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# **Resources for high throughput marker development and large-scale gene silencing**

## **Genyi Li**

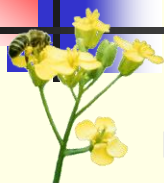
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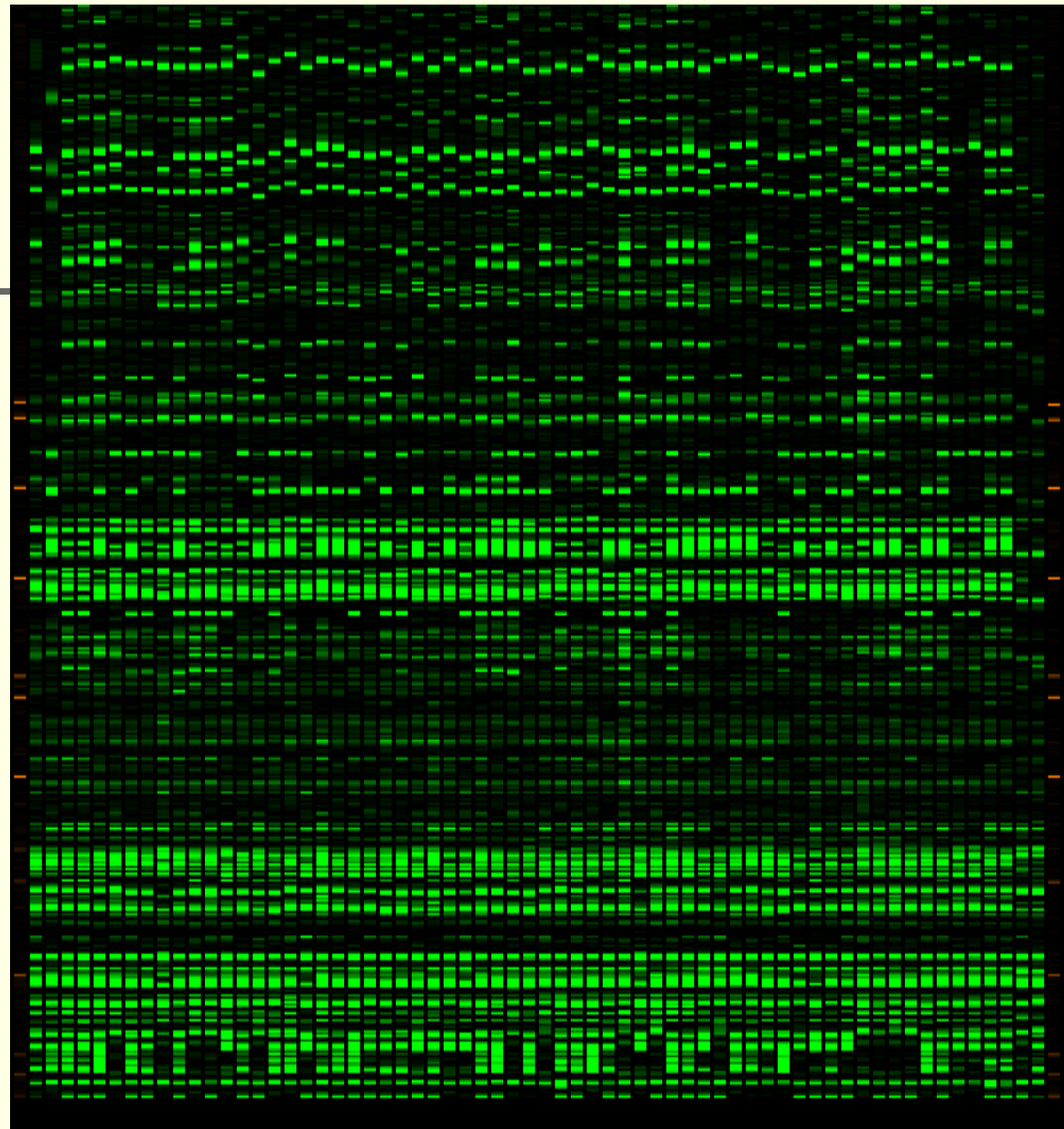
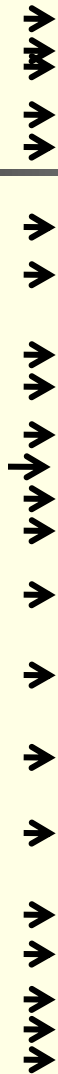
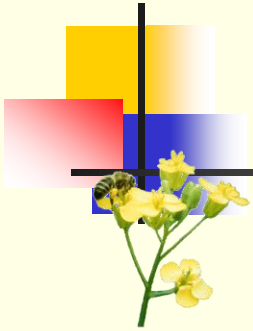


