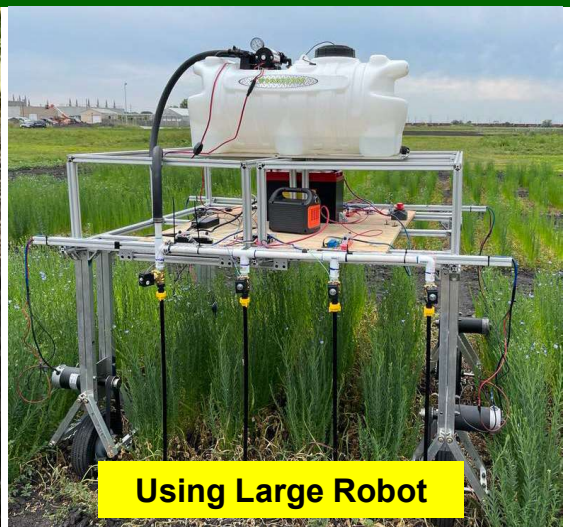
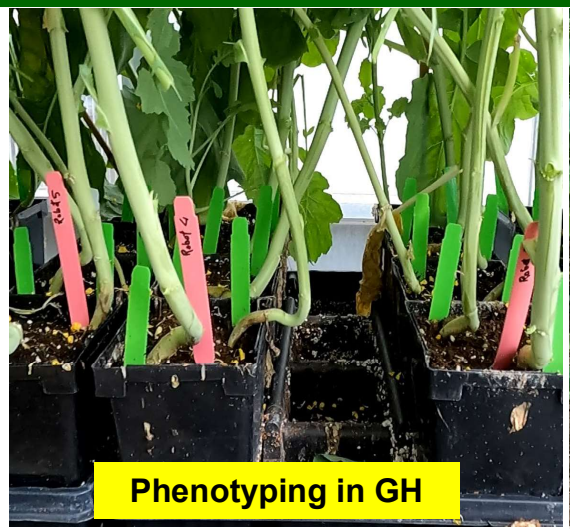
Application of ROBOT for Precision Agriculture


Using Small Robot


Using Large Robot


Phenotyping in GH


Phenotyping in Field

Artificial Intelligence and Machine Learning on Stem Diameter and Stand Count
At the University of California Los Angeles

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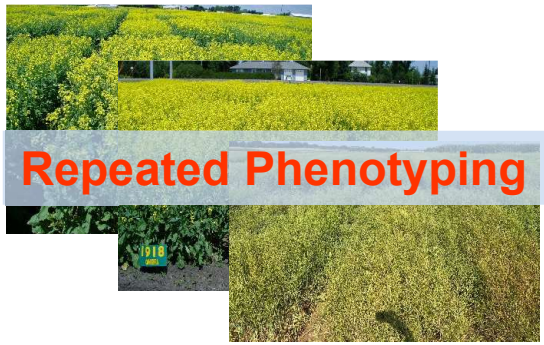
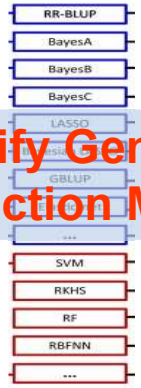
Training Population (~200 lines)



Repeated Phenotyping

Genotyping ~200 lines

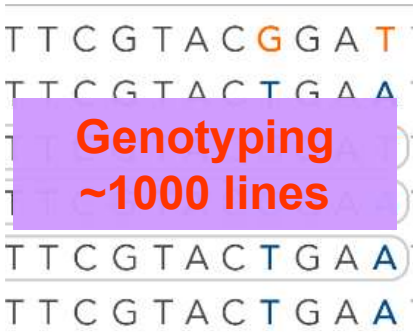


Identify Genomic Prediction Model

Genomic Selection

Breeding or unknown Population (~1000)

No Phenotyping



Genotyping ~1000 lines

Best lines (eg. 100) selection based on the best Pred model

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Genomic Selection – Pod Shattering in Canola

Method: BWGS pipeline in R using CCAST

CCAST= Center for Computationally Assisted Science and Technology (**Provides high-performance computing capabilities for big data analysis**)

Data

- **Rapeseed/canola germplasm accessions = 150**
- **Design = RCBD** with 3 reps
- **Environments = 5** (E1=2020 Osn, E2= 2020 Fargo, E3= 2020 Car, E4= 2021 Osn, E5= 2021 GH)

