

# Journal of the Mississippi Academy of Sciences

Volume 62

January 2017

Number 1



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*The Journal of the Mississippi Academy of Sciences* (ISSN 0076-9436) is published in January (annual meeting abstracts), April, July, and October, by the Mississippi Academy of Sciences. Members of the Academy receive the journal as part of their regular (non-student) membership. Inquiries regarding subscriptions, availability of back issues, and address changes should be addressed to The Mississippi Academy of Sciences, Post Office Box 55709, Jackson, MS 39296-5709, telephone 601-977-0627, or email [msacademyofscience@comcast.net](mailto:msacademyofscience@comcast.net).

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unknown. We addressed this gap by conducting the 16S rDNA-based profiling of microbial communities from the rhizosphere of wheat grown in adjacent irrigated and non-irrigated field plots. Results of these experiments revealed that irrigation and plant monoculture lead to strong shifts in the composition of rhizobacterial communities. Among taxa with differential response to soil moisture were fluorescent pseudomonads that produce bioactive metabolites and protect wheat from soilborne fungal pathogens. We sequenced genomes of several *Pseudomonas* strains and screened them for pathways involved in water stress response. We also produced and analyzed plant root exudates and demonstrated that they contain diverse types of osmoprotectants. The amendment of culture medium with the sterile root exudates markedly improved growth of pseudomonads under conditions of water stress. Our findings suggest that rhizodeposition strongly modulates bacterial pathways involved in the mitigation of water stress and contributes to the selection of specific types of beneficial rhizobacteria in arid soils. Understanding how plants and rhizosphere bacteria respond under water stress will help to predict how climate change in the 21st century could impact the rhizosphere microbiome that contributes to the productivity of agroecosystems worldwide.

### **EVOLUTION OF THE GENOMES OF THE *COXIELLA*-LIKE ENDOSYMBIONTS OF TICKS**

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**Introduction:** Ticks transmit the second largest number of vector-borne pathogenic bacteria causing disease in humans and vertebrates. Many studies suggest that many ticks harbor and are obligately dependent on *Coxiella*-like endosymbionts (CLEs) that are closely related, but genetically distinct from the pathogen *Coxiella burnetii*, which causes Q fever in human and domestic ruminants. Understanding the interactions between arthropod hosts and these abundant endosymbionts is crucial for developing novel symbiont-based control measures for ticks and the pathogens they vectors. We assembled two CLE genome sequences from metagenomes of individual *Rhipicephalus sanguineus* (Rs) from Oklahoma (OK) and *Amblyomma americanum* from Georgia (AaGA) and bioinformatically compared them with two recent CLE assemblies from pooled tick DNAs (*R. turanicus* (Israel) Rt; AaOK).

**Methods:** The CLE-AaGA genome (CLC Genomics Workbench) was assembled from sequences from a 100 bp library obtained on an Illumina HiSeq. A partial CLE-Rs genome was assembled (Geneious) from sequences from a 200 bp library using Ultra REPLI-g amplified DNA on an Ion Torrent Personal Genome machine with an Ion 318 chip. Extensive bioinformatics approaches were employed to determine i) the phylogenetic relationships and the level of genome reduction in CLEs, ii) most affected functional categories of proteins encoded by the four CLE genomes, and iii) the genes involved in amino acid biosynthetic pathways.

**Results:** CLEs from AaGA and AaOK were quite similar but not identical. Phylogenetic and network analyses showed Rs-CLE and Rt-CLE clustered differently from AaGa/AaOK, suggesting CLE and *C. burnetii* are distantly evolutionarily related and thus probably derived from an ancient ancestor. The Rt (1.73 Mb, 38.2 % G+C), Rs (1.2 Mb, 38.0% G+C), and AaGA/AaOK (657 Kb, 34.6% G+C) CLE genomes are significantly reduced compared to the genomes of *C. burnetii* isolates (1.95-2.21 Mb, 42.3-42.8 % G+C). No plasmids or IS1111 sequences were found in the CLEs. The proteomes of each agent were annotated using BLAST-KOALA into 18 categories and pathways with KAAS and while the distribution of proteins CLE-Rt, CLE-Rs was different from that of CLE-AaGA/AaOK, *C. burnetii* had many more functional proteins. The CLE proteomes retained some major amino acid biosynthetic pathways. CLE appears to provide both essential amino acids and vitamins to its host but CLE-AaGA/AaOK appears to be more highly adapted than CLE-Rs or CLE-Rt to its tick host since it has undergone a much higher loss of functional proteins.

**Conclusion:** The loss of protein encoding genes in CLE genomes may contribute to their greater fitness in ticks. Small differences in closely related CLE proteomes may help identify those genes that are least critical to the endosymbiotic interaction. CLE-Rs and CLE-Rt may still be cultivable but this seems unlikely for the CLE-Aa given its advanced genome reduction compared to *C. burnetii*. It seems unlikely that horizontal exchange of CLE between ticks has contributed significantly to their evolution as current information suggests they are highly host-specific.

**Acknowledgements:** Drs. Ramaiah and Williams-Newkirk were both Bioinformatics Postdoctoral Fellows of the Association of Public Health Laboratories when they performed this work. The findings and conclusions in this report are those of the authors and do not necessarily represent the official position of the Centers for Disease Control and Prevention.