# In-Pipe Technology

## Introduction

In-Pipe Technology (IPT) bacteria are heterotrophic bacteria commonly found in soil. They are part of a group of microorganisms termed “decomposers” and are “generalists” in regards to their broad capabilities of using many different carbon sources to fuel their metabolism. In their natural soil environment, similar bacteria feed on decaying material and by-products produced by the other organisms in the food chain. These organisms contain a great diversity of enzymes that are both excreted and retained within the cells and are very active degrading complex organic matter. The IPT bacteria can be found in the human gastrointestinal tract but in very low numbers and usually in a low metabolic state. They are naturally occurring and are not pathogenic or genetically modified. IPT bacteria can operate using aerobic respiration, fermentation, and anaerobic respiration using nitrate or fumarate as the final electron acceptor. They are vigorous growers and are more than capable of degrading pollutants normally found in municipal wastewater.

The predominant bacteria in the human intestinal tract are strict anaerobes (Clark, 1977). A recent article in Science (Eckburg et al, 2005 with supporting online materials) found that 51% of the total bacteria detected within stool and pooled mucosa samples were *Firmicutes* (low G+C Gram-positive bacteria). Of the *Firmicutes*, 95% belonged to the *Clostridia* class, while 4.5% and 0.2% were members of the *Mollicutes* and *Bacilli* classes, respectively. The *Clostridia* class contains 274 phylotypes including *Eubacterium*, *Ruminococcus*, *Dorea*, *Lachnospira*, *Butyrivibrio*, and *Coprocuccus*. The *Bacilli* class representatives were identified as *Streptococcus*, *Gemella*, and *Lactococcus* genera. The other dominant phylum was that of *Bacteroidetes* (48% of total) containing *Bacteroides* and *Prevotellaceas* species. The

*Proteobacteria* were found to be very minor constituents of the samples and those found included *Desulfomonas*, *Bilophila*, *Escherichia*, *Camphylobacter* and *Sutterella*.

Bacteria that thrive continuously in a contained environment such as the intestinal tract tend to become specialized in that ecosystem (Casjens, 1998). In order to compete effectively, the expressed genomes of bacteria that grow within living hosts tend to become smaller, becoming specialized to that particular environment. When these bacteria are shed from this environment in feces, they are less capable than wild-type organisms of the same *Genus species* of adapting to the new environment and will not be as efficient as generalist organisms. It has been determined that some species of these bacteria do survive and proliferate in the new environment (Cho, 2000). In particular, the *Proteobacteria* which are found in extremely low quantities in the gut, seem to thrive in the wastewater environment. These include the various sulfate reducing bacteria and *Escherichia coli*. Under conditions without IPT treatment, the bacteria present in collection systems (and therefore entering wastewater treatment plants) are primarily from the intestinal tract and their preferred environment has similar conditions as the intestinal tract. These bacteria are not the most capable for metabolizing wastewater pollutants effectively nor have the least detrimental impact (odors, corrosion, disease).

Please remember these general ideas as you read further on the particular application(s) that you are interested in applying In-Pipe Technology to. If your problems include Odor/Corrosion, FOG, poor BNR, we have further publications available.

## References

Casjens S. 1998. The Diverse and Dynamic Structure of Bacterial Genomes. Annu. Rev. Genet. 32:339-377.

Clark RT. 1977. The Gut and its Micro-organisms. In *Microbial Ecology of the Gut.* Clark RT and Bauchop J (editors). Academic Press, New York. pp 36-71.

Cho JC, Kim SJ. 2000. Increase in Bacterial Community Diversity in Subsurface Aquifers Receiving Livestock Wastewater Input. *Appl Env Microb*. **66(3)**:956-965.

Eckburg PA, Bik EM, Bernstein CN, Purdom E, Dethlefsen L, Sargent M, Gill SR, Nelson KE, Relman DA. 2005. Diversity of Human Intestinal Microbial Flora. *Science*. **308**:1635-1638, (plus supporting online material at www.sciencemag.org/cgi/content/full/1110591/DC1.