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Subject: CONFIDENTIAL-BCRT STUDY FOIA DOC
Date: May 21, 2015 at 2:25 PM
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DS

Marianne:

I'm not sure if you've seen the attached or not.

We have the subsequent draft proposals (post FB, Cargill, C & H input) which illustrate how the plan changed from monitoring and finding a problem to one that added Ag Ext to help Jason stay in watershed.

Re item #4 -bacterial indicators, pathogens and genetic markers to identify public health risks-These items did not make it into BCRT official study. Re integrator liability -If Cargill saw this proposal- Did Cargill have input and might Cargill have paid for recommended tests? If so, and these test results do in fact exist, any results would not be subject to FOIA as these tests are not part of the BCRT scope of study.

Dane

Microbial Source Tracking in a Stream Draining a Rural Watershed, Northern Arkansas

Objective

To identify the fate and transport of bacterial and fecal indicators in Big Creek, Arkansas.

Study Area

C&H Farm and Big Creek, Newton County, AR

Approach

1. Collect water samples longitudinally along the river channel at frequent intervals to pinpoint where *Escherichia coli* numbers are high. This should start before the farm property begins, all along the property, and after it ends. Thus, the number of samples collected and analyses to be conducted will depend on the stream length we are talking about. One possible way to do this would be to identify 2 to 3 sampling locations above, then 4 to 5 sampling spots along the farm property (before and after fields receiving manure, and then 2 to 3 locations downstream of the property. Initially, *E. coli* will be measured as that is the EPA standard freshwater indicator (and what has been measured in the past) in order to ascertain where bacterial levels are consistently elevated.
2. As far as additional microorganisms to target, we recommend measuring both the traditional bacterial indicators as well as actual human pathogens to understand the potential public health risk. Specific markers of swine contamination such as viruses should be measured, as well as compare microbial markers from the animals and other important sources to the microbial markers in the stream using molecular techniques.
3. In addition samples will be collected on transects across the stream to determine if there are flow regimes within the stream channel influencing bacterial transport and persistence.
4. Determine diversity and potential regrowth (especially in locations with high numbers) in "hot spots" of the stream by investigating if the *E. coli* population is clonal (i.e. the same) and also using molecular approaches to compare *E. coli* collected in the water.

from these rain events per year

5. Sample water collected in runoff and in streams in a time course after three rain events per year. Rain events (increased inputs from watershed and increase of flow above base flow) increases microbial abundances in streams.
6. Dye tests on farm land water flow paths are important to determine any preferential movement to the stream. Possible dyes are fluorescein and rhodamine-WT. Dye tests are beyond the scope of this proposal.
7. A simple alternative to dye testing to evaluate where groundwater inputs enter the stream (to see if the elevated microbial counts correspond with subsurface flow pathways) is to conduct longitudinal surveys of stream water pH, alkalinity and temperature to calculate the excess partial pressure of CO_2 (EpCO_2 ; a simple calculation). It is expected that subsurface flow with high organic matter content from animal waste to have a very high EpCO_2 . The longitudinal profiles of EpCO_2 would help locate the input of subsurface flow along the stream reach