

MicroScoop

eNewsletter from ATCC



New Microbial Panels

Microbial Panels are groupings of **ATCC Genuine Cultures**[®] that are designed to accelerate research in drug discovery, assay development and inclusivity/exclusivity testing. Cultures in each panel are chosen according to official industry guidance and characterized for relevant traits such as serotype, genotype, antibiotic resistance/susceptibility and the presence or absence of virulence or antibiotic resistance genes – saving you time and money. Check out the first of the ATCC Microbial Panels – a unique collection of vancomycin resistant Enterococci (VRE) useful for developing and validating new methods to detect VREs in clinical and environmental settings:

- **[Vancomycin Resistant Enterococci Panel](#)**

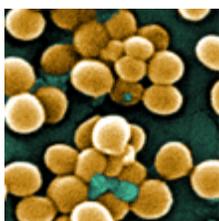
Events and Conferences

American Society for Microbiology (ASM) General Meeting
Booth #616
 San Francisco, CA
 June 16 – 19, 2012

International Association for Food Protection (IAFP)
 Providence, RI
 July 22 – 25, 2012

Parenteral Drug Association's (PDA) Global Conference on Pharmaceutical Microbiology
Booth #26
 Bethesda, MD
 October 22 – 24, 2012

Association of Molecular Pathology (AMP)
 Long Beach, CA
 October 25 – 27, 2012



New Clinically Significant MRSA Isolates with Novel Resistance Gene

The 2010 recall of an FDA-approved commercial PCR-based MRSA/SA blood culture assay prompted research on the emergence of two clonal complex 130 (CC130) methicillin-resistant *Staphylococcus aureus* harboring a novel resistance gene designated SCCmec XI. Both isolates, **ATCC[®] BAA-2312[™]** and **ATCC[®] BAA-2313[™]**, were obtained from hospitalized patients in Ireland, where MRSA has been endemic since the 1980s. Researchers report that this mobile genetic element, staphylococcal cassette chromosome *mec* (SCCmec), showed highly divergent *mecA*, *mecI*, *mecR1*, *blaZ*, and *ccr* genes, and significant similarity to an unpublished SCCmec element previously isolated from a bovine source.¹ To read the article in its entirety in *Antimicrobial Agents and Chemotherapy*, [click here](#).

¹ Shore, et. al. *Antimicrob Agents Chemother* 55(8):3765, 2011.

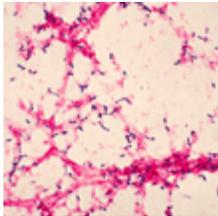


Pathogen Responsible for White-Nose Syndrome—*Now Available*

Geomyces destructans, a novel, cold-loving fungus, is the pathogen responsible for White-Nose Syndrome (WNS) – a devastating disease that has killed at least 6 million bats in North America.¹ Deposited by the USGS National Wildlife Health Center, the type strain of *Geomyces destructans* (**ATCC® MYA-4855™**) is now available. This strain has been sequenced, but not yet formally annotated, by the Broad Institute as part of the [Geomyces destructans Sequencing Project](#).

¹Blehert, et al. Science 323:227, 2009.

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Improving Pneumococcal Disease Therapies

Streptococcus pneumoniae continues to pose a major health threat to children less than 5 years of age. Currently, 14.5 million children display symptoms of serious pneumococcal disease each year,² whereas WHO reports that children infected with HIV are 20 to 40 times more likely to contract the disease.³

One of the most effective treatments for *S. pneumoniae* infection is linezolid, a 1,3-oxazolidinone antibiotic. In a 2009 paper published in *Genomic Research* investigators noted that, although linezolid still remains an effective treatment for *S. pneumoniae*, clinical strains not susceptible to linezolid (MIC \geq 8 micrograms/mL) have been reported. In an attempt to understand the genomic events related to linezolid resistance, 2 strains of linezolid-resistant *S. pneumoniae* were developed in vitro from the parental R6 strain (**ATCC® BAA-255™**). Sequencing highlighted mutations in two genes already linked with resistance along with 27 additional genes never previously associated with resistance.¹

While vaccine manufacturers have focused primarily on the use of the organism's polysaccharide capsule in disease prevention, funding supported by WHO, CDC and many major pharmaceutical companies have encouraged researchers to perform ongoing whole genome sequencing of *S. pneumoniae* to understand how genes are transferred and expressed among strains. Gaining a better understanding of recombination events that occur among different strains of *S. pneumoniae* will lead to the development of novel diagnostics and drug therapies to combat pneumococcal disease.

ATCC houses 3 fully sequenced strains of *Streptococcus pneumoniae* for use in pneumococcal disease research, including **ATCC® 700669™**, **ATCC® BAA-255™** and **ATCC® BAA-334™**. ATCC also offers a total of 24 types of purified pneumococcal polysaccharides that can be used to study pneumococcal disease.

¹Feng, et. al. Genome Research 19:1214-1223, 2009.

²Golubchik, et. al. Nature Genetics (doi:10.1038/ng.1072) Published online 29 January 2012.

³WHO, Acute Respiratory Infections (Update September 2009): *Streptococcus pneumoniae*, www.who.int/vaccine_research/diseases/ari/en/index3.html.

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