

## 4th International Conference on

## **Agriculture & Horticulture**

July 13-15, 2015 Beijing, China

The rapid response of agricultural biosafety via modern mass spectrometry-based microorganism identification technology

Chinese Academy of Tropical Agriculture Sciences, China

ass spectrometry (MS) has been widely used for specific, sensitive, and rapid analysis of proteins and has shown a high potential for bacterial identification and characterization. In the present study, four well-characterized rhizobia strains and E. coli DH5α, as a reference, were chosen to optimize applications of MALDI TOF MS for rhizobia species identification. The four rhizobia strains were Sinorhizobium/Ensifermeliloti USDA 1015T, Rhizobium leguminosarum USDA 2370T, Mesorhziobium tianshanense USDA 3306T, and Bradyrhizobium yuanmingense CCBAU 10071T. Bacterial cultivation, colony storage conditions and sampling time were studied to evaluate the effects on protein mass spectra. In comparison with 16S rDNA phylogenetic tree, the optimized method was further evaluated with 75 rhizobial strains of 40 characterized species in 4 genera (6 Mesorhziobium spp., 22 strains; 9 Rhizobium spp., 49 strains; 3 Sinorhizobium/Ensifer spp., 3 strains; and 1 Azorhizobium sp., 1 strain). The potential of developing a mass spectrum database for rhizobial species determination was demonstrated with blind samples. A dendrogram of 75 rhizobial strains of 4 genera was constructed based on MALDI-TOF mass spectra and the topological patterns agreed well with those in the 16S rDNA phylogenetic tree. The potential of developing a mass spectrum database for all rhizobia species was assessed with blind samples. The entire process from sample preparation to accurate species identification and classification required approximately 1 hour.

## **Biography**

Ruizong Jia had done his PhD from China Agricultural University (2016-2009), Post Doctorate from University of Hawaii (2009-2010), Hawaii Agricultura Research Center (2010-2013), Currently he is Associate Researcher and Associate Professor in Institute of Tropical Bioscience and Biotechnology, Chinese Academy of Tropical Agriculture Sciences (2013- present).

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