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Research in S.Epstein's lab falls into two categories: culture-dependent and culture-independent. The first focuses on the "Great Plate Count Anomaly" – and reasons why so many (prokaryotic) microbes refuse to grow in the lab. Synergistic projects aim at design alternative cultivation approaches, ways to domesticate uncultivated species, and explore their biotechnological potential. The second group of projects is more relevant to the goals of the ICoMM meeting. This (culture-independent) direction is developing in three venues:

1. Nature of microbial species. Two projects in the lab aim at determining the level of genetic variations within classical taxonomic units vs among such units, looking at reconciliation of taxonomic schemes produced by alpha-taxonomists and molecular phylogenetists. The focus is on microbial eukaryotes. At a minimum, we would like to find a practical measure of rRNA gene divergence that separates organisms into morphologically and ecologically meaningful clusters. At this time, 1% divergence seems to be a good candidate for a species cut-off value at least in marine ciliates. A separate project studies ecological differences and similarities between strains identical – or nearly identical – in their conserved genes' sequences.

2. Microbial discovery. Three projects in the lab, mostly in collaboration with other scientists (V.Edgcomb, D.Patterson, G.Taylor, T.Stoeck, M.Yakimov, L.Giuliano), aim at surveying, discovering, describing, and eventually cultivating representatives of novel lineages of microbial eukaryotes. The largest of the three is represented by a Microbial Observatory in the Cariaco Basin off the coast of Venezuela. The other two focus on extreme environments of Arctic (Greenland) and high salinity/deep sea (Mediterranean). Not surprisingly, each of the three has uncovered an enormous diversity and richness of novel protistan forms, but going beyond a simple detection of novel sequences proves challenging.

3. Patterns of diversity. Two projects, both in collaboration with John Bunge, focus on local and global diversity of both pro- and eukaryotes. The long-term goals are a) to understand if microbial communities are indeed composed of thousands of interacting species – or most of them are essentially inconsequential in the given community, and b) if there are meaningful patterns in global microbial distribution. The immediate objectives are more modest: to develop statistically valid tools to measure and predict microbial diversity based on small samples of this diversity (as all our clone libraries are). Parametric distributions appear to be good candidates for analyses of local diversity. Global diversity and its patterns are more difficult to handle; these seem to require completely new statistical approaches (under development).