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Marker assisted selection for rubber yield potential of Hevea brasiliensis genotypes suitable for stress prone non-traditional rubber growing areas

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Background: Hevea brasiliensis is the primary source of natural rubber (NR) which is an important industrial raw material. As the current NR production in our country is not sufficient to meet the demand, rubber cultivation is being expanded to non-traditional regions which experience extreme climatic conditions during summer and winter. The genotypes that perform well in the traditional regions have often been noted to suffer yield reduction in such regions. Hence, it is necessary to develop/identify genotypes with high yield potential and stress tolerance. Genes encoding key rubber biosynthesis enzymes can be used as marker for high yield potential. In this study, attempts would be made to identify genotypes with high yield potential under stress conditions using yield specific markers.

Objectives: The main objective is to identify high yielding genotypes of Hevea suitable for drought/cold stress prone regions using marker assisted selection approach.

Methodology: About 100 genotypes with high yield potential would be evaluated under stress conditions for their yield potential. Validation of markers will be evaluated by quantitative PCR and marker-trait relationship will be established.

Concept: Many studies indicate the direct correlation between genes such as HMGR1, FPPS, RuT2, SRPP and REF related to rubber biosynthesis pathway, HbACO mediating ethylene biosynthesis, HbSUT, HbBAM and HbPK facilitating carbohydrate metabolism and ATP synthase in energy metabolism with yield. Genes related to efficient water inflow into laticifers such as HbPIP1;3, HbPIP1;4 and HbPIP2;3 also have been found to be positively correlated with yield. While chitinase is positively correlated, hevein is negatively correlated with yield. Expression of all these markers will be evaluated in a large set of genotypes with varying yield potential grown in non-traditional regions and eventually markers exhibiting strong association with high yield (under stress conditions) would be identified which would be further employed in crop improvement programmes.

Conclusion: The markers having strong association with yield need to be evaluated in a large set of genotypes to further identify high yielding elite genotypes for non-traditional regions experiencing drought or cold stress.

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