

Fate of Antibiotic Resistance Genes (ARG) in On-Farm Lagoons

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Abstract. Antibiotic resistance is a growing human health problem. Reservoirs of antibiotic resistance are known to exist in the environment, however, little practical understanding is available to guide potential strategies to contain resistance. The purpose of this study was to explore the effect of on-farm treatment of animal waste in lagoons on antibiotic resistance genes (ARG), which are segments of DNA that give bacteria the ability to survive in the presence of antibiotics. ARG concentrations were monitored in the lagoons of several confined animal feeding operations (CAFO), including: two conventional dairies, two organic dairies, two beef feedlots, a swine feedlot, and a poultry egg producing facility on the eastern plains of northern Colorado. These lagoons were sampled at four different time points (to represent the four seasons), with water and sludge sampled from each lagoon. Two tetracycline ARGs (tet(O) and tet(W)), and two sulfonamide ARGs (sul(I) and sul(II)) were quantified using real-time quantitative polymerase chain reaction (Q-PCR). The ARGs were normalized to the 16S gene copy numbers. Additionally, nutrient and metal analysis were performed to explore potential correlations with the concentrations of ARGs. All four ARGs were found on all farms at all time points. The poultry egg producing facility had significantly lower levels of tet(W) than all the other farms. In some cases, lagoon treatment resulted in an apparent reduction in ARGs, however, the effect was variable among the farms. Since ARGs are gaining attention as emerging contaminants, studies such as this are important to environmental scientists and engineers to design effective treatment processes.