

Pathogenicity and Host Range of soilborne fungi Associated with *Ammophila arenaria*

Haivan Ngo (University of California, Santa Cruz), Advisors: Ingrid Parker (University of California, Santa Cruz), Julie Beckstead (Gonzaga University).

Ammophila arenaria (European beachgrass) is currently invading coastal dune systems in California. A previous study found that the invasive success of *A. arenaria* is not explained by a release from pathogenic fungi, instead soilborne fungi increased seedling mortality and reduced plant biomass. This study investigated whether four fungal species, *Fusarium culmorum*, *F. oxysporum*, *Phytophthora sp.*, and an unidentified species in the Pleosporales that were isolated from the previous study were responsible for the disease symptoms. Two inoculation experiments of these fungi on seedlings of *A. arenaria* led to reduce biomass in comparison to controls. Moreover, the inoculated treatment showed a trend for shorter culm height and greater number of dead leaves. These results suggest that the four fungi tested contribute to the measured reduction in *A. arenaria* growth, providing further evidence that its invasive success is not attributed to a release from pathogenic fungi. A survey of fungal incidence in ten co-occurring host species showed that the host range of these fungi spans beyond *A. arenaria*. Host range of the four soilborne fungi associated with *A. arenaria* was explored via inoculation experiments on three co-occurring plant species, *Cakile maritima*, *Camissonia cheiranthifolia*, and *Chorizanthe pungens var. pungens*. Fungal inoculation experiments on co-occurring species resulted in reduced biomass in comparison to controls, indicating that these species have a wide host range and therefore can be considered as generalist pathogens on the plant communities at Sunset State Park. Furthermore, the results from this study suggest that although invasive species may escape specialist enemies from home range, it may not escape generalist enemies that have a broad range. Secondly, escaping specialist and generalist enemies does not mean that the species cannot acquire new generalist enemies in home range.

Prediction of Metabolite Binding Sites in Bacterial mRNA

Vlad Codrea (University of Texas at Austin), Advisors: Andrew D. Ellington (University of Texas at Austin), Jay Hesselberth (University of Texas at Austin).

There is a pressing need to use bacteria to create medically important products and to stop pathogenic bacteria from producing toxic proteins and metabolites. Manipulation of gene expression can address both of these objectives, and can be achieved by identifying the regulatory pathways.

Riboswitches, the recently discovered highly conserved regulatory intergenic regions of some mRNA genes, serve to down regulate the production of metabolites by directly binding to those metabolites. This computational comparative genomics algorithm, which was implemented using the Python programming language and MySQL relational databases, generalizes the search for riboswitches by determining the type and extent of co-conservation of intergenic regions with their neighboring genes. Gene/intergenic-region pairs were isolated from *Escherichia coli* K12, *Bacillus subtilis*, and *Pseudomonas aeruginosa*, and identified in the other sequenced bacterial genomes. The pair's co-conservation could be the manifestation of a functional, regulatory relationship.

The relative position of the gene to the intergenic region was conserved in 98.6% of pairs derived from *E. coli*, 62.7% from *P. aeruginosa* and 69.4% from *B. subtilis*. 64.1% of target intergenic regions derived from *E. coli* did not overlap a gene, compared to 48.9% from *P. aeruginosa* and 71.4% from *B. subtilis*. The positive control riboswitches, *thiC*, *thiM*, and *btuB*, were significant matches in *E. coli*.

This novel algorithm may locate possible drug targets in bacterial genomes that can be jammed with antisense RNA or designer organic molecules mimicking natural metabolites. Resultant drugs may be effective without disrupting translation and metabolism in higher organisms.