

RESEARCH

A convergence in interest: Mutability of PE_PGRS genes in mycobacteria

Researchers in the Wits node have developed a versatile assay system for monitoring the rates and spectra of mutations in a variable region of the PE-PGRS gene Rv0746 from *Mycobacterium tuberculosis*. Application of this assay in a *Mycobacterium smegmatis* host allowed a wide range of mutations that resulted primarily from replication slippage between PGRS repeats to be detected, thus confirming the plasticity of such sequences inferred from the inter-strain sequence variation observed in clinical isolates of *M. tuberculosis*. However, the mutation rates measured using this assay argued against marked hypermutability of PGRS-containing loci in mycobacteria. This study, led by postdoctoral fellow Edith Machowski and MSc student Samantha Barichiev, was published in the March 2007 issue of the *Journal of Bacteriology* (<http://jb.asm.org/cgi/content/full/189/5/2190?view=long&pmid=17172340>).

In the same area of research, researchers in the SU node recently published an article entitled "Evolution and expansion of the *Mycobacterium tuberculosis* PE and PPE multigene families and their association with the duplication of the ESAT-6 (*esx*) gene cluster regions." This study by Nico Gey van Pittius, Samantha L Sampson, Hyeyoung Lee, Yeun Kim, Paul van Helden and Rob Warren was published in the November 2006 issue of the open access journal, *BMC Evolutionary Biology* (<http://www.biomedcentral.com/1471-2148/6/95>). This paper has been accessed 1162 times in the first three months after its publication. An earlier paper in *Genome Biology* by Nico Gey van Pittius and co-workers has reached 10 000 accesses in 6 years. These access statistics demonstrate the high visibility that is achieved by open access publication and the interest in this area of research.