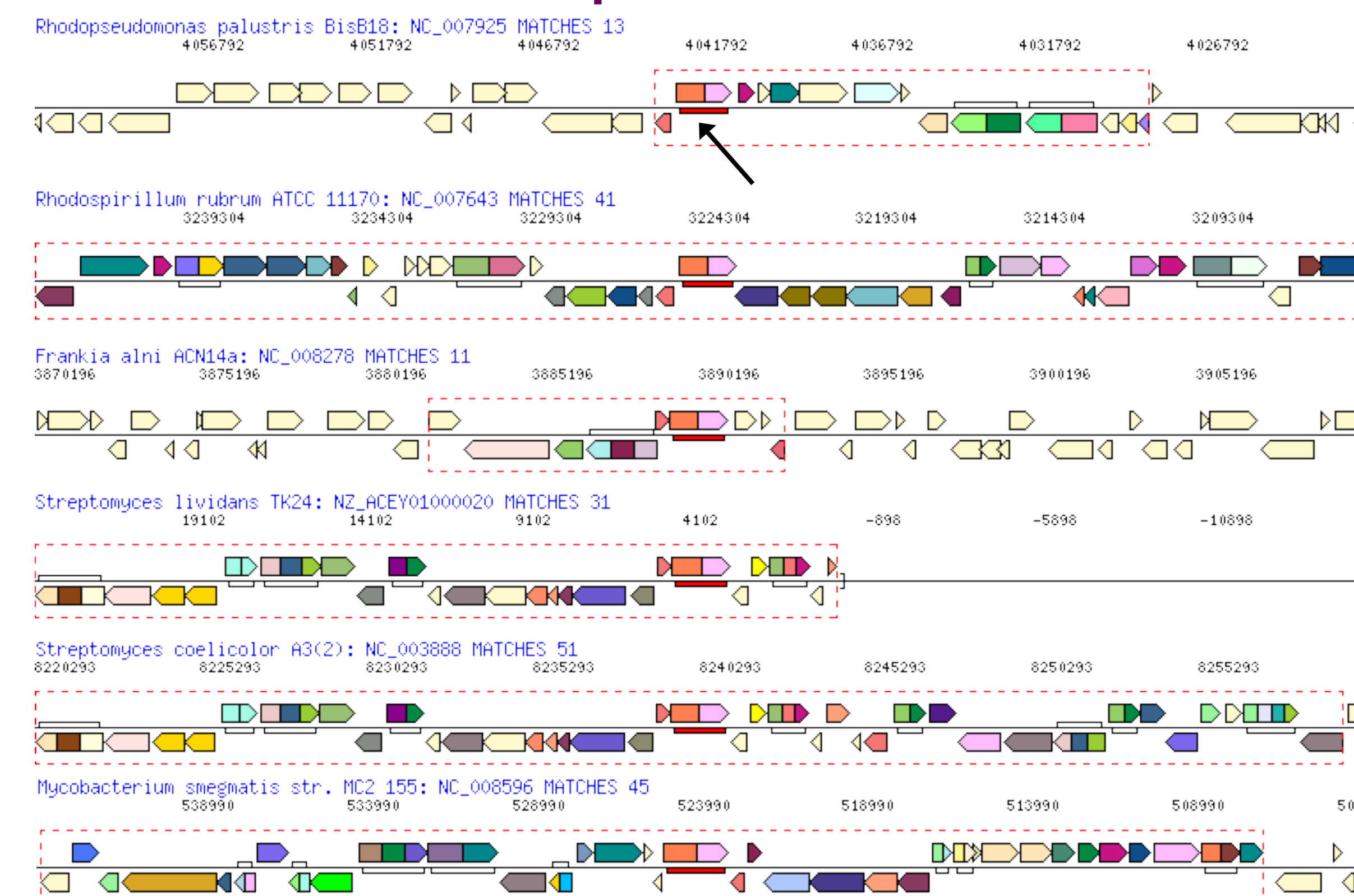
METHODS



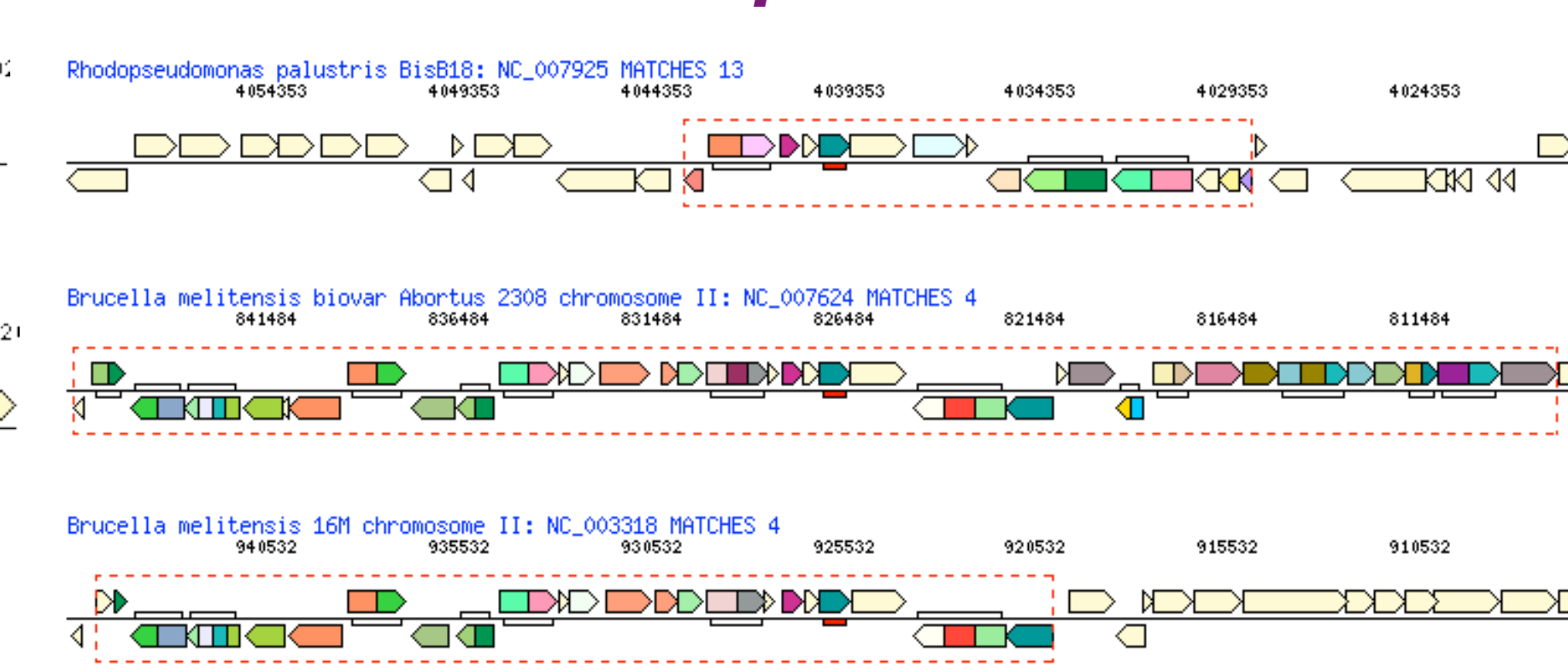
RESULTS

- Usp gene (RPC_3634 or UniProt Q210L7) encodes a 565 aa protein containing a USP domain fused to a carbohydrate transport Major Facilitator Superfamily (MFS_1) domain and is present only in the genome of BisB18
- A total of 5 additional microbial genomes contained the MSF-1 fused Usp domain
- Pfam functional annotation of the upstream gene cluster of RPC_3634 revealed genes encoding transporters of iron.
- Genes (RPC_3632, RPC_3631, and RPC_3630) were predicted to be in a transcription unit in the BioCyc database.

Chromosomal Cassette Reveals MSF-1 fused Usp in Select Genomes



Neighborhood of gene RPC_3634 of *R. palustris*



Chromosomal cassette of RPC_3631 to infer other genomes (*Brucella*) with gene cluster upstream RPC_3634

Pfam functional annotation of upstream adjacent genes in a BioCyc transcription unit

- RPC_3633 is iron (Fe²⁺) transport (PF10634)
- RPC_3631 is a Iron permease FTR1 family a high-affinity iron transporter (PF03239)
- RPC_3629 is a carbohydrate-selective porin, OprB family (PF04966)
- RPC_3628 had unknown function

CONCLUSION

- One Usp gene of 62 found in *R. palustris* finished genomes encodes a MSF-1 fused Usp, indicating a strain-specific universal stress protein for solute transport
- Pfam chromosomal cassette for the uniquely annotated *R. palustris* MSF-1 fused Usp gene contains 18 genes in the conserved neighborhood view with six genes upstream that are in the same transcription direction.
- Chromosomal context obtained from IMG reveals 5 microbial genomes with similar architecture to *R. palustris* MSF-1 fused Usp
- Five additional genes were in the same transcriptional direction as RPC_3634

DISCUSSION

- Chromosomal cassette alignment using RPC_3631 as gene of focus was performed to determine the other prokaryotes with the iron transport cluster.
- The cluster of 4 genes upstream of RPC_3634 was observed in genomes of *Brucella* species, where they exist as transcriptional units.

Future Studies:

- Determine the selective pressures that affect gene organization in various chromosomal regions

REFERENCES

- Nachin L, Nannmark U, Nyström T. 2005. Differential roles of the universal stress proteins of *Escherichia coli* in oxidative stress resistance, adhesion, and motility. *J Bacteriol.*18:6253-4.

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