# Most saturated genetic map with 13,551 SRAP molecular markers in canola/rapeseed



- SRAP technology: one step PCR with two primers
- One labeled primer combined with many unlabeled primers
- High throughput based on the individuals and marker number.
- QTL mapping with multiple populations
- Map-based gene cloning





SRAP  
Markers

A SRAP image for map construction

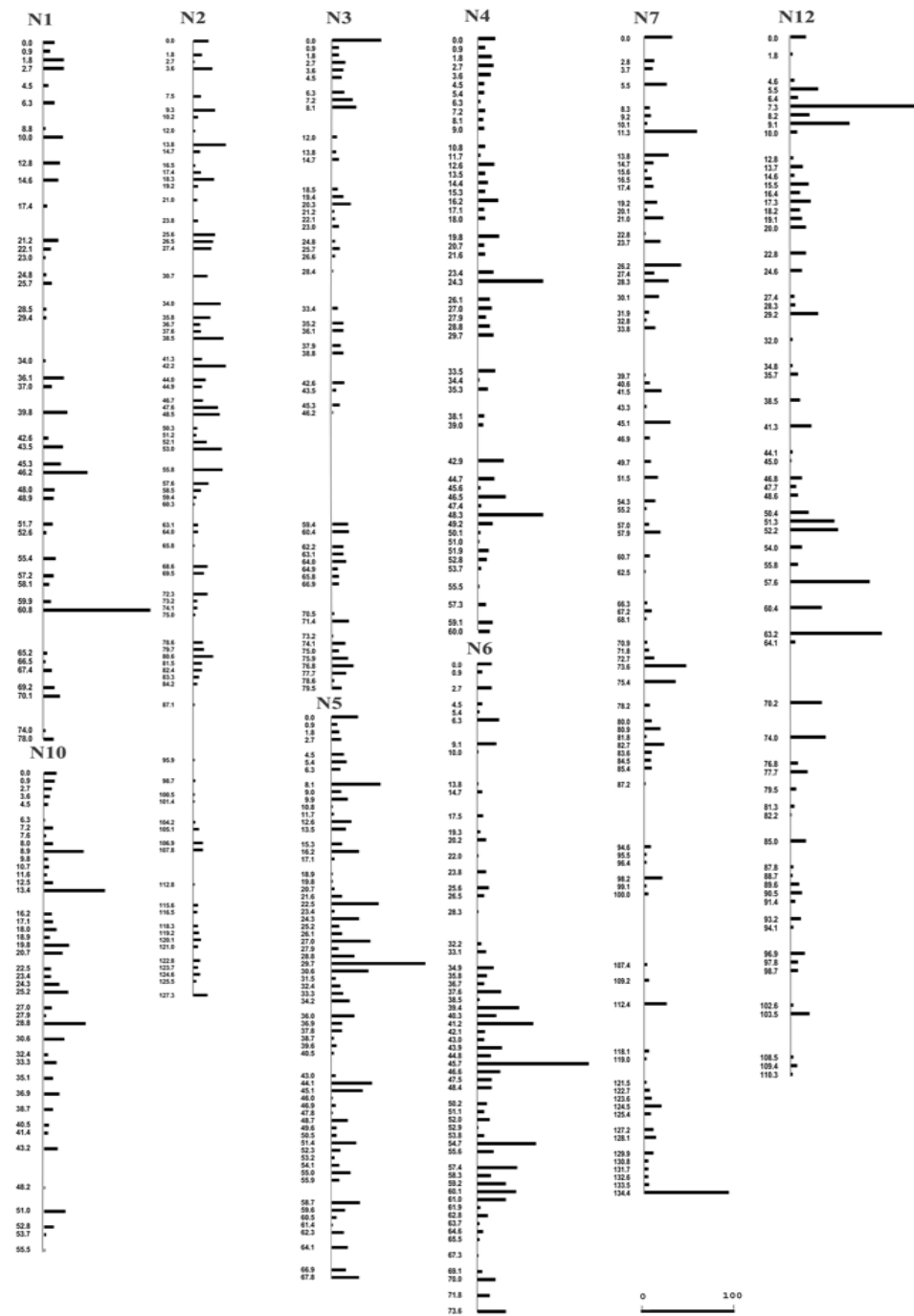


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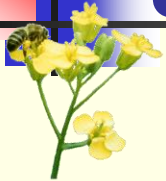
# Most saturated Genetic map 13551 SRAPs (Nine LGs)



