Title: Low genetic diversity of bovine *Mycobacterium avium* subspecies *paratuberculosis* isolates originating from the Republic of Ireland detected by MIRU-VNTR genotyping

Authors: Marcel de Kruijf, Olga N. Lesniak, Dermot Yearsley, Elvira Ramovic, Aidan Coffey, Jim O'Mahony

PII: S0378-1135(17)30201-8
DOI: http://dx.doi.org/doi:10.1016/j.vetmic.2017.03.029
Reference: VETMIC 7590

To appear in: *VETMIC*

Received date: 13-2-2017
Revised date: 22-3-2017
Accepted date: 24-3-2017

Please cite this article as: de Kruijf, Marcel, Lesniak, Olga N., Yearsley, Dermot, Ramovic, Elvira, Coffey, Aidan, O'Mahony, Jim, Low genetic diversity of bovine Mycobacterium avium subspecies paratuberculosis isolates originating from the Republic of Ireland detected by MIRU-VNTR genotyping.Veterinary Microbiology http://dx.doi.org/10.1016/j.vetmic.2017.03.029

Low genetic diversity of bovine *Mycobacterium avium* subspecies *paratuberculosis* isolates originating from the Republic of Ireland detected by MIRU-VNTR genotyping

Marcel de Kruijf[a], Olga N. Lesniak[a], Dermot Yearsley[b], Elvira Ramovic[b], Aidan Coffey[a], Jim O'Mahony[a*]

[a]Cork Institute of Technology, Department of Biological Sciences, Rossa Avenue, Bishopstown, Cork, Republic of Ireland
[b]Central Veterinary Research Laboratory, Department of Agriculture, Food and the Marine, Backweston, Celbridge, Kildare, Republic of Ireland

* Corresponding author:
Dr. Jim O'Mahony
Cork Institute of Technology, Department of Biological Sciences, Rossa Avenue, Cork, Ireland.
Tel.: +353 21 4326833
Email address: jim.omahony@cit.ie

Highlights for Journal of Veterinary Microbiology:

- First time a large scale MAP genotype study was performed in Ireland.
- The INMV 3 genotype has been reported for the first time in Ireland.
- The INMV 116 genotype has been reported for the first time among dairy herds.
- The study provided important groundwork for future MAP genotype studies in Ireland.

Abstract

Mycobacterial interspersed repetitive unit and variable number tandem repeat (MIRU-VNTR) has been developed as a simple, rapid and cost efficient molecular typing method to differentiate *Mycobacterium avium* subspecies *paratuberculosis* (MAP) isolates. The aim of this study was to determine the genomic diversity of MAP across the Republic of Ireland by utilising the MIRU-VNTR typing method on a large collection of MAP isolates.
A total of 114 MAP isolates originated from 53 herds across 19 counties in the Republic of Ireland were obtained and genotyping on these MAP isolates was based on eight established MIRU-VNTR loci.
Four INMV groups were observed during this study. INMV 1 was found in 67 MAP isolates (58.8%) and INMV 2 was observed in 45 isolates (39.4%). INMV 3 and INMV 116 recorded only one isolate each (0.9%). The unique INMV 116 group has never been reported among herds thus far and the molecular pattern of the MAP isolate classified in INMV 116 showed a difference at the MIRU-VNTR X3 locus compared to the other three INMV groups observed.
INMV 1, INMV 2 and INMV 3 are observed frequently in Europe and comprised 99.1 % of the total MAP isolates characterised in this study, indicating that MAP exhibited low level of genetic diversity across the Republic of Ireland using the MIRU-VNTR method. By the implementation of SNP analysis or MLSSR as an additional typing method, MAP genetic