Heterotic Gene Pool Development in *Brassica napus*

Corey Lees and Robert W. Duncan
Department of Plant Science

Introduction

- *Brassica napus* is the second most important oilseed crop in the world.

- To continually match global demand, plant breeding programs must improve seed quality and agronomic performance.

- Hybrid heterosis is a common method for improving agronomic performance.

- Heterotic gains are linked to the genetic distance between each parent used in hybrid development (Falconer and Mckay 1996).

- Genetic distance is the measure of variation between populations or genotypes.

- Phenotypic and genotypic characterization methods are commonly used as measures of variation.

Objectives

- The objectives of this study were to determine the genetic distance between 95 *B. napus* genotypes and separate them into heterotic gene pools.

- Using these gene pools, putative high heterotic hybrid crosses were created.

- The genetic distance and heterosis of each parental cultivar was measured compared to the check cultivar, HYHEAR 1.

Methods

- Two years of phenotypic data as well as two genotypic methods, Sequence Related Amplified Polymorphism (SRAP) and Genotype-by-Sequencing (GBS) were used determine the genetic distance between 95 genotypes.

- Phenotypic evaluations included: flowering date, flower morphology, lodging, maturity, oil content, fatty acid profile, protein and yield.

- SRAP (Li and Quiros, 2001) produced 314 polymorphic bands scored on a presence/absence basis.

- GBS (Elshire et al, 2011) was conducted at Cornell University. Cornell completed all bioinformatics in Tassel version: 3.0.166. Analysis identified 80,005 Single Nucleotide Polymorphisms (SNP's).

- The GBS data set was analysed in Geneious V.8.03 software and a neighbour-joining method of hierarchical clustering was used to create dendrograms based on Tamura-Nei genetic distance.

- Crosses were developed from these gene pools using the *ogu*-INRA hybrid system to assess whether genetic distance based on Tamura-Nei is a true predictor of high heterosis.
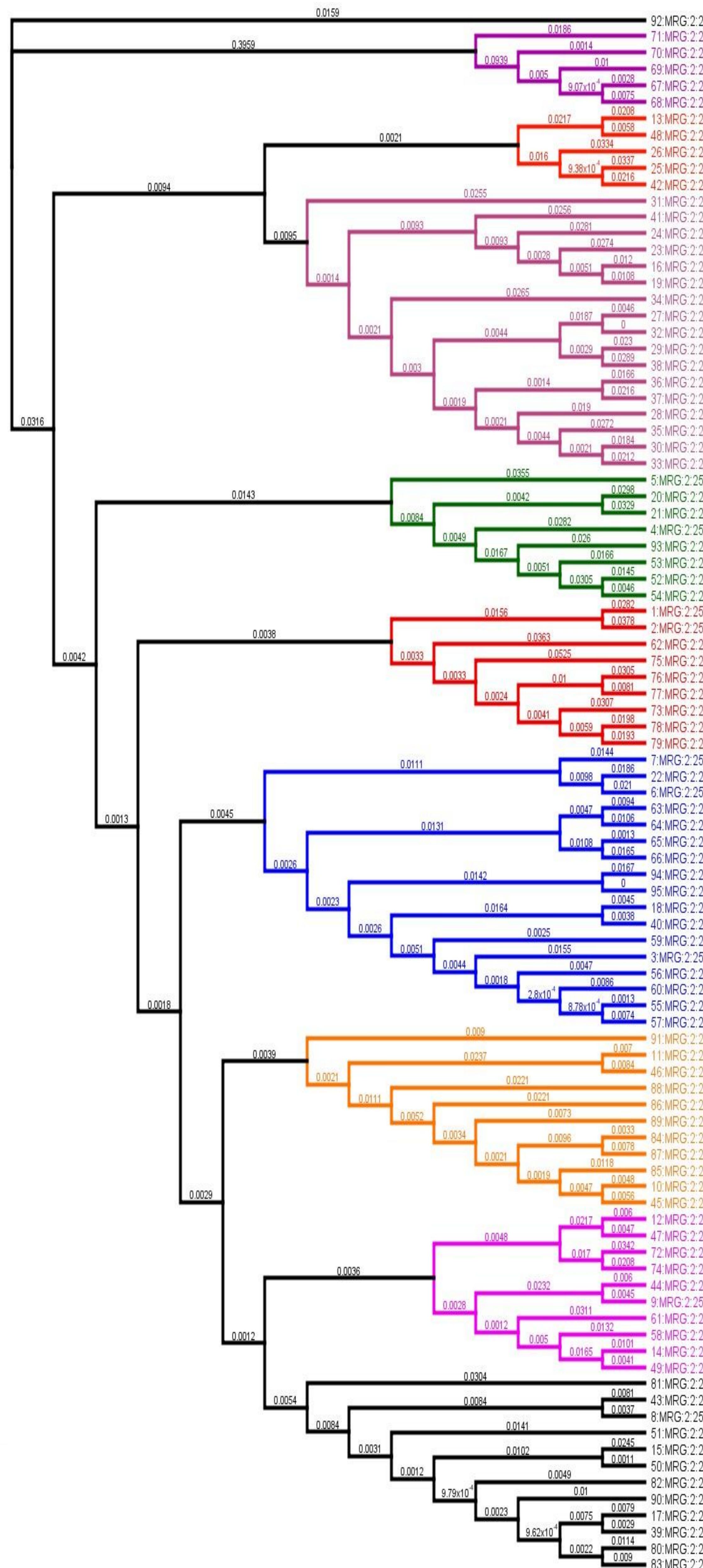
Results

Figure 1: Neighbour joining dendrogram of 95 genotypes based on the genetic distance formula of Tamura-Nei using 80,005 SNP's completed in Geneious V.8.03.

Table 1: Genetic distance, yield and commercial heterosis for select *B. napus* hybrids grown in Winnipeg, Manitoba in 2014

Hybrid Pedigree	GD (%)	Yield Kg/Ha	Commercial Heterosis (%)
53MRG X 31MRG	12.0	3327	118.7
53MRG X 32MRG	12.2	3243	116
53MRG X 26MRG	12.8	3105	110.8
HYHEAR 1 (Check)	8.0	2803	100
50MRG X 34MRG	10.0	2338	88
10MRG X 34MRG	7.8	2014	76
CV		14.8	
LSD		583.6	
R^2 (GD and Yield)		.188	

Conclusions

- Genetic distance as calculated by Tamura-Nei based on 80,005 SNP's from GBS is positively correlated to yield.

- GD alone is not sufficient to accurately predict high heterotic parental combinations.

Research supported by

BUNGE   DL seeds   NSERC CRSNG

UNIVERSITY OF MANITOBA

Email:
Leesc3@myumanitoba.ca