

Category	: International Rice Research Conference
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Keyword 1	: Healthy food systems
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Keyword 3	: Glycemic index
Title of Entry	: Identification of key regulatory genes involve in the biosynthesis of native Resistance Starch(RS) in rice through multi-omics approach.
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Abstract	: Among cereals rice( <i>Oryza sativa</i> L.)is the major source of starch consumed by billions of people. Digestion of carbohydrate eaten as a starch began at mouth than proceed to stomach and duodenum where its further bio-chemically broken down to monosaccharides. The portion of starch that skips the digestion and breakdown by microbes of gut into compounds other than glucose is called resistance starch(RS).Unlike the starch,calories from RS is unavailable in blood as glucose or in liver as glycogen as it starts its journey towards large intestine and by the process of fermentation they are metabolized as short chain fatty acids (SCFA). Different RS fractions have been identified in cereals products such as native starch,retrograded amylose,the chemically modified starch the amylo-lipid complex. In this study, the key regulatory genes,transcription factor and signaling pathways involve in the formation of native RS biosynthesis in rice has been identified. We selected the natural occurring high and low RS lines from indica rice population. Through genome wide association analysis (GWAS) and targeted association,SSIHA along with other novel unknown genes located at Chr6 region were found to be strongly associated with RS phenotype. Differential gene expression analysis (DEGS) between contrasting RS lines at system-based level identified the hub candidate gene which found to be mostly unknowns and some associated with different functions like glycosyl hydrolase,pectin esterases,splicing factor,aspartate protease,signaling kinases,OsSAUR53,NAC domain, TCP and bHLH etc. All of the candidate genes were found to be associated with major starch metabolism gene such as GBSS1(granule bound starch synthase),SSs(starch synthases) and SBE,DBE(starch branching,debranching enzymes).Positive correlation of RS was detected with gelatinization temperature(GT) and amylose structure(AM1,AM2) and negative with glycemic index(GI).The metabolic pathway overview reveal certain genes to be specifically up and down regulated in high and low RS lines. Thus our analysis identified the key regulatory genes present at a neighbors of known starch biosynthesis genes which are essential for native RS formation. We can use this genes as markers in breeding program to develop the rice varieties with high RS content. Consumption of such variety will helps us to maintain a healthy digestive system and prevention from modern lifestyle diet

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