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Interrogating Microbial Communities: New Approaches, New Challenges but New Insight

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In 1992 at ISME Kevin Marshall indicated that we were entering the decade of 'Microbial Communities'. He was correct in his vision, though his time-table was short. Fifteen years later we still recognize the importance of this topic for many microbial problems but we are only beginning to understand the composition and interactions of simple communities. We have host of new molecular methods, genome sequences and now sequencing technologies that is making our job easier but this information has also revealed that our goal is more complex than we imagined. I will present information about microbialcommunity complexity and patterns using the 454FLX (pyro) sequencing technology, what I think is the next step in resolving communities at a functional and finer level than allowed by rRNA gene sequences, and about the gene diversity found among close relatives, i.e. within currently named species. I will also comment on the problem of the Bacteria species definition in that it may or may not be useful in predicting phenotypic features of importance. Microbes have a 3.8 billion year evolutionary history and would be expected to explore many strategies leading to their current successes. There is yet no sign of nearing a plateau in the discovery of new species, genera, families or orders.