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**INVESTIGATION OF GENE ACTIVATION OF BACTERIAL SPECIES
ISOLATED FROM UNITED STATES AIR FORCE AVIATION FUEL USING
DNA MICROARRAYS**

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Since the United States Air Force (USAF) assumed use of a kerosene-based aviation fuel it has been well documented that the fuel can be degraded by microorganisms. However, the ability of the bacteria and fungi to sequester the fuel and suspend it within the aqueous phase for subsequent metabolism, particularly in aviation fuel, is not well understood. The microorganisms present with the water bottoms of fuel storage tanks have been shown anecdotally to produce surfactant and or polymer molecules as evidenced by the disarming of refueling truck filter/coalecers. As described in Rauch et al (2006) a 2002-2003 Air Force Research Laboratory (AFRL) study isolated ten genera of bacteria from USAF aviation fuel storage tanks. Of those ten genera the organism *Bacillus licheniformis* was found to be the most prevalent at the eleven USAF bases sampled. *Bacillus licheniformis* has been shown to produce a high molecular weight poly-glutamate polymer. There is some evidence that a negatively charged carboxyl containing polymer may indeed bind to and reduce the corrosion of a metal surface. While isolation of individual suspected polymer species produced by *Bacillus licheniformis*, *Dietzia sp.* and other microorganisms is feasible, advances in identifying and quantitating mRNA transcripts opens an avenue to expeditiously investigate organism expression of multiple proteins/polymers. Exploitation of DNA microarrays allows researchers to visualize which genes are being expressed in a particular organism or cells. Knowing which genes are expressed by probing for complementary mRNA gives information as to what proteins are being ordered into production upon cell exposure to a particular environment, without the actual production or isolation of those proteins. This paper describes the use of DNA microarrays to exam which genes are “turned on” upon *Bacillus licheniformis* exposure to JP-8. The data provides crucial insight as to how the bacteria metabolizes the aviation fuel resulting in protein/polymer products. The application of this information may in turn unveil potential chemical indicators of aviation fuel microbial contamination which may be exploited for detector design or other novel uses.