

IN BRIEF

BACTERIAL PHYSIOLOGY***Bacillus* sporulation goes interactive**

Publishing in *Nucleic Acids Research*, Eijlander and colleagues present a database that aims to provide an interactive guide to the sporulation cycle of *Bacillus subtilis*, from the vegetative state through to germination and outgrowth. The database, known as Sporeweb (<http://sporeweb.molgenrug.nl>), provides a bird's eye overview of each of the key developmental stages and their regulatory networks. For each stage, the key regulators and the genes that they control are linked to further information pages within the accompanying Sporeweb database or SubtiWiki (<http://subtiwiki.uni-goettingen.de>; the latest release of which was also recently described in *Nucleic Acids Research*). In addition, the relevant gene regulatory networks can be visualized using Cytoscape, and these visualizations can be individually tailored to include a specific subset of genes of interest.

ORIGINAL RESEARCH PAPERS Eijlander, R. T. *et al.* SporeWeb: an interactive journey through the complete sporulation cycle of *Bacillus subtilis*. *Nucl. Acids Res.* <http://dx.doi.org/10.1093/nar/gkt1007> (2013) | Michna, R. H. *et al.* SubtiWiki — a database for the model organism *Bacillus subtilis* that links pathway, interaction and expression information. *Nucl. Acids Res.* <http://dx.doi.org/10.1093/nar/gkt1002> (2013)

MICROBIOME**Revealing deficiencies**

To assess the impact of the cutaneous immune response on the structure and composition of the skin microbiome, Oh *et al.* examined the skin microbiomes in patients with three rare monogenic primary immunodeficiencies (PIDs). Although these diseases have different extracutaneous clinical manifestations, they are all associated with atopic dermatitis (AD)-like eczema. Using 16S rRNA sequencing, the authors compared the bacterial microbiomes that were present at four different skin sites in 41 patients with PID with those that were present in patients with classical AD who were undergoing treatment and healthy controls. The PIDs were associated with increased permissivity to colonization and altered community diversity, along with decreased site specificity and longitudinal stability. Patients with PID often develop fungal infections, and internal transcribed spacer region 1 (ITS1) sequencing of a subset of these patients showed an increased abundance of *Aspergillus* and *Candida* spp. compared with controls, leading the authors to suggest that the skin may function as a reservoir for recurrent fungal infections.

ORIGINAL RESEARCH PAPER Oh, J. *et al.* The altered landscape of the human skin microbiome in patients with primary immunodeficiencies. *Genome Res.* <http://dx.doi.org/10.1101/gr.159467.113> (2013)

BACTERIAL PHYSIOLOGY**HD-GYP domain structure solved**

The second messenger cyclic di-GMP, which is involved in many different aspects of bacterial physiology and development, is synthesized by GGDEF-domain diguanylate cyclases (DGCs) and degraded by EAL- or HD-GYP-domain phosphodiesterases (PDEs). Although the DGCs and EAL PDEs have been intensively investigated, much less is known about the HD-GYP PDEs. Bellini *et al.* now describe the crystal structures of a catalytically active HD-GYP domain protein alone and in complex with its cyclic di-GMP substrate and the final reaction product, GMP. The structures show that the mode of substrate binding differs from that of the EAL PDEs and involves a novel trinuclear, rather than a binuclear, catalytic iron centre.

ORIGINAL RESEARCH PAPER Bellini, D. *et al.* Crystal structure of an HD-GYP domain cyclic-di-GMP phosphodiesterase reveals an enzyme with a novel trinuclear catalytic iron centre. *Mol. Microbiol.* <http://dx.doi.org/10.1111/mmi.12447> (2013)