

# DNA STRAIN TYPING IN TB CONTROL

## FACTSHEET TB04

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During the 1980s it was identified that possums in different parts of New Zealand were infected by different strains of the bovine TB bacterium (*Mycobacterium bovis*) which could be identified by DNA typing. The same DNA strains were present in livestock in the same area.

This led to the development of DNA strain typing of *M. bovis* as a tool to help determine likely causes of new TB infection cases in cattle and deer herds – and especially whether the infection was caused by local contact with infected possums, or by the introduction of infected stock into the herd.

This can greatly help in TB control decision-making. For example if we get a new herd TB case in Southland, but the DNA type turns out to be a typical Central North Island strain, then it's most likely the herd was infected through livestock movement and we can rule out local infection from possums as a cause. We would also look into the livestock movement picture in more detail, which might even lead us back to an unknown infected herd back in the Central North Island.

Alternatively, if the herd infection matched the local TB strain, then we would investigate possible infection from local livestock movement, but would also look very hard at the need for further possum survey or control work, especially if the area was thought to be close to TB eradication.

A number of techniques have been developed and become available for use in DNA typing *M. bovis* strains since the early 1980s. The simplest, known as spoligotyping, has been used extensively for typing *M. bovis* in other parts of the world. However, under New Zealand conditions, spoligotyping provided very little discrimination and was only able to identify about eight different strains.

Given the poor discrimination available from spoligotyping, New Zealand scientists developed a new method that provided far greater ability to discriminate between different *M. bovis* strains. This method, called Restriction Endonuclease Analysis (REA) has allowed us to identify about 320 different *M. bovis* strain types throughout New Zealand. Of these, 51 predominate on the West Coast. Use of the REA typing method has thus often enabled our vets to determine whether a new TB infection diagnosed in a cattle or deer herd was likely to have been locally acquired, or brought in from another part of New Zealand, and if so, from where.

However REA typing is technically very complex to perform and the outputs can't be digitised for archiving or analysis. This led to investigation of a new method known as Variable Number Tandem Repeats (VNTR) which appeared in the mid to late-2000s. While VNTR does not discriminate between different strains as well as the REA method, it still provides very useful information while being far simpler to perform, and the results can be digitised. The VNTR method was thus adopted for wide use in New Zealand from 2010/11. VNTR currently provides for typing of 125 different *M. bovis* strains, of which at least 48, and possibly 50, predominate on the West Coast.

In 2012/13, with the rapid reduction in the price of performing whole genome sequencing (WGS) on DNA from bacteria, TBfree New Zealand began funding research to evaluate this method and compare it with VNTR. So far the use of WGS for *M. bovis* strain typing looks promising and affordable.

The real benefit of this method is that it will provide a unique TB DNA fingerprint for each individual infected animal. This will give us a much more precise tool for identifying sources of infection when investigating both livestock and wildlife TB cases.

**For more information, please visit the [OSPRI](#) website, or phone OSPRI on 0800 482 463.**