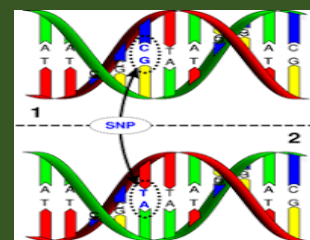


<b>Technology</b>	<b>1. Genomic selection models and SNP markers for red rot resistance</b>
<b>Year</b>	2024
<b>Features</b>	<ul style="list-style-type: none"> <li>• A set of markers with largest effect on red rot resistance was found in sugarcane.</li> <li>• The most significant SNP is co-locating with a cluster of four Chitinase A genes, NBS LRR and DMR region.</li> <li>• SNP marker AX-118043322 and AX-117916984 from linkage group A and markers AX-117251209 and AX-117216196 from linkage group B is associated with red rot resistance.</li> </ul>
<b>Use of the Technology</b>	<ul style="list-style-type: none"> <li>• SNP markers are used to scan for the presence of the major QTLs in sugarcane germplasm</li> </ul>
<b>Impact</b>	<ul style="list-style-type: none"> <li>• SNP markers are used to select red rot resistant parental clones in early selection stages of sugarcane breeding program.</li> </ul>
<b>Developers</b>	R. Manimekalai, G. Hemaprabha, R.Viswanathan, K. Mohanraj, R. Viswanathan, A. Selvi, O connel, Deo, J., deomano,E., Wei, X., Jackson, P., Aitken, K., Ram, B., and Lakshmanan, P.

### SNP markers for red rot resistance in sugarcane

Genotyping with SNPs



Red rot resistance

Predictive Genomic selection models

Linked SNP makers for red rot resistance