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Model microbial communities for biocellulose production: dynamics, labour division and functionalities

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Bacterial cellulose (BC) is a biopolymer useful for several food and biomedical applications. BC production suffers from several constraints (strain-dependent, variability, high costs) and, therefore, strategies to improve BC yield is of practical relevance.

In the Project SynBioCell, 12 model microbial communities (MMC) were constructed by assembling, through a combinatorial approach, 4 acetic acid bacteria (AAB, core strains and BC-producers), 3 lactic acid bacteria (LAB, helper) and 3 yeasts (Y, helper), to boost BC yield, compared to individual AAB strains. The best MMC (including 2 AAB and 3 LAB) was select and re-combined to evaluate the microbial dynamics, cell compartmentalisation and strain functionalities during BC production (plate counting, BC yield, 16S rRNA-based qPCR, qPCR on cellulose sintasi complex, ^{1}H-NMR spectroscopy). Metatranscriptomic analyses were also performed to investigate the metabolic interaction of MMCs members.

The composition of MMCs significantly affect the BC production and, generally, LAB stimulated the BC yield. A good correlation was found for strain occurrence detected with plate counting and *16S rRNA* gene. qPCR confirmed the overexpression of CS genes in LAB-containing consortia. Metatranscriptomic data revealed that AAB functionalities significantly changed in MMC compared to the single AAB cultures, due to the shift in metabolic pathway stimulated by the presence of LAB. Our results showed that targeted MMCs could be an efficient machinery to improve BC production and provided further insights on metabolic networks and dynamics of microbial consortia.

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