

# Enrichment and High Throughput Screening of POME Metagenomic Libraries for Bioprospecting Novel Cellulose-degrading Enzymes

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## INTRODUCTION

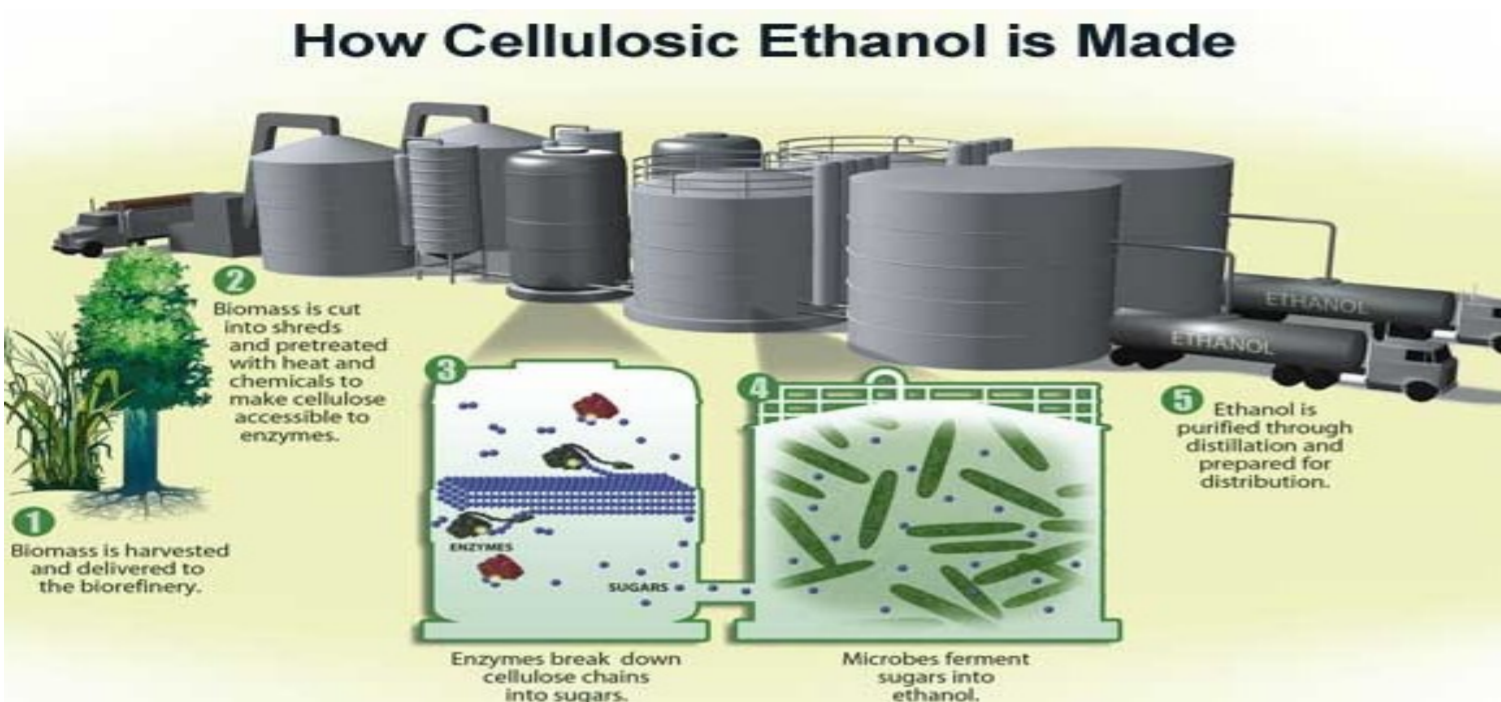


Fig. 1: Production of cellulosic ethanol by enzymatic degradation of cellulose and microbial fermentation.

