Identification, astaxanthin production and genome sequence of yeasts from flowers

Patcharaporn Hoondee[1,2], Engkarat Kingkaew[1], Sukanya Phuengjayaem[1], Nisachon Tedsree[1], Pornchai Rojsitthisak[3], Boonchoo Sritularak[4], Worrathat Thitikornpong[3], Somphob Thompho[5], Natapol Pornputtapong[1], Somboon Tanasupawat[1]

[1] *Department of Biochemistry and Microbiology, Faculty of Pharmaceutical Sciences, Chulalongkorn University, Bangkok 10330, Thailand*
[2] *Division of Biology, Faculty of Science and Technology, Rajamangala University of Technology Krungthep, Bangkok 10120, Thailand*
[3]*Department of Food and Pharmaceutical Chemistry, Faculty of Pharmaceutical Sciences, Chulalongkorn University, Bangkok 10330, Thailand*
[4]*Department of Pharmacognosy and Pharmaceutical Botany, Faculty of Pharmaceutical Sciences, Chulalongkorn University, Bangkok 10330, Thailand*
[5]*Pharmaceutical Research Instrument Center, Faculty of Pharmaceutical Sciences, Chulalongkorn University, Bangkok 10330, Thailand*

*Corresponding author: Tel. +66(0)2-218-8376; Fax. +66(0)2-254-5195; E-mail address: Somboon.T@Chula.ac.th

Keywords: Astaxanthin, Carotenoid, Whole genome sequencing, Pigment, Yeast, *Rhodotorula paludigena*

Astaxanthin is a natural carotenoid pigment with high antioxidant activity and commercial value. Microbial astaxanthin production has become a promising alternative. A total of 29 yeasts were isolated from 50 flower samples collected in Lampang province, Thailand. Of these, 17 isolates were determined to be Basidiomycota, belonging to *Rhodotorula paludigena* (11 strains), *R. mucilaginosa* (3 strains), and potential new species closely related to *R. kratochvilovae* (3 strains). Meanwhile, the 12 remaining isolates were classified as 9 species in 7 genera of Ascomycota. Surprisingly, all the basidiomycetous yeasts found in this study were pink to orange-red pigmented and showed positive astaxanthin formation when determined on a TLC-developed plate. Analysis of their intracellular astaxanthin accumulation by UV spectrometry revealed that *R. paludigena* TL35-5 was the greatest astaxanthin-producing strain with an astaxanthin content of 275.94 ± 0.16 g/g DCW. *R. paludigena* was first reported as astaxanthin-producing yeasts in this study. *R. paludigena* TL35-5 was then selected for further astaxanthin production optimization and genome sequence analysis. The whole genome of *R. paludigena* is the second to be reported to date for its species. *R. paludigena* TL35-5 genome was 20,982,417 bp long with a GC content of 63.75%. A total of 6,701 protein-encoding genes were predicted, with a total length of 10,181,859 bp. Essential genes required for the biosynthesis of β-carotene, and other derivative biosynthesis pathways namely terpenoid backbone biosynthesis, xanthophyll biosynthesis, and β-carotene degradation, could be identified. Our findings indicated that *R. paludigena* TL35-5 had the potential to be an astaxanthin-producing yeast.