

" male *Encarsia* that took longer to develop expressed much stronger CI than their faster-developing brothers.

Abstract Category

16 Microbial Symbioses

**PS.16.046 ADAPTIVE EVOLUTION VIA SYMBIOSIS: RAPID SPREAD OF A DEFENSIVE SYMBIONT IN *DROSOPHILA***

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There is a growing awareness that many organisms harbor microbial symbionts that provide protection against natural enemies. We have identified a novel defensive symbiosis in the mycophagous fly *Drosophila neotestacea*, and show that this is its primary mode of defense against a virulent nematode parasite. We show that *D. neotestacea* harbors an inherited *Spiroplasma* symbiont that protects it against the sterilizing effects of the parasitic nematode, *Howardula aoronymphium*, both in the lab and in the wild. Flies are parasitized at high frequencies in nature, and until recently, almost all infections resulted in complete sterility. While the mechanism of resistance to sterility is not yet known, nematodes in *Spiroplasma*-positive flies are half as small as in *Spiroplasma*-negative ones. This is the first reported case of natural symbiont-mediated defense against nematodes, which are among the most diverse and widespread macroparasites known. This is also the first report of *Spiroplasma* acting as a mutualist. Although *Spiroplasma* are widespread invertebrate symbionts, their role is mostly unknown. *Spiroplasma* infections appear to be spreading rapidly in *D. neotestacea*. Almost all infected flies collected in New York in the 80s were sterile, suggesting that *Spiroplasma* infection was rare or absent. To confirm this, a sample of museum-preserved specimens was screened for *Spiroplasma* and was shown to be uninfected. There is a dramatic continent-wide cline for *Spiroplasma*, with infections at high frequency in eastern N. America but absent in British Columbia. We are actively monitoring infection spread across the Rocky Mountains. Finally, sequencing of mitochondrial haplotypes in infected and uninfected flies is also consistent with spread. This study demonstrates the profound and potentially rapid effects of defensive symbionts, which are increasingly recognized as major players in the ecology of species interactions.

Abstract Category

16 Microbial Symbioses

**PS.16.047 FROM SPONTANEOUS TO INOCULANT SYMBIOTIC NODULATION OF LEGUME TREES: THE EXAMPLE OF *ACACIA MANGIUM***

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*Acacia mangium* is a legume tree native of Australasia. It has been introduced in many tropical countries especially in the context of industrial plantations. It has the exceptional capacity to establish symbioses with three types of microorganisms: nitrogen-fixing bacteria, arbuscular and ecto-mycorrhizal fungi, enabling a great productivity and adaptability. In this context, many field trials were established to test the effects of controlled inoculation with selected symbiotic bacteria versus natural colonization with indigenous strains. In introduction areas, *A. mangium* spontaneously nodulate with local and often ineffective bacteria. When inoculated, the persistence of inoculants, their impact on local biodiversity and possible genetic recombination with local strains have to be explored. The aim of this study was to describe the genetic diversity of bacteria spontaneously nodulating *A. mangium* in Brazil and to evaluate, by molecular tracing, the durability of selected strains used as inoculants. Three different sites, several hundred kilometres distant, were studied, each with inoculated and non inoculated plots. About one hundred strains were isolated and sequenced on three housekeeping (*glnB*, *dnaK* and *recA*) and one symbiotic (*nodA*) genes. We showed that, whatever the site and the treatment, *A. mangium* is nodulated by bacteria of the genera *Bradyrhizobium* and *Mesorhizobium*. We observed a significant genetic differentiation not only among the three sites, but also between inoculated and non-inoculated plots in each site. The two inoculated strains were never detected, even few months after inoculation, be they in nursery or in plantation, raising the question of the usefulness of such artificial inoculation. At last, *Mesorhizobium* strains, display a genetic diversity within the housekeeping genes, shared exactly the same symbiotic sequence gene, opening the door to the possible transfer of the symbiotic island from unknown symbiotic strain.

Abstract Category

16 Microbial Symbioses

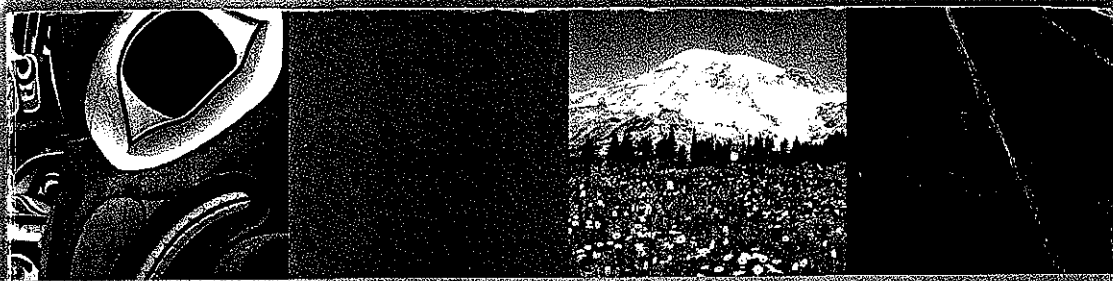
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**PS.16.048** TEMPORAL ANALYSIS OF DIVERSITY AMONG SYMBIOTIC  
VI 0 FISCHER STRAINS

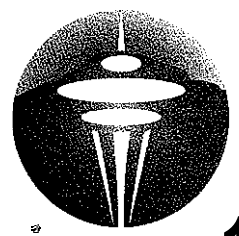
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The symbiotic association between the bacterial species *Vibrio fischeri* and its squid host, *Euprymna tasmanica* (Mollusca: Cephalopoda), is a well-known and extensively studied example of mutualistic symbiosis. Both squid are benthic organisms found in shallow waters throughout the world. Several *V. fischeri* strains inhabit these waters before many environmentally infect the light organ of their squid host during the first stage of the symbiotic life cycle. Previous studies have analyzed bacterial diversity found within *Euprymna* light organs on a geographical scale, but few, if any, have observed diversity on a temporal scale. This study aims at determining the diversity of *V. fischeri* strains by creating a haplotype network from sequencing multiple individuals on a yearly basis from a single population of *Euprymna-Vibrio* pairs. We primarily focused on the variation



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