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Understanding the mechanisms underlying bacterial bio-flocculant production

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Bio-flocculants are increasingly employed in water and waste water treatments for solid-liquid separation because they are biodegradable, environmentally safe and non-toxic. Several flocculant-producing bacteria species have been identified, but there exists variability both in their flocculant production ability and efficiency of produced flocculants. To maximize industrial application of bio-flocculants, optimization of several culture parameters is required to ensure high production of efficient bio-flocculants. This requires understanding of the mode of bacterial flocculant production at the molecular level. The aims of the study were to isolate and identify bacterial bio-flocculant producers from Eastern Cape Province of South Africa, and to determine their mechanisms of flocculant production using comparative proteomic approach and pathway analysis. Brackish waters, marine sediments, marine rock scrapings and sand samples from some marine environments inthe Eastern Cape Province of South Africa were collected and screened for bio-flocculant producing bacteria in accordance with the description of Zhang et al. After incubation, culture broth was processed for flocculating activity using kaolin clay suspension. Thereafter, flocculating activity of flocculants from different isolates was calculated by determining their flocculation rates. Actinobacteria species including *Streptomyces* spp., *Brachybacterium* spp., and *Cellulomonas* spp., showed high level of flocculant production: *Streptomyces* spp. (3.88±0.432 g/l), *Brachybacterium* spp. (4.06±0.62 g/l), and *Cellulomonas* spp. (3.99±0.79). Flocculant activity for Streptomyces spp., Brachybacterium spp., and Cellulomonas spp. was 92%, 89% and 83% respectively. The 3 isolates with high production of efficient flocculants have been selected for proteomic analysis to determine bacterial metabolic pathways that are important in flocculant production. Characterizing these pathways will provide a better understanding of the mechanisms underlying bacterial flocculant production, and could lead to improving industrial flocculant production and efficiencies.

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