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Cloning and characterization of seed specific transcription factor for regulating anthocyanin biosynthesis in Indonesia black rice (*Oryza sativa* ‘Cempo Ireng’)

Yekti Asih Purwestri
Universitas Gadjah Mada, Indonesia

Black rice is considered as functional food which containing bioactive compounds such as anthocyanin. It is our interest to determine genes responsible for anthocyanin biosynthesis. In this research, we obtained cDNA library from different developmental stages of black rice seeds and white rice seeds as control. Seeds were harvested at different developmental stages (at pollination time, 2, 7, 14 and 21 days after pollination) for RNA isolation. One μg of RNA were subjected for obtaining cDNA library. Semi-quantitative RT-PCR showed that several seed-specific transcription factors regulating anthocyanin biosynthesis were expressed in Indonesian local black rice. Our previous result showed that two of down regulating genes showed small differences with control rice (white rice cv. Ciherang). Interestingly, one of up-regulating (*Os1lg059600*) demonstrated the high expression level at all four seed developing stages, however only expressed at the day of pollination in white rice control. This result indicated that this gene may play a role in the anthocyanin production during seed development. This gene was reported as conserved hypothetical protein located at chromosome 11 (RAP-DB). The down regulating genes were assumed inhibit anthocyanin metabolism or had a negative effect on the anthocyanin biosynthesis pathway. Further characterization to get insight the function of this gene in the biosynthesis of anthocyanin in black rice cv Cempo ireng was important to develop black rice or other crops as functional food.

yektiugm@yahoo.com

Connotation of glutathione-S-transferase enzyme expression (GST) and glutathione (GSH) in human head and neck squamous cell carcinoma cancer

Sami Ullah Khan, Abdul Qayyum, Faraz Arshad Malik and Mahmood Akhtar Kayani
Kazan Federal University, Russian

A series of enzymes deliver protection from harmful injury by toxic chemicals. Among these, Glutathione-S-transferase (GST) is most imperative for detoxifying exogenous and endogenous substances to protect cells from the toxic effects of ROS. Reactive oxygen free radicals are implicated in the pathogenesis of a multistage process of head and neck carcinogenesis which are proposed to cause DNA base alterations, strand breaks, damage to tumor suppressor genes and an enhanced expression of proto-oncogenes. This study was conducted in COMSATS institute of Information Technology Islamabad supported by a grant from Higher Education Commission, Islamabad (Pakistan). In the present study, alterations of Glutathione S-transferase (GST) enzyme activity were investigated in 500 samples (cohort 1 containing 200 head and neck cancer blood samples along with 200 healthy controls and cohort II with 50 head and neck squamous cell carcinoma tissue samples along with 50 control tissues) by high performance liquid chromatography and ELISA techniques. The results specified that mean blood GSH levels were significantly reduced in head and neck squamous cell carcinoma patients ($p < 0.001$) blood samples as compared to respective controls. In contrast, the levels of GSH ($p < 0.05$) were significantly elevated in head and neck squamous cell carcinoma tissues compared with adjacent cancer free control tissues. The Glutathione S-transferase (GST) enzyme activity, ($p < 0.05$) were significantly reduced in head and neck squamous cell carcinoma patient's compared to adjacent cancer-free control tissues. Our study suggests that dysregulation of glutathione (GHS) levels and Glutathione S-transferase (GST) enzyme activity in head and neck cancer may have potential to contribute to the pathogenesis of HNSCC malignancies. This investigation of the expression of GST-activity and GSH levels may have the potential to predict metastasis and may serve as a prognostic marker.

skmwt2003@gmail.com