

## ENVIRONMENT

**Title:** Microbial Community Analysis to Identify Risk Factors in Manure Foaming –  
**NPB #11-039**

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**Scientific Abstract:** Extensive foam production in Midwestern U.S. deep-pit swine operations has become a serious concern to the pork industry. In recent years, a number of explosions and flash fires have been reported in swine facilities as foam production has developed and spread to numerous deep-pit manure storages. Efforts have been made to document and assess the severity of foaming in these swine facilities, however to date no cause has been identified. The purpose of this project was to analyze the microbial communities present in these deep-pit manure storages and to determine if presence of foaming in these storages is correlated to the differences in microbial communities between foaming and non-foaming swine facilities. Samples for this study were collected from fifty-nine barns from twenty-six deep-pit swine operations located in the states of Illinois, Iowa, and Minnesota from both foaming and non-foaming facilities. The bacterial community composition was assessed using automated ribosomal intergenic spacer analysis (ARISA). The results indicated that microbial communities do indeed differ between foaming and non-foaming manure samples. It was found that manure from foaming storages had reduced microbial richness, but increase dominance of specific bacterial populations. Results also indicated that some manure storages have more stable microbial communities while others are in a state of transition from foaming to non-foaming (or vice versa). These results support the idea that foam production in deep-pit manure storages is correlated with distinct bacterial populations present in the manure; however more research is needed to determine if the bacterial communities are the cause of foaming, or merely an indicator of the foaming condition.

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