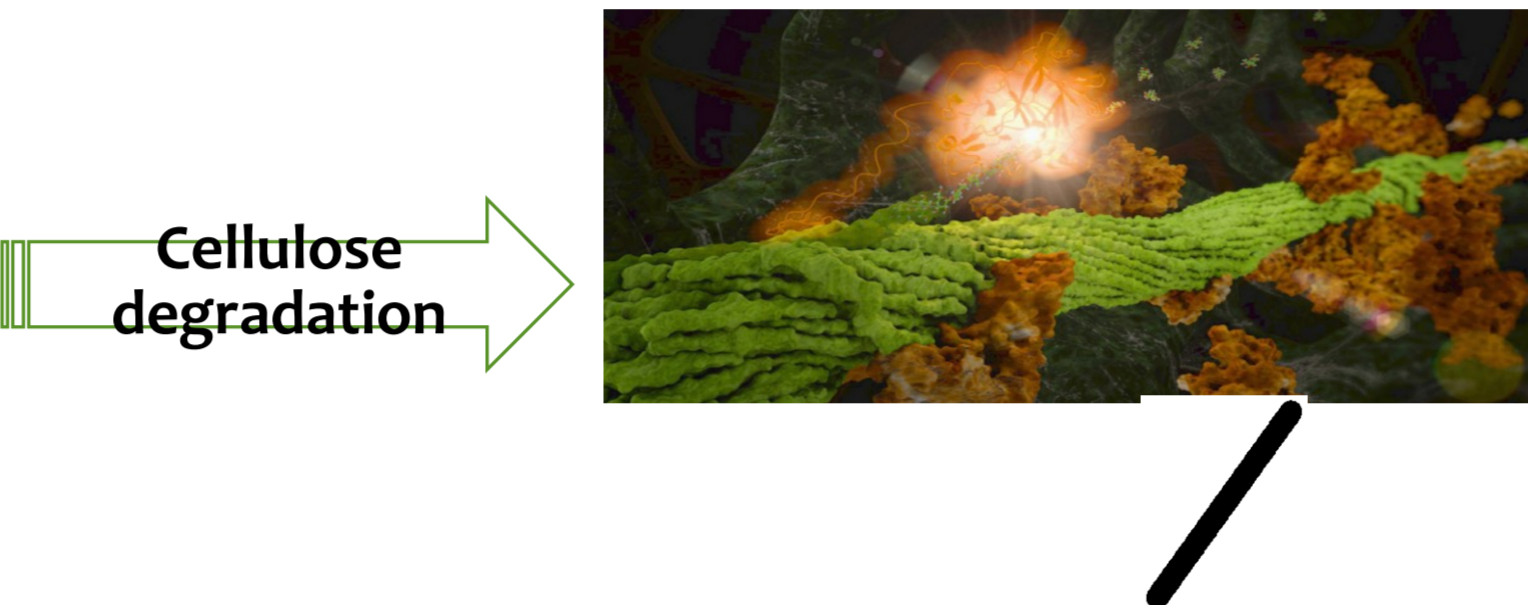


Fig. 2: Deconstruction of polysaccharides to oligo- & monosaccharides by the cellulose-degrading enzymes

