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ISOLATION AND CHARACTERIZATION OF "WILD" MICROBES FOR BREWING

Marissa Yost Katherine Napoli Nauel Tejada

The craft beer brewing industry has enjoyed explosive growth over the past decade and as component of this expansion interest in the production of "wild" or spontaneously fermented alcoholic beers and ales has increased dramatically. Unlike traditionally fermented ales, the vast majority of which are brewed with less than a dozen well characterized domestic strains of *Saccharomyces cerevisiae*, "spontaneous fermentation typically depends on environmental yeasts of the Saccharomycetaceae family. We report here a recharacterization and comparison of a number of previously isolated yeast species from various environmental sources as their characterization of a strain newly isolated from a New England malting facility is presented. This comparison has confirmed that yeasts of potential use in the brewing industry can vary widely in terms of species, secondary metabolite production, carbohydrate use, and fermentation characteristics.

COMPARISON OF PLANKTONIC MICROBIAL DIVERSITY IN TWO WATERSHEDS ON THE DINGLE PENINSULA Nicole Longo Jessica Zolatarevsky

Anthropogenic impacts on water quality in coastal ecosystems is of increasing concern given current land-use and population patterns. In particular, sustainable development in areas of high population/tourism pressure in coastal watersheds is of concern and demands an understanding of the complex relationships between the "natural" and "human" systems affecting the ecosystem. Two adjacent watersheds on the on the Dingle Peninsula in Ireland (Dingle and Ballyferriter) provide an interesting opportunity to separate the effects of natural/agricultural impacts (Balleyferriter) vs. natural/agricultural/tourism (Dingle) effects on water quality in the primary river systems draining the two watersheds. As part of a larger effort to conduct a thorough environment assessment of the two watersheds, we have completed an initial 16S rRNA community profile of the planktonic microbial communities in the Milltown (Dingle) and Feohanagh (Ballyferriter) rivers. Our data indicate substantial and significant differences both within and between sample sites in the different river systems. In addition, instances of clear relationships between microbial community composition and both stream level classification/surrounding terrestrial habitat are apparent.