

BRIDGING THE GAP IN SOIL METAGENOMICS: THE POWER OF PACBIO HIFI READS FOR IMPROVED DE NOVO ASSEMBLY AND ACCURATE BACTERIAL PROFILING IN DDT-CONTAMINATED ENVIRONMENTS



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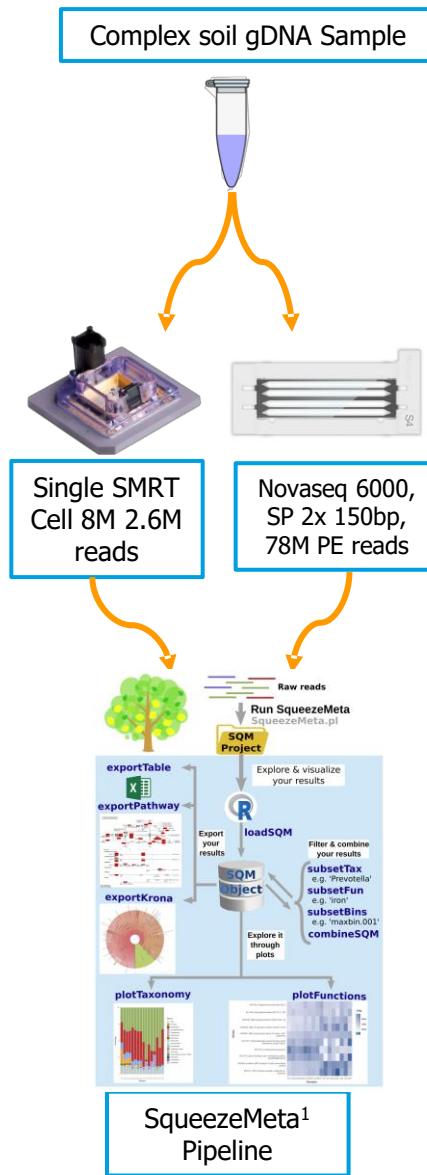
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De novo assembly of complex metagenomic samples has traditionally provided a challenge in the bacterial genomics space. To date, most metagenome assemblies are undertaken using short read (Illumina) datasets, producing highly fragmented contigs, resulting in assembly errors when clustered into metagenome-assembled genomes (MAGs). PacBio HiFi sequencing has shown to produce MAGs with a low error rate and significantly longer read length. This study leverages the power of HiFi reads to directly compare metagenomic sequencing results from the same sample, with the aim of building a database of targets for further research in DDT-contaminated agricultural environments.

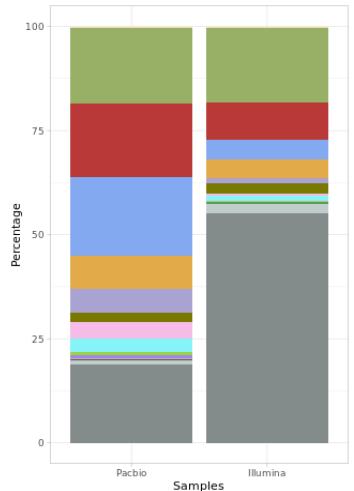
Methods



Results

Longer, contiguous assemblies generated with HiFi data		
	PacBio	Illumina
Number of contigs	49,136	702,853
Longest contig	5,856,797	363,466
Shortest contig	2694	200
N50	38,776	591
Number of ORFs	1,850,942	943,481

Higher accuracy in Taxonomic classifications



Better MAG binning

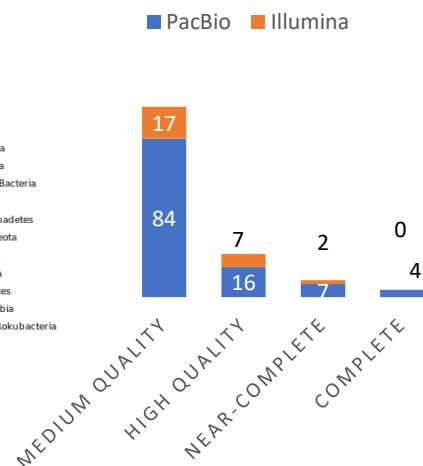


Fig. 1. MAG Binning results. Medium quality: >50% completeness. High Quality: >70% completeness, <10% contamination. Near-complete: >90% complete, <5% contamination

Conclusion

- HiFi reads show significant improvement in all areas of shotgun metagenomics.
- Circularised, complete genomes now possible in complex samples.
- Pathway analysis can now be started to identify DDT-related targets for rehabilitation.

References

- Tamames, Javier, and Fernando Puente-Sánchez. "SqueezeMeta, a highly portable, fully automatic metagenomic analysis pipeline." *Frontiers in microbiology* 9 (2019): 3349.