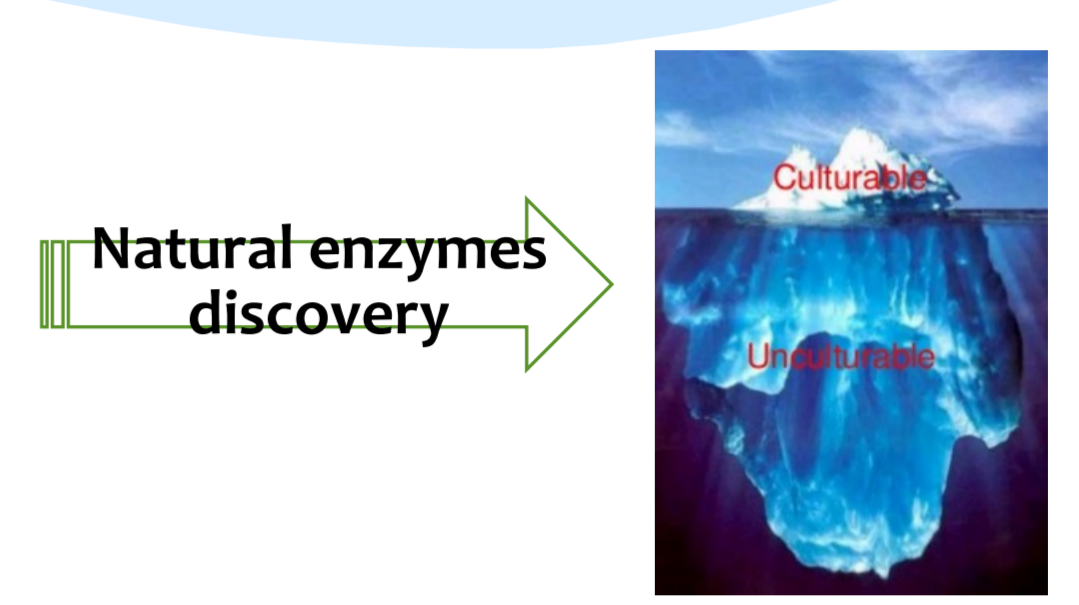


Fig. 3: Only a fraction (~1%) of microorganisms is culturable as potential resource of enzymes.

## METHODOLOGY

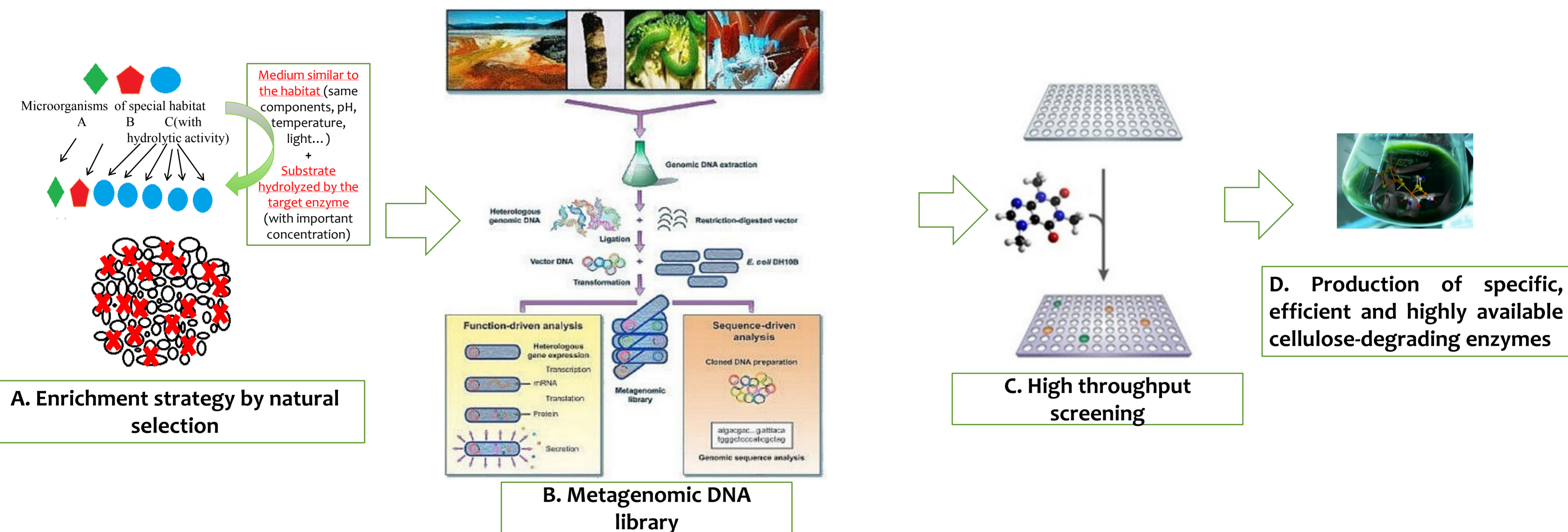


Fig. 4: Overview of bioprospecting novel cellulose-degrading enzymes from POME microorganisms