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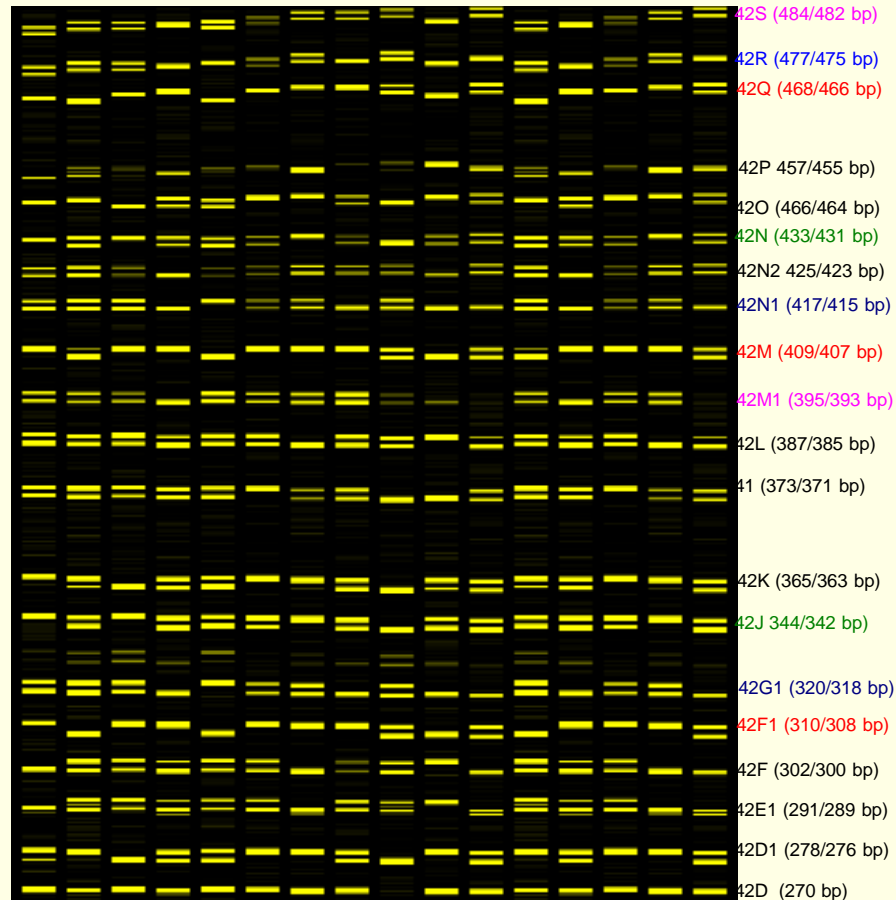
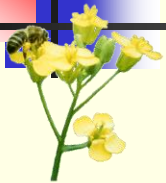
# High throughput genome specific markers for erucic acid content



- Two genes FAE1-1 and FAE1-2 controlling erucic acid content
- Three nucleotide difference between rapeseed and canola
- Obtaining genome sequences flanking the FAE1 genes
- Finding genome sequence differences between the A genome and C genome
- One base change in the A genome for SNP markers
- Two base deletion for multiplexing SCAR markers



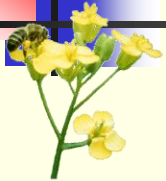
# High throughput multiplexing SCAR molecular markers For erucic acid content





# Large-scale RNAi transformation

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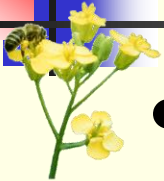
- RNA interference (RNAi)
- Silencing a gene family with one construct
- Creating phenotypic changes more easily in canola
- Deciphering gene function
- Creating beneficial traits





# Large scale RNAi transformation

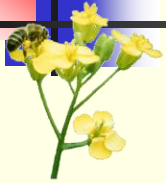
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- RNA interference (RNAi)
- Silencing a gene families with one construct
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# Sequence analysis of cloned SRAP amplicons from cDNA



	Leaves	Isolated PMC	Total
Sequences	6528	8832	15360
Hitting Arabidopsis genes	1284	2698	5290
Non-redundant genes	492	816	1308
Over-lapping between leaf and PMC cDNA			82
Uni-genes			1226





# RNAi constructs and large-scale transformation (Goals in two years)

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- 1000 RNAi constructs
- 25-50 transgenic plants
- 25000-50000 transgenic plants





# Acknowledgement

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- U of Manitoba

Zudong Sun, Jingxing Tu, Jiefu Zhang, Mingjuan Tong, Yu Chan, Feng Gao, Ying Lu, Jianfeng Geng, Yuming Long, Zheng Liu, Zening Wang, Mukhlesur Rahman , Zixia Niu, Ravneet Behla, Arvindkumar H. Hirani, Peter B. E. McVetty, Fouad Daayf and others.

- Institute of Plant Biotechnology, Saskatoon  
Wilf Keller, Joe Hammerlindl

- UC Davis

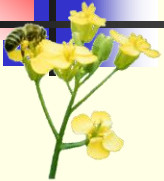
Carlos Quiros, Muqiang Gao, Bo Yang





# Acknowledgement

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- NSERC discovery project.
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