

SIG2-3

Marker gene profiling toward larger sample size and lower biases using MGISEQ platform

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Inference community composition from marker genes has come to the age of flourish, which researcher without much molecular background can use it as a common tool. The future for the usage of marker genes, is however, facing various challenges. The science community need next generation marker gene profiling to be accurate, fast, and at a lower cost so that it can fit into a large-scale research accommodating the increasing global collaborations. Here we present an alternative platform for marker gene profiling using the MGISEQ platform. By using short primers, and a new sequencing chemistry called CPas and pattern array, we have achieved a much higher throughput of marker gene profiling at the same cost as the current options. We have benchmarked our solution with the current option using 1,276 soil samples from three 20 ha permanent forest plots. We concluded with layout of near future plan including a multi-PCR solution for library prep and a new algorithm for utilizing multiple regions.