

IN BRIEF

GENETIC TESTING**Genetic risk and statin preventative therapy**

Mega, Stitzel *et al.* test the clinical use of a multi-locus genetic risk score including a composite of 27 genetic variants associated with coronary heart disease. In community-based and primary or secondary prevention studies, they find that a higher genetic risk score is associated with increased risk of incident or recurrent coronary heart disease events, adjusted for clinical risk factors. Those in the highest genetic risk score categories derived greater benefits from statin preventative therapy, with greater relative and absolute disease risk reductions in randomized controlled trials for primary and secondary prevention. Although further testing in stratified prospective trials will be needed to directly test the clinical benefit of using a genetic risk score as the basis of selective statin therapy, the current study provides an indicator of how genetic screening may prove useful in identifying subpopulations that are more likely to benefit from preventative therapy.

ORIGINAL RESEARCH PAPER Mega, J. L., Stitzel, N. O. *et al.* Genetic risk, coronary heart disease events, and the clinical benefit of statin therapy: an analysis of primary and secondary prevention trials. *The Lancet* [http://dx.doi.org/10.1016/S0140-6736\(14\)61730-X](http://dx.doi.org/10.1016/S0140-6736(14)61730-X) (2015)

PATHOGEN GENETICS***S. aureus* multi-host tropism**

The *Staphylococcus aureus* clonal complex CC121 is a common cause of human skin and soft-tissue infections, as well as the source of a recent epidemic in rabbits. Viana *et al.* track the evolution of the multi-host tropism of this lineage. Phylogenetic analysis based on whole-genome sequences of a global collection of CC121 clinical strains showed a high level of diversity for the strains isolated from human cases, whereas the strains isolated from rabbits fell into a single clade. The authors' analyses suggest that the most likely explanation for the emergence of the rabbit clade is a single human-to-rabbit host jump occurring more than 40 years ago. They demonstrate that a single naturally occurring mutation in the *dltB* gene is necessary and sufficient to convert a human-specific *S. aureus* strain into one that infects rabbits, and they find evidence for convergent evolution at this locus.

ORIGINAL RESEARCH PAPER Viana, D. *et al.* A single natural nucleotide mutation alters bacterial pathogen host tropism. *Nature Genet.* <http://www.dx.doi.org/10.1038/ng.3219> (2015)

GENOMICS**Benchmarking genome analysis pipelines**

Highnam *et al.* present an open online platform to facilitate the testing and comparison of genome analysis methods using a standardized set of performance metrics and datasets. The platform hosts selected sets of raw sequence reads, which users can download for use in their own analysis pipelines and then return results for benchmarking. They currently offer an alignment test for short-read mappers and a variant calling test for single nucleotide polymorphism (SNP) and indel variant callers. An initial benchmarking survey shows the continued improvement of short-read mapping algorithms in both alignment accuracy and the precision and sensitivity of variant calls. The genome comparison and analytic testing (GCAT) platform is freely accessible at <http://www.bioplanet.com/gcat>.

ORIGINAL RESEARCH PAPER Highnam, G. *et al.* An analytical framework for optimizing variant discovery from personal genomes. *Nature Commun.* **6**, 6275 (2015)