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Study of Metabolic Flux Distribution in Rice (*Oryza sativa*) Cultures for Starch Production

Nuri, Nur Aqila Syafiqah Abdul^a ; Puad, Noor Illi Mohamad^a ; Abduh, Muhammad Yusuf^b ;Azmi, Azlin Suhaida^a [Save all to author list](#)^a Department of Chemical Engineering and Sustainability, Kulliyyah of Engineering, International Islamic University Malaysia, P.O. Box 01, Kuala Lumpur, 50728, Malaysia^b School of Life Sciences and Technology, Institut Teknologi Bandung, Jalan Ganesha, No. 10, Bandung, 40132, Indonesia [View PDF](#) [Full text options](#) [Export](#)**Abstract****Author keywords**

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Abstract

The demand for starch-rich crops remains high due to their wide applications, and one of them is rice (*Oryza sativa*). However, large-scale rice production faces challenges such as unstable productivity, climate changes and excessive use of agrochemicals. Plant cell culture technology is proposed to increase rice yield and produce a drought-resistance variety of rice to sustain its demand. However, the amount of starch in rice cultures is expected to be smaller compared to the planted ones. The main aim of this study is to apply Flux Balance Analysis (FBA) to optimize starch production in rice cultures. This study reconstructed the stoichiometric metabolic model for rice culture based on the published articles. It consists of 160 reactions and 148 metabolites representing rice's main carbon metabolism towards starch production. The model was then formulated in GAMS v31.1.0, and the objective function was set to the maximization of biomass and starch. The selected constraints (sugar uptake rates and cell growth rates) from previous studies were utilized. The simulated starch production rate values were achieved at the highest glucose uptake rates with the value of 0.0544 mol/g CDW.h. The internal metabolic flux distributions demonstrated that the incoming carbon fixes were directed towards the glycolysis pathway, TCA cycle, PPP cycle, and starch biosynthesis reactions. The study results serve as a starting point to further understanding the starch production mechanism in plants known to be complex. © Universiti Putra Malaysia Press.

Author keywords

FBA; General Algebraic Modeling System (GAMS) software; metabolic flux distribution ; rice ; starch

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✉ Puad, N.I.M.; Department of Chemical Engineering and Sustainability, Kulliyyah of
Engineering, International Islamic University Malaysia, P.O. Box 01, Kuala Lumpur,
Malaysia; email:illi@iium.edu.my
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