

# Microbial Genomics & Bioprocessing Research

---

## Alejandro P. Rooney

Microbiologist

**Ph.D. Genetics, Texas A&M University**  
**B.S. Biology, University of Cincinnati**

Microbial Genomics and Bioprocessing Research Unit  
National Center for Agricultural Utilization Research  
United States Department of Agriculture  
Peoria, IL 61604-3999

Tel: (309)-681-6395

Fax: (309)-681-6672

E-mail: [rooney@ncaur.usda.gov](mailto:rooney@ncaur.usda.gov)

---

## Research

The goal of my research is to characterize the mechanisms and processes that shape genome structure, function, and evolution in agriculturally important organisms.

### Evolutionary Genomics

An understanding of how multigene families evolve and diversify is crucial for understanding the processes that underlie genome evolution. Current and past research in my laboratory shows that many multigene families undergo differential rates of gene duplication and loss, resulting in some genes being maintained in the genome for long evolutionary time periods while others exist for relatively short periods. This pattern has been termed "birth-and-death evolution". We are currently investigating the extent to which multigene families in a variety of eukaryotic and prokaryotic genomes undergo birth-and-death evolution. Two recent studies published from our laboratory (Rooney 2004; Rooney and Ward 2005) show that ribosomal RNA genes can undergo birth-and-death evolution, which is surprising because most researchers consider ribosomal RNA to be a paradigm of concerted evolution. Moreover, in our study on fungal 5S ribosomal RNA genes (Rooney and Ward 2005) we also found that these genes undergo a mechanism of amplification that bears striking similarity to retrotransposition. Interestingly, this mechanism appears to operate in the genomes of certain plant pathogenic fungi that are supposedly devoid of or immune to the propagation of mobile genetic elements. We are also interested in understanding how birth-and-death evolution can give rise to novel genetic systems and complex phenotypic traits. One example concerns the evolution of chemical communication systems. These systems are used in bacteria and insects for a variety of purposes. In my laboratory, we are especially interested in sex pheromones. Over the course of our long-term collaboration with

Dr. Wendell Roelofs at Cornell University, we have found that the sex pheromone desaturase multigene family of moths and flies evolves under a birth-and-death process (Roelofs and Rooney 2003; Liu et al. 2004). This provides an explanation for our discovery of sex pheromone desaturase gene nonfunctionalization as a mechanism for speciation in moths of the genus *Ostrinia* (Roelofs et al. 2002). We have recently begun studies on the sex pheromone systems of bacteria that are important public health and food safety pathogens.

### **Microbial Population Genetics, Molecular Ecology, and Biogeography**

Most studies in the field of population genetics are concerned with patterns at the level of the individual gene or among a few genes. The goal of our research in this area is to understand how genetic polymorphism arises and is maintained across the entire genome in natural populations of bacteria. We are particularly interested in understanding the causes underlying the fluctuation of genetic variability between different regions of the genome in bacterial pathogens. Of special interest to us are genes that are involved in virulence and toxin production. The major emphasis of our research in this area concerns members of the genera *Clostridium* and *Bacillus* that are important in the areas of food safety and biosecurity. We are also interested in the development of new methods for identifying and monitoring microbes. While some microorganisms are highly clonal, others possess a tremendous amount of genetic diversity, especially those that are cosmopolitan and found on every continent. These widespread species are not only important for the study of microbial evolution but for application to forensic microbiology. We recently completed a study in collaboration with the United States Army on the identification of bacteria present in cigarettes associated with an outbreak of acute eosinophilic pneumonia among military servicemen deployed in Southwest Asia during Operation Iraqi Freedom (Rooney et al. 2005). Finally, we also study the molecular ecology of extremophiles, which are unusual microorganisms that live in conditions that are inhospitable to most other forms of life, such as thermal hot springs, volcanic fields, and hyperalkaline lakes. Our studies are geared towards characterizing the microbial community composition of these unique environments and identifying the unique molecular adaptations that allow extremophiles survive in them.

---

## **Selected Publications**

**A. P. Rooney** and T. J. Ward. 2005. Evolution of a large ribosomal RNA multigene family in filamentous fungi: Birth and death of a concerted evolution paradigm. *Proceedings of the National Academy of Sciences of the USA* 102:5084-5089.

**A. P. Rooney**, J. L. Swezey, D. T. Wicklow, and M. J. McAtee. 2005. Bacterial species diversity in cigarettes linked to an investigation of severe pneumonitis in U.S. military personnel deployed in Operation Iraqi Freedom. *Current Microbiology* in press.

**A. P. Rooney**. 2004. Mechanisms underlying the evolution and maintenance of functionally heterogeneous 18S rRNA genes in apicomplexans. *Molecular Biology and Evolution* 21:1704-1711.

C. M. Seabury, R. L. Honeycutt, **A. P. Rooney**, N. D. Halbert, and J. N. Derr. 2004. Novel Prion Protein Gene (PRNP) Variants and Evidence for Strong Purifying Selection in Functionally Important Regions of Bovine Exon 3. *Proceedings of the National Academy of Sciences of the USA* 101:15142-15147.

W. Liu, **A. P. Rooney**, B. Xue B, and W. L. Roelofs. 2004. Desaturases from the spotted fireworm moth (*Choristoneura parallela*) shed light on the evolutionary origins of novel moth sex pheromone desaturases. *Gene* 342:303-311.

**A. P. Rooney**. 2003. Selection for highly biased amino acid frequency in the TolA cell envelope protein of proteobacteria. *Journal of Molecular Evolution* 57: 731-736.

W. L. Roelofs and **A. P. Rooney**. 2003. Molecular genetics and evolution of pheromone biosynthesis in Lepidoptera. *Proceedings of the National Academy of Sciences of the USA* 100:9179-9184.

**A. P. Rooney**, H. Piontkivska, and M. Nei. 2002. Molecular evolution of the histone 3 multigene family. *Molecular Biology and Evolution* 19:68-75.

W. L. Roelofs, W. Liu, G. Hao, H. Jiao, **A. P. Rooney**, and C. E. Linn, Jr. 2002. Evolution of moth sex pheromones via ancestral genes. *Proceedings of the National Academy of Sciences of the USA* 99:13621-13626.

C. E. Patterson, J. Gao, **A. P. Rooney**, and E. C. Davis. 2002. Genomic organization of mouse and human 65 kDa FK506-binding protein genes and evolution of the FKBP multigene family. *Genomics* 79:881-889.

**A. P. Rooney**, J. Zhang, and M. Nei. 2000. An unusual form of purifying selection in a sperm protein. *Molecular Biology and Evolution*. 17:278-283.

K. Takahashi, **A. P. Rooney**, and M. Nei. 2000. Origins and divergence times of mammalian class II MHC gene clusters. *Journal of Heredity* 91:198-204.

**A. P. Rooney**, J. Zhang, and M. Nei. 1999. Rapid evolution of a primate sperm protein: relaxation of functional constraint or positive selection? *Molecular Biology and Evolution* 16:706-710.

M. Nikaïdo, **A. P. Rooney**, and N. Okada. 1999. Phylogenetic relationships among cetartiodactyls based on insertions of short and long interspersed elements: Hippopotamuses are the closest extant relatives of whales. *Proceedings of the National Academy of Sciences of the USA* 96:10261-10266.

*Last Revised: March 25, 2005*