



## **CARE Cross-sectoral framework for quality Assurance Resources for countries in the European Union –PIWET's first experiences**

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### **INTRODUCTION**

CARE is an OHEJP international project aimed at strengthening cooperation between the public health, food and animal health sectors in the EU (<https://onehealthjep.eu/>). It involves 16 partners from 8 countries. Partner institutions function as reference centres and, using their own collections of microorganisms, operate as Biological Resource Centres (BRCs). The main objectives of CARE are: development of guidelines for the organisation of cross-sector proficiency tests; creation of an inventory of available reference materials in the context of One Health; identification and filling of possible shortages; creation of a reference database of strains and genomes for effective quality control analysis in food safety and public health protection across sectors; development of a permanent public portal ensuring transparent access to strains and necessary information from the microbial collection; and international harmonisation of metadata databases between OHEJP partners.

### **METHODOLOGY**

For the study, 36 *Salmonella* and 6 *Bacillus cereus* strains were selected from the bacterial culture collection of the National Veterinary Research Institute (PIWET). The *Salmonella* strains belonged to serovars deemed relevant for animal health (i.e. *Choleraesuis*, *Dublin*, *Typhimurium*, *monophasic Typhimurium*, *Newport*), with a rare antigenic structure (i.e. *S. bongori* 48:z65:-) and were multi-drug resistant or derived from uncommon sources such as wildlife or reptiles. All *Bacillus* strains were of reptilian origin. Precise characterisation was obtained through validated standard methods, including macroscopic evaluation of the microorganisms on the culture medium, a biochemical characterisation by the VITEK system. *Salmonella* was tested according to the ISO 6579 standard. All bacterial strains were also identified and characterised via MALDI-TOF mass spectrometry and whole genome sequencing (WGS).

### **RESULTS**

The strains were fully characterised phenotypically and genotypically. Characteristic MALDI-TOF spectra were obtained. Whole genome sequencing made it possible to confirm the

Salmonella serovar identification and led to identification of the resistance and virulence genes. Bacillus strains were identified as *B. cereus*, *B. toyonensis* and *B. paranthracis*. An application of a wide range of available phenotypic and genotypic methods made it possible to obtain fully characterised bacterial isolates which can be considered candidates for the bacterial reference materials.

## DISCUSSION

CARE emphasises the development of collaboration between the public health, food and animal health sectors to increase joint preparedness and the reaction rate in relation to bacterial zoonoses. Numerous advanced reference identification methods based on both phenotype and genotype analysis make it possible to maintain high quality standards in the creation of a database of the certified reference materials. Obtained reference materials will be placed on a public portal created to facilitate access to a collection of selected certified reference materials along with complete genomic data and confirmed correlations between genotypes and phenotypes.

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