Models (14)

- GBLUP, RRBLUP, EGBLUP, LASSO, EN, BRR, BL, BA, BB, BC, RKHS, MKRKHS, SVM, RF

Markers used

- 24540 SNP

CCAST Platform

CCAST is the largest academic supercomputing facility in the state of North Dakota, with more than 12,000 CPU cores and 70 GPUs

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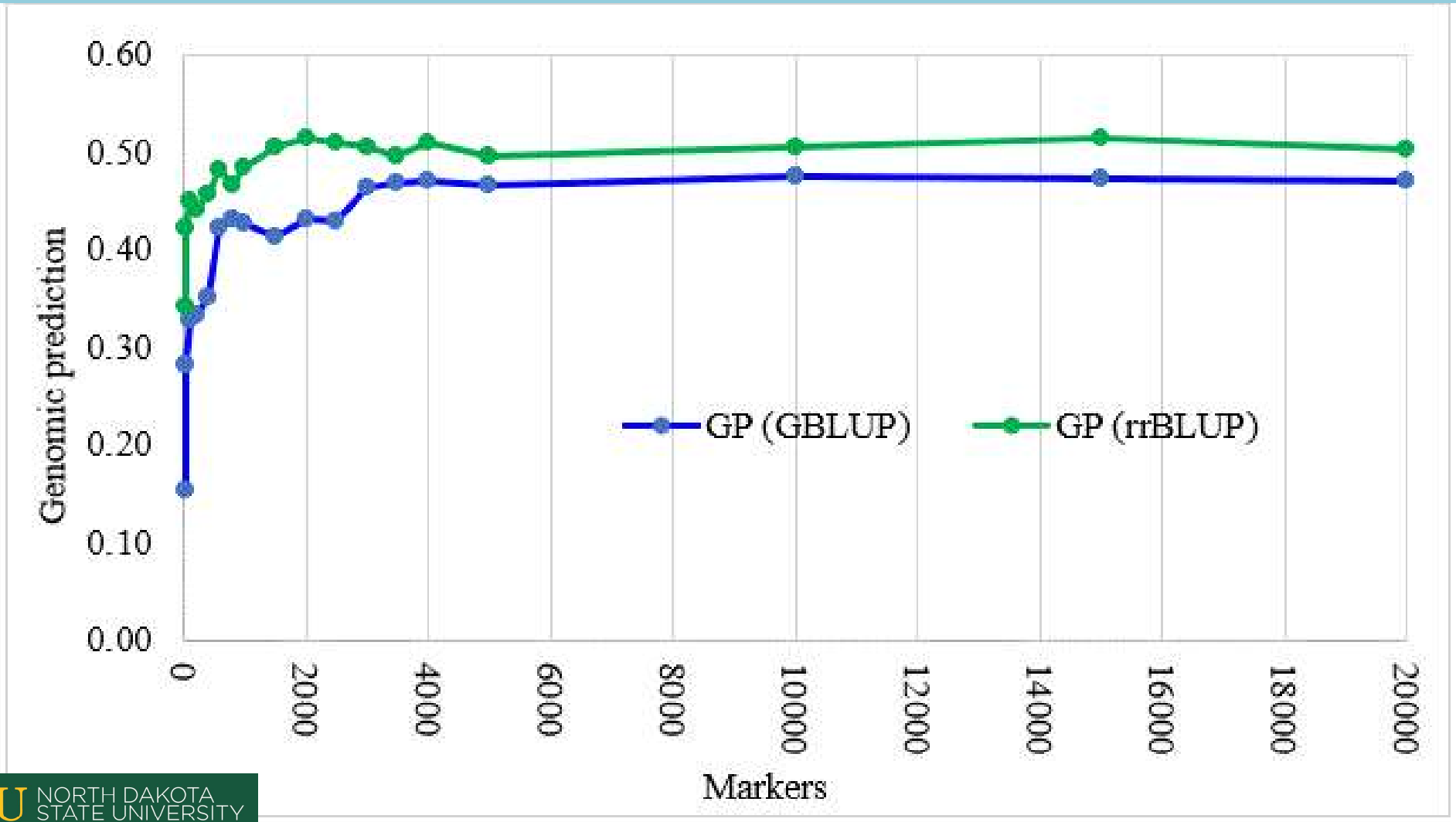
Genomic prediction – using different models - Canola

