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Omics Advancements for Bacterial Bioethanol Production

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ABSTRACT

Zymomonas mobilis is an α-proteobacterium that ferments simple sugars to produce ethanol, to near perfect yields. Corn ethanol and 2nd generation cellulosic ethanol continue to dominate the biofuels domain. Given the global mandate for cleaner, safer and renewable energy, *Z. mobilis* has been rigorously studied in academia and in industry as a platform organism for the production of 1st and 2nd generation bioethanol, for over three decades. In order to optimize *Z. mobilis*, of interest to us has been the understanding of the *Z. mobilis* genome – core and pangenome – to a comparative, structural and functional level. To this end, we have sequenced different strains that were obtained from various parts of the globe, as well as transcriptomes harvested at different growth conditions. This genomic endeavour has helped us recognize the collective gene pool, discriminate essential from accessory genes, observe genomic division between chromosomal and extrachromosomal elements, and gain evidence for gene flows and horizontal transfer events. It has also enabled us to choose the most suitable modules – genes or *cis*-acting elements – in order to enhance the bacterium's performance and/or create designer strains. Gene networks contributing to cell-cell signalling and mutagenic stress have also been of interest. In terms of elucidating responses brought forth by a mutagenic stressor, transcriptional profiling has been carried out and revealed the vast numbers of genes implicated in SOS induction, in DNA repair and cell-cycle regulation, as well as other versatile functions, expected or unforeseen. Lastly, we undertook to complement the otherwise truncated TCA cycle of this bacterium and inquired on concurrent metabolomic profile changes as well as productivity. The suitability of the newly constructed TCA-proficient strain for future biorefinery use is under further investigation.

Keywords: bioethanol, zymomonas, genomics, transcriptomics, TCA cycle

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