Isolating novel enzymes and microorganisms from Yellowstone National Park for use in food waste degradation.

In the United States, 2 billion pounds of food waste are discarded yearly, an amount equivalent to $161 billion or 30-40% of all food production. Food waste also makes up the largest portion of landfill waste. A small amount of food scraps are recycled through compost and re-purposed into animal feed, but these processes are costly, have minimal benefits, and have limitations. One of the most promising routes is converting food waste into value added products through microbial fermentation. Food waste is rich in carbohydrates, proteins, lipids, vitamins, and other trace minerals, making it the ideal environment for microbes. Unfortunately, food waste is highly variable with a variety of contaminant native microbes. Native microbial species compete with industrial strains used in fermentation to create target downstream products such as 2,3-butanediol (2,3-BDO), lactic acid, and bioethanol. This competition between microbes presents the need for sterilization, which accounts for approximately 41% of the cost in conventional fermentation. Currently, bacteria and fungi that are generally regarded as safe (GRAS) are desired for use in industrial microbiology and fermentation. GRAS microbes that are known to produce target products are *Paenibacillus* and *Bacillus*, *Lactobacillus*, *Leuconostoc*, *Pediococcus*, *Lactococcus*, and the most common *Saccharomyces* (bioethanol). A new species of bacteria, *Bacillus licheniformis YNP5-TSU*, was discovered to create 2,3-BDO in non-sterile fermentation temperatures greater than 50°C and an alkaline pH. The goal of this project is to identify similar novel thermophilic microorganisms and/or enzymes from Yellowstone National Park hot springs through phentoyping, genomic isolation and metagenomic sequencing. Results from this study can lead to advancements in food waste fermentation by increasing bio-conversion rates.