Effect of genotype and location on yield and seed quality of canola across western Canada over three years

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Introduction

Selecting genotypes that are stable in yield and seed quality across a wide geography is key to the successful development of new canola (*Brassica napus* L.) cultivars for western Canada. A study was conducted to determine the effect of genotype and location on yield, oil, protein, glucosinolates and total saturates.
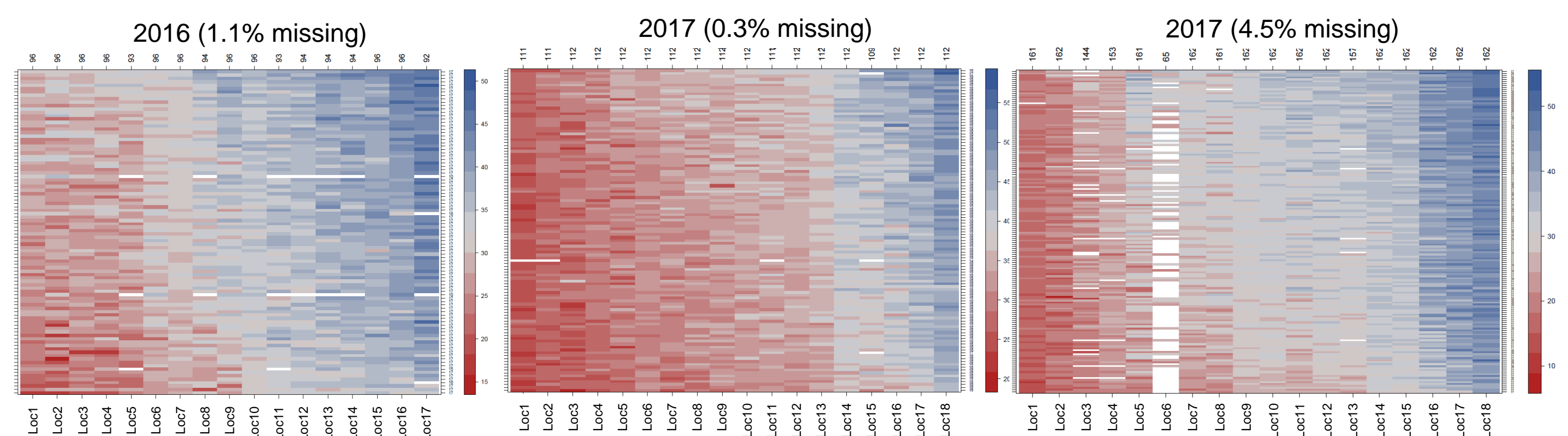
Materials and Methods

A total of 97, 112 and 162 genotypes were evaluated in 2016, 2017 and 2018 growing seasons, respectively, in Manitoba (MB), Saskatchewan (SK) and Alberta (AB) provinces in replicated trials. Genetic variance for each province, covariance of the genotypes between pairs of provinces, genetic correlation between pairs of provinces, and GxE variance among locations within each province for each trait were calculated with Factor Analytic (XFA) GxE model using ASREML. Entries with missing values were removed to meet <10% missing value threshold for each trait. Heatmaps (Fig 1.) were generated using R Studio®.

Results and Discussion

A high genetic correlation was observed between pairs of provinces for all traits tested in 2016, 2017 and 2018. Lower genetic variance for yield was observed in SK in 2016 and 2017 however, in 2018 SK had the highest. Genetic variance for yield, protein and saturates was higher in 2018 compared to 2016 and 2017. Similar pattern was observed for covariance of genotypes between pairs of provinces for above traits (Fig 2.). For both SK and AB, GxE for yield was highest in 2018 (Fig 3.). This study indicates that province specific selections would be very similar to selections across all of western Canada. The data generated in this study will allow more focus on the number of high quality locations to use in future studies.

Fig 1. Heatmaps for Yield trait for 2016, 2017 and 2018 data across all locations.

Correlation	Covariance	Variance

Yield

	SK	AB	MB
2016			
SK	2.03	0.96	0.73
AB	2.19	2.55	0.70
MB	2.53	2.72	5.87
2017			
SK	1.20	0.89	0.79
AB	1.76	3.28	0.74
MB	1.27	1.96	2.16
2018			
SK	4.09	0.94	1.00
AB	3.34	3.11	0.94
MB	3.60	2.94	3.17

Oil

	SK	AB	MB
2016			
SK	1.42	0.96	0.94
AB	1.54	1.78	0.91
MB	1.25	1.34	1.22
2017			
SK	1.11	0.97	0.96
AB	0.96	0.89	0.93
MB	1.06	0.92	1.10
2018			
SK	1.00	0.82	0.88
AB	0.92	1.27	0.87
MB	0.87	0.98	1.00

Protein

	SK	AB	MB
2016			
SK	0.37	0.93	0.93
AB	0.45	0.63	0.86
MB	0.42	0.51	0.55
2017			
SK	0.31	0.96	0.95
AB	0.28	0.27	0.92
MB	0.27	0.24	0.27
2018			
SK	0.69	0.85	0.96
AB	0.60	0.72	0.88
MB	0.71	0.67	0.80

Glucosinolates

	SK	AB	MB
2016			
SK	3.22	0.99	0.97
AB	3.94	4.97	0.96
MB	3.90	4.80	4.98
2017			
SK	3.04	0.98	0.98
AB	2.99	3.09	0.95
MB	2.57	2.52	2.27
2018			
SK	3.50	0.90	0.97
AB	3.04	3.28	0.89
MB	3.71	3.28	4.19

Saturates

	SK	AB	MB
2016			
SK	0.01	0.91	0.82
AB	0.01	0.01	0.75
MB	0.01	0.01	0.01
2017			
SK	0.03	0.99	0.98
AB	0.03	0.03	0.97
MB	0.03	0.03	0.03
2018			
SK	0.05	0.96	0.96
AB	0.04	0.04	0.94
MB	0.04	0.03	0.04

Fig 2. Genetic variance for each province, covariance of genotypes between pairs of provinces and genetic correlations between pairs of provinces for yield, oil, protein, glucosinolates and saturates in 2016, 2017 and 2018.

Fig 3. GxE variance for yield, oil, protein, glucosinolates and saturates in three provinces for 2016, 2017 and 2018.