Substantial breeding efforts in the last century led to the improvement of agronomic traits of many crops including yield, grain quality, heading date and stress tolerance…

Agronomic traits are influenced by a number of genes, gene x gene interaction and gene x environment interaction. Consequently, continuously phenotypic variation occur in hybrid progenies.

The genes are generally referred to as quantitative trait loci (QTL).
For the past ten years, molecular markers have been used successfully in gene mapping and QTL analysis based on high density linkage map for identifying chromosomal regions that controlling quantitative traits.

Genetic markers represent genetic differences between individual organisms or species.

There are three major types of genetic markers:

1. Morphological markers
2. Biochemical markers
3. Molecular markers
**QTL ANALYSIS**

**Anthesis silking interval (ASI)**

![Bar chart](image)

The frequency distributions of 194 F$_2$ plants of maize for ASI

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**QTL ANALYSIS**

**Grain yield (g)**

![Bar chart](image)

The frequency distributions of 194 F$_2$ plants of maize for grain yield
QTL ANALYSIS

The genetic linkage map contains 85 SSR markers and covers 1350 cM, using 194 F\textsubscript{2} plants derived from a cross between D12 and CLM161.

QTL analysis for ASI and GY in 194 F\textsubscript{2} plants of D12 and CML161.

<table>
<thead>
<tr>
<th>Condition</th>
<th>QTL</th>
<th>Chromosome</th>
<th>Interval markers</th>
<th>Nearest marker (cM)</th>
<th>Additive effect</th>
<th>Dominant effect</th>
<th>Phenotype variation (%)</th>
<th>LOD</th>
</tr>
</thead>
<tbody>
<tr>
<td>Water stress</td>
<td>GY</td>
<td>1</td>
<td>bnlg1429-bnlg1811</td>
<td>bnlg1429(2.6)</td>
<td>-7.26</td>
<td>-3.66</td>
<td>10.60</td>
<td>2.87</td>
</tr>
<tr>
<td>ASI</td>
<td>1</td>
<td>bnlg1811-umc2228</td>
<td>bnlg1811(9.1)</td>
<td>-0.92</td>
<td>-0.01</td>
<td>12.10</td>
<td>2.6</td>
<td></td>
</tr>
<tr>
<td>GY</td>
<td>9</td>
<td>umc1804-umc1675</td>
<td>umc1804(2.0)</td>
<td>4.314</td>
<td>7.212</td>
<td>13.69</td>
<td>4.02</td>
<td></td>
</tr>
<tr>
<td>ASI</td>
<td>9</td>
<td>umc1078-bnlg1091</td>
<td>bnlg1091(3.7)</td>
<td>-0.299</td>
<td>-0.188</td>
<td>12.80</td>
<td>3.67</td>
<td></td>
</tr>
<tr>
<td>ASI</td>
<td>3</td>
<td>umc1588-umc1399</td>
<td>umc1399(7.3)</td>
<td>0.215</td>
<td>0.202</td>
<td>5.00</td>
<td>2.78</td>
<td></td>
</tr>
</tbody>
</table>
Bacterial blight (BB) of rice is considered the serious disease in rice-growing countries worldwide. Since there is no bactericide effective to the disease, introduction of resistance varieties is the most effective measure to control disease.

In Vietnam, bacterial blight of rice is one of major rice diseases affecting to yield, grain quality and productivity. The change of rice ecosystem, cropping pattern, and intensive farming as well as susceptible varieties are significantly influenced to disease.

The objective of this study to develop the restorer lines containing Xa7 and Xa21 by a combination of phenotype against Xoo diagnostic strains and marker-assisted selection.
MARKER ASSISTED SELECTION

Genetic linkage map of Xa7 AND Xa21 resistance genes in chromosome 6 and chromosome 11

MARKER ASSISTED SELECTION

Electrophoresis result of PCR product using marker RM20590. Note, M: Marker ladder, 1: Que99, 2: IR24, 3 to 14 BC$_3$F$_1$ population Que99(Xa21)3*/IRBB7

Electrophoresis result of PCR product using marker RM20590. Note, M: Marker ladder, 1:MK63, 2: IR24, 3 to 13 BC$_3$F$_1$ population MK63 (Xa21)3*/IRBB7
Soybean production in Vietnam has recently been threatened by the widespread dissemination of soybean rust (SBR) caused by the fungus *Phakopsora pachyrhizi*. Currently, chemical spray containing fungicides is the only effective method to control the disease. This strategy increases production costs and exposes the environment to higher levels of fungicides; introduction of resistant varieties is the most effective measure to control this disease. As first step towards the development of SBR resistance cultivars, we have used PCR based molecular markers in a backcross-breeding program to introgress *Rpp5* gene of SBR resistance into HL203 from two donor lines (DT2000 and Stuart 99084B-28).
Breeding schemes were produced for developing backcrossing population containing SBR resistant gene with genetic background of HL203.

Genetic linkage map of *Rpp5* locus
PCR detection of Rpp5 gene in representative in BC$_2$F$_1$ plant. Marker used was Sat_275 (M: 100bp ladder, 1: HL203 recurrent parent, 2: DT2000 donor, 3-13: BC$_2$F$_1$ plants)

MARKER ASSISTED SELECTION

Late blight disease of tomato
MARKER ASSISTED SELECTION

Ph-3 resistant gene on chromosome 9

PCR product with marker SSR383 on chromosome 9. Note: 1, 2: resistant lines, 3: susceptible line.

PCR product with marker SSR69 on chromosome 9. Note 1-2: resistant lines, 3: susceptible line.
Phenotype

Population

Segregation

F2, BC, RILs, DH

- Continuously distribution
- 3:1 or 1:1

QTL analysis

Detect QTL

QTL

- Effect
- Position

Mapping

N = 100-200

- ANOVA
- SIM
- CIM

Making NIL

High resolution mapping

N = 3000-10000

Cloning

THANKS FOR YOUR ATTENTION!