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Bacterial speciation by sequencing of the 16S rRNA gene

Fact Sheet

Bacterial speciation by sequencing of the 16S rRNA gene is now available at the University of Minnesota Veterinary Diagnostic Laboratory. The 16S rRNA gene is highly conserved within bacterial species, and sequencing of variable regions can be used to characterize bacterial isolates to the species level (Fig. 1).

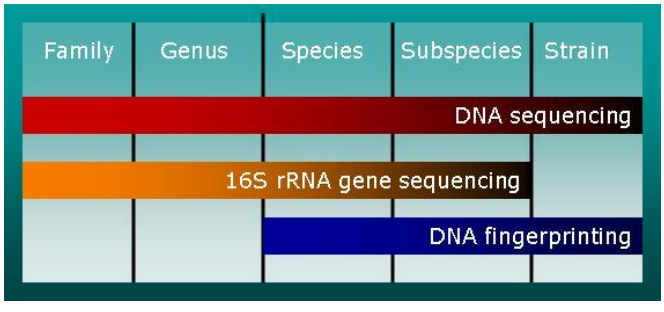

Figure 1 – Comparison of different molecular techniques for characterization of bacterial isolates.

Sequencing of the 16S rRNA gene from pathogens isolated at the University of Minnesota Veterinary Diagnostic Laboratory has been shown to be useful for speciation of bacterial isolates recovered from different animal species, as shown in Table 1. The new speciation method enabled the differentiation between closely related organisms (*Haemophilus* sp, and *Actinobacillus indolicus*) and the identification of gram-negative rods that were non-reactive when tested using traditional biochemical tests (*Actinobacillus delphinicola* and *Riemerella anatipestifer*). It also helped to identify the *Campylobacter* sp. isolated from the intestine of a healthy pig as *Campylobacter lanienae.*

Table 1. Comparison of biochemical and sequence-based identification of bacterial pathogens.

Animal species	Biochemical Identification	16S rRNA gene sequence identification
Swine	*Haemophilus* sp.	*Actinobacillus indolicus*
Dolphin	Gram-negative rod*	*Actinobacillus delphinicola*
Mallard duck	Gram negative rod*	*Riemerella anatipestifer*
Swine	*Campylobacter sp.*	*Campylobacter lanienae*

* non-reactive on biochemical tests.

Samples to be submitted for testing (refrigerated):

1. Tissues for bacterial isolation.
2. Bacterial isolates (pure cultures)

If you have any questions about these procedures, or proper submission of samples, please contact Dr. Stephanie Rossow at 1-800-605-8787 or by Email at rosso003@umn.edu.

This test was standardized and validated by Dr. Yogesh Chander, Research Associate at the University of Minnesota VDL.
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