HIGHLIGHTS

HIGHLIGHT ADVISORS

ADRIANO AGUZZI

UNIVERSITY HOSPITAL OF ZÜRICH, ZÜRICH, SWITZERLAND

NORMA ANDREWS

YALE UNIVERSITY SCHOOL OF MEDICINE, NEW HAVEN, CT, USA

ARTURO CASADEVALL

THE ALBERT EINSTEIN COLLEGE OF MEDICINE, BRONX, NY, USA

RITA COLWELL

UNIVERSITY OF MARYLAND BIOTECHNOLOGY INSTITUTE, BALTIMORE, MD, USA

STANLEY FALKOW

STANFORD UNIVERSITY SCHOOL OF MEDICINE, STANFORD, CA, USA

TIMOTHY FOSTER

TRINITY COLLEGE, DUBLIN, IRELAND

KEITH GULL

UNIVERSITY OF OXFORD, OXFORD, UK

NEIL GOW

UNIVERSITY OF ABERDEEN, ABERDEEN, UK

HANS-DIETER KLENK

PHILIPPS UNIVERSITY, MARBURG, GERMANY

BERNARD MOSS

NIAID, NATIONAL INSTITUTES OF HEALTH, BETHESDA, MD, USA

JOHN REX

ASTRAZENECA, CHESHIRE, UK

DAVID ROOS

UNIVERSITY OF PENNSYLVANIA, PHILADELPHIA, PA, USA

PHILIPPE SANSONETTI INSTITUT PASTEUR, PARIS, FRANCE

CHIHIRO SASAKAWA UNIVERSITY OF TOKYO, TOKYO, JAPAN

ROBIN WEISS

UNIVERSITY COLLEGE LONDON, LONDON, UK

ENVIRONMENTAL MICROBIOLOGY

Diet and diversity

A new study in *Applied and Environmental Microbiology* has provided an inventory of the bacteria that populate the gypsy moth midgut, an alkaline environment. The composition of the simple bacterial community that was found largely depends on the diet of the larval moth.

The midgut of the gypsy moth is typically pH 8-10, but can reach pH 12, making this an excellent model for investigating how bacterial inhabitants cope with alkaline conditions. Microbial communities that thrive in acidic conditions have been documented in environments including the human stomach or hot springs, but communities that can contend with alkaline environments are less understood. Culturing, PCR and terminal restriction fragment length polymorphism (T-RFLP) were combined in this study to analyse the moth's bacterial community.

Broderick and colleagues analysed the microbial community in the guts of individual gypsy moth larvae hatched in sterile conditions and fed an artificial diet, from eggs that either originated from a culture collection, or were collected from field sites. PCR and T-RFLP revealed that the microbial composition was surprisingly consistent and wasn't dependent on the egg source.

Several new bacterial phylotypes were identified, but the overall diversity, which ranged from 7–15 phylotypes, was low compared with the human intestine — at least 500 phylotypes — and the termite gut — at least 50 phylotypes. Not surprisingly, new phylotypes were found by culture-independent methods, but more surprisingly, culturing also yielded new phylotypes, some of which were only distantly related to known bacterial species.

By analysing the guts of larvae hatched from one type of egg but fed different diets, the authors found that diet had a big effect on bacterial diversity in the moth gut. However, regardless of the food eaten, *Enterococcus faecalis* and an uncultured *Enterobacter* species were always resident in the moth gut. *E. faecalis* isolates were physiologically quite different from clinical isolates — this species might be more diverse than previously suspected.

Few studies have addressed the relationships of microbial symbionts

with moths and butterflies, one of the largest insect orders. Where the gut bacterial inoculum comes from, how the bacterial community copes with alkaline conditions, and whether the bacterial symbionts contribute to insect physiology and development are all good questions. By using this model system, combined with metagenomics, researchers can now try and link the community structure in the insect gut to community function. Susan lones

() References and links

ORIGINAL RESEARCH PAPER Broderick, N. A. et al. Census of the bacterial community of the gypsy moth larval midgut by using culturing and culture-independent methods. *Appl. Environ. Microbiol.* **70**, 283–300 (2004) WEB SITES

Jo Handelsman's laboratory:

http://www.plantpath.wisc.edu/fac/joh.htm Kenneth F. Raffa's laboratory: http://entomology.wisc.edu/%7Eraffa