## RESULTS AND DISCUSSION

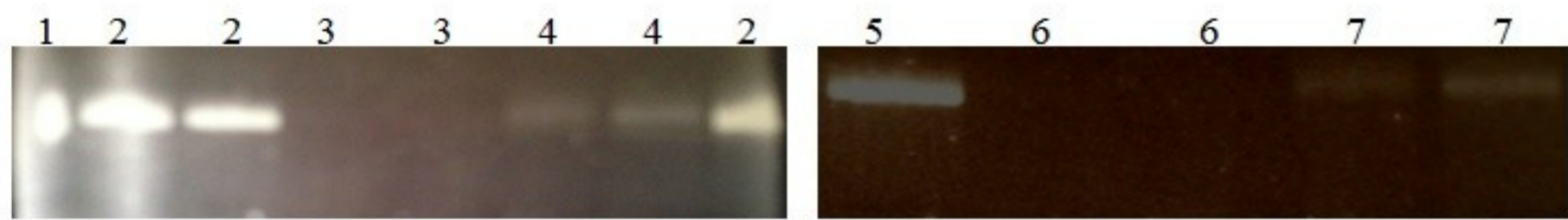


Fig. 5: LMP agarose gel electrophoresis of different enriched and non-enriched metagenomic DNA of POME. 1: fosmid control, 2: enriched-anaerobic, 3: enriched-cooled, 4: anaerobic, 5: enriched-fresh, 6: cooled, 7: fresh. The enriched-anaerobic metagenomic DNA presents the highest quantity of DNA; it is 5 to 7 times more higher than non-enriched metagenomic DNA, while the quantity of enriched-fresh is 5 times more important than non-enriched fresh

