Actinobacterial Activities

A recent meeting of the Society for Applied Microbiology highlighted organisms involved in potato scabs, nitrogen fixation and desert-based alchemy

Bernard Dixon

Had a local journalist, seeking material for a sensational article, dropped into the summer meeting of the Society for Applied Microbiology (SfAM), held this year in Cardiff, Wales, he or she might have spotted one particularly promising source. It was a poster entitled “Potentially zoonotic viruses circulating in wildlife in China,” written by Guangjian Zhu of East China Normal University in Shanghai with other colleagues in China and in the United States and United Kingdom.

Even without journalistic embellishment, the report was of considerable interest. It summarized the results of tests on swabs and blood samples from over 2,000 mammalian species, including bamboo rats, masked palm civets, and Malayan porcupines, caught in the wild or acquired from markets. The main findings, confirmed by sequencing, were an approximately 10% prevalence of astroviruses, and a high incidence of SARS-like coronaviruses in Chinese horseshoe rats. Most of the coronavirus positives showed 90–98% homology with various bat coronaviruses.

If the same journalist had needed enticement to listen to a scientific lecture (a rare scenario these days), he or she might have attended one of four remarkably cogent yet entertaining talks by students at the SfAM meeting. Given by Suzy Moody of Swansea University, Wales, it highlighted what she called “a model organism, and a bit of a show-off.” Accompanied by conversational asides (“and that set me thinking . . . I struck lucky . . . something was definitely going on . . . ”) which in no way detracted from the scientific importance of her talk, Moody described her efforts to identify the in vivo role of albaflavenone, a sesquiterpene antibiotic synthesized by Streptomyces coelicolor.

“We found that a disruption mutant incapable of producing albaflavenone had a specific phenotype when grown under osmotic stress, being unable to generate the pigmented antibiotics for which S. coelicolor is renowned,” Moody said. “Our aim was to find out how albaflavenone mediated this alteration in phenotype.” She and her coworkers used antibiotic assays to quantify the change in pigmented antibiotic production, and qRT-PCR to determine the specific regulators affected by albaflavenone. Bioinformatic analysis and modelling identified a possible araC family transcriptional regulator (AFTR) to which the albaflavenone is a ligand.

Moody and her collaborators next constructed a disruption mutant of the AFTR. Further antibiotic assays indicated that the AFTR-albaflavenone partnership is an important regulatory system for the formation of pigmented antibiotics. “Our work provides evidence that albaflavenone is a novel bacterial hormone,” Moody concluded. “The phenotype, assays and qRT-PCR data all point to a new signalling role for this antibiotic.”

Actinobacteria were one of the principal themes of the Cardiff meeting, not least for the potential of those found in extreme environments as sources of new drugs. While some would question the assertion by Michael Goodfellow of Newcastle University that “it is rarely acknowledged that bacteria are the dominant forms of life on Earth,” most would support his enthusiasm for studying and indeed harnessing actinobacteria living in places such as the Atacama Desert in northern Chile, where he has worked in recent years.

“Actinobacteria have an unrivalled capacity to synthesize a wide spectrum of bioactive compounds, and it is now becoming apparent that taxonomically novel isolates need to be screened in drug discovery programs if we are to avoid the costly rediscovery of known chemical entities,” Mike said. “Research on isolates from the Atacama Desert, the oldest and driest desert in the
world, has led to the recognition of innumerable novel actinobacterial species, including some belonging to so-called rare genera. This work not only emphasizes the importance of establishing cultural actinobacterial diversity in extreme habitats. It also paves the way for the selection of candidate strains for genome mining and systems/synthetic biology."

One of Goodfellow’s collaborators, Gilles van Wezel of Leiden University in the Netherlands, described a new way of classifying actinomycetes—one that addresses a limitation in current approaches. With large whole-genome bacterial data sets being generated apace these days, rapid and accurate molecular taxonomy is increasingly important. The existing method, based on the sequence divergence of 16S ribosomal RNA, reveals differences that are too small to allow accurate discrimination between strains. The new technique developed by van Wezel is based on what he called the “extraordinary” conservation of SsgA and SsgB proteins.

“SsgA-like proteins are developmental regulators, which streptomycetes require for septum-specific cell division during sporulation-specific cell division,” van Wezel explained. “The almost specific cell division during sporulation-specific targets cellulose biosynthesis. Although this has revealed differences that are too small to allow accurate discrimination between strains. The new technique developed by van Wezel is based on what he called the “extraordinary” conservation of SsgA and SsgB proteins.

The data obtained in Leiden clearly validate Kitasatospora as a sister genus to Streptomyces in the family Streptomycesae and indicate that Micromonospora, Salinospora, and Verrucosispara represent different clades of the same genus. The amino acid sequence of SsgA is an accurate determinant of the ability of streptomycetes to make submerged spores.

Introducing a subsequent speaker, Martha Trujillo of the Universidad de Salamanca, Spain, Goodfellow commented that even five years ago we would not have believed anyone who said that Micromonospora was involved in nitrogen fixation. Yet here we were, hearing that species of this actinobacterium were normal inhabitants of the root nodules formed in legumes and actinorhizal plants as a result of symbioses established with rhizobia and Frankia respectively. Moreover, most of these actinobacterial populations represent newly recognized species.

“Recent studies suggest that Micromonospora is a growth-promoting bacterium, interacting with rhizobia or Frankia in a tripartite process.” Trujillo said. “Other work indicates that Micromonospora, co-inoculated with rhizobia or Frankia, can promote both nodulation and plant growth. Reinfection experiments not only show that Micromonospora induces nodules but also suggest that a rhizobial organism is necessary for it to penetrate the tissues. It is still too early, however, to explain the exact role which Micromonospora plays inside root nodules or how it penetrates.”

Trujillo and colleagues have very recently determined the genome sequence of Micromonospora lupini strain Lupac 08 from lupine nodules. Their genomic information points to a large number of putative genes coding for hydrolytic enzymes, which may be involved in the process of infection—as suggested for other microorganisms living symbiotically with plants.

This was by no means the only actinobacterial advance reported at the SfAM conference, which in turn raises new questions about their activities. Dawn Bignell of Memorial University, St John’s, Newfoundland, Canada, discussed her work on Streptomyces species that cause scab disease on economically important root and tuber crops such as potatoes, carrots, radishes and beet. The main known virulence determinant made by S. scabies and its relatives is thaxtomin A, which targets cellulose biosynthesis. Although this has prompted suggestions that its suppression might be harnessed to prevent scabs, Bignell and others have found that some of the pathogens work in other ways.

The St John’s group recovered strains of Streptomyces from scab lesions on infected potatoes, and used plant bioassays to determine the virulence phenotype of each isolate. Morphological characterization plus 16S rDNA sequencing then identified pathogenic isolates, while a combination of genetic and chemical approaches showed the capacity of each strain to produce thaxtomin A. The results clearly demonstrated that some pathogenic streptomycetes do not generate this secondary metabolite but use other virulence factors when infecting hosts and causing disease.

One aspect of the otherwise excellent SfAM conference was less appealing—mobile phones not only ringing during presentations but being answered, leaving people seated nearby to hear one half of a heated conversation. Is such behavior becoming socially and professionally acceptable?