



Request for Oral Presentation for FDA/CVM Public Meeting, April 10, 2007

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Time requested: 10 minutes

Statement summary: The NARMS program is an essential component in the effort to preserve the efficacy of antibiotics through the prevention of the rise and spread of antibiotic resistance. Not only is NARMS vital for monitoring the spread of antibiotic resistance through the food chain, but it also is one of the few continuous sources of antibiotic resistance data for bacteria that live as both pathogens and commensals (e.g., *E. coli*, *Enterococcus*). For the last five years, the Alliance for the Prudent Use of Antibiotics (APUA), in collaboration with the National Institute of Allergy and Infectious Diseases, has conducted the Reservoirs of Antibiotic Resistance (ROAR) project, which examines the role of commensal bacteria in the spread of antibiotic resistance. This project combines molecular and epidemiological data from ROAR-funded studies, as well as previously published studies by other researchers. During the ROAR project, we have gained much experience in surveillance design, data collection, and data integration. Based on our experience, we offer the following suggestions to further strengthen the NARMS program:

On-farm sampling: APUA would encourage NARMS to structure the on-farm sampling scheme to focus on the use of antibiotics. With the appropriate sampling scheme, there is an opportunity to conduct a ‘natural experiment’ that could assess the effect of antibiotic use on antibiotic resistance in food-borne organisms.

Integration of results: Currently, most of the NARMS data are published as separate studies by the different researcher arms. Consequently, it is difficult for independent researchers and groups to determine how antibiotic resistance could be spreading through the food chain. APUA recommends that there be more integration of analysis and publication of the NARMS findings among the different arms.

Molecular epidemiology: One of the most difficult issues in assessing the spread of resistance is the lack of common and portable molecular epidemiological techniques. Consequently, it is difficult to compare results from different studies; cross-dataset analyses among NARMS project arms and external studies would maximize the power of the NARMS data. APUA recommends that NARMS increase the molecular epidemiological component of NARMS to not only focus on resistance genes, but also the genomic background in which these resistance genes are found in order to track the spread of resistance genes *and* clones. In addition, ‘portable’ techniques that are robust among laboratories, such as multi-locus sequencing typing and common microarray schemes to detect virulence genes should be adopted.

International surveillance: Developing nations have dramatically increased their capacity to accurately assess antimicrobial resistance in food-borne pathogens. However, most developing countries lack the resources to assess antimicrobial resistance, and many of those that do agricultural surveillance are not integrated into with NARMS (e.g., Thailand). APUA has 57 chapters worldwide, with over 25 in the developing world. We offer our advice and expertise to NARMS on possible integration with surveillance systems in these countries.

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