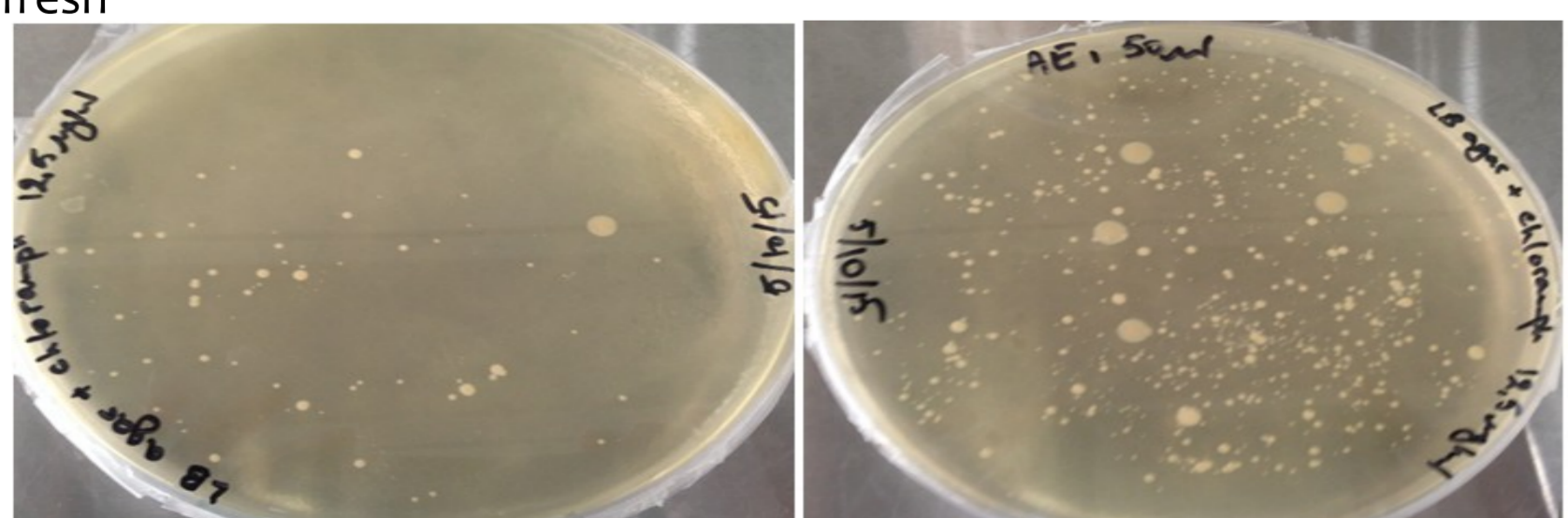
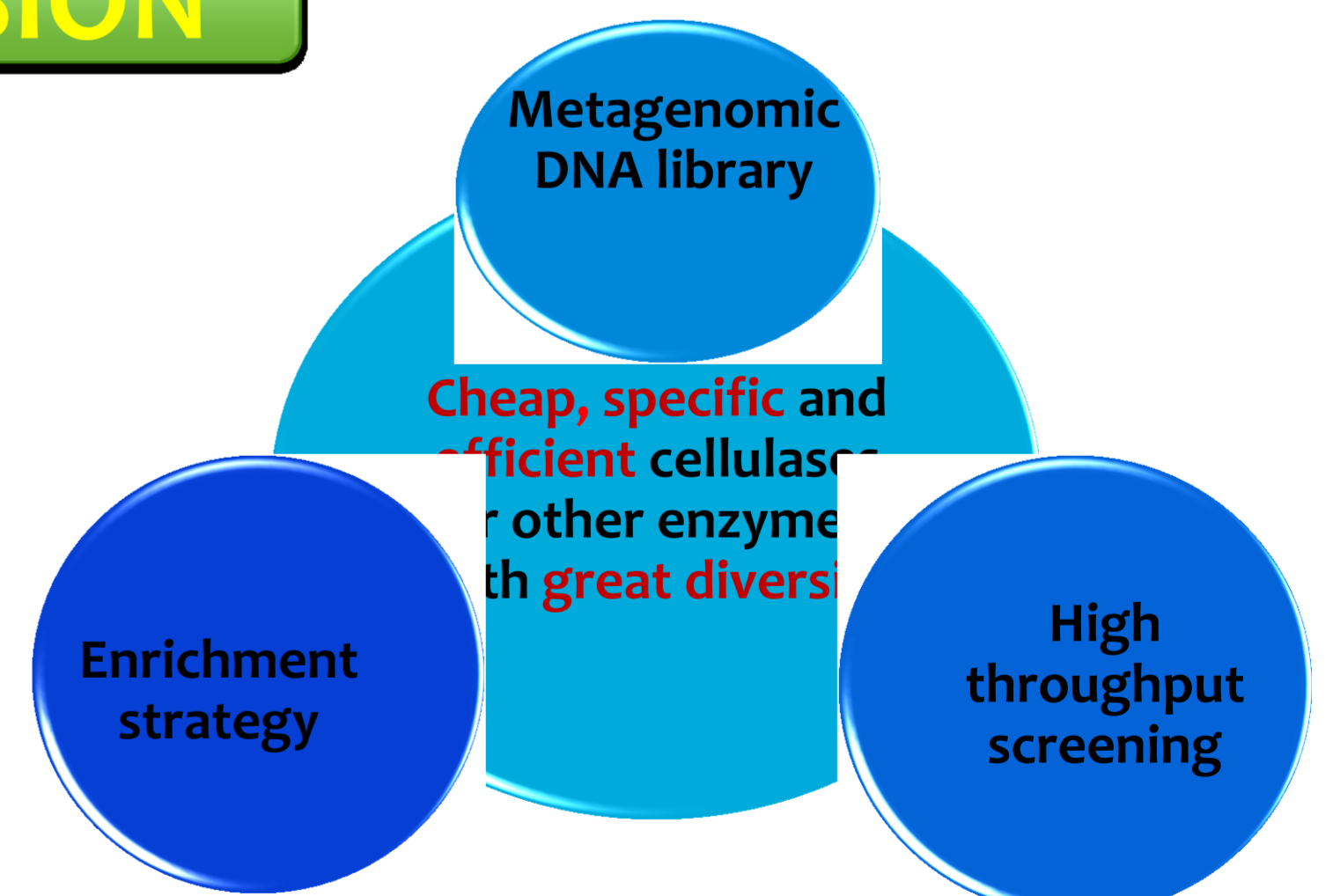


Fig. 6: Large Petri-dishes of transformed EPI300T1 plated on LB agar with 12.5 µg/ml antibiotic. (right) 400 to 600 colonies per Petri-dish from enriched cultures; (left) 70 and 100 colonies per Petri-dish from non-enriched cultures.



- Strategies namely «Metagenomic DNA library construction» combined with «high-throughput screening» and enhanced with «enrichment strategy» can improve the bioprospecting of novel catalysts from Nature.
- This study shows the potential of **bioprospecting** natural enzymes for green industry; cheaper, specific and efficient and highly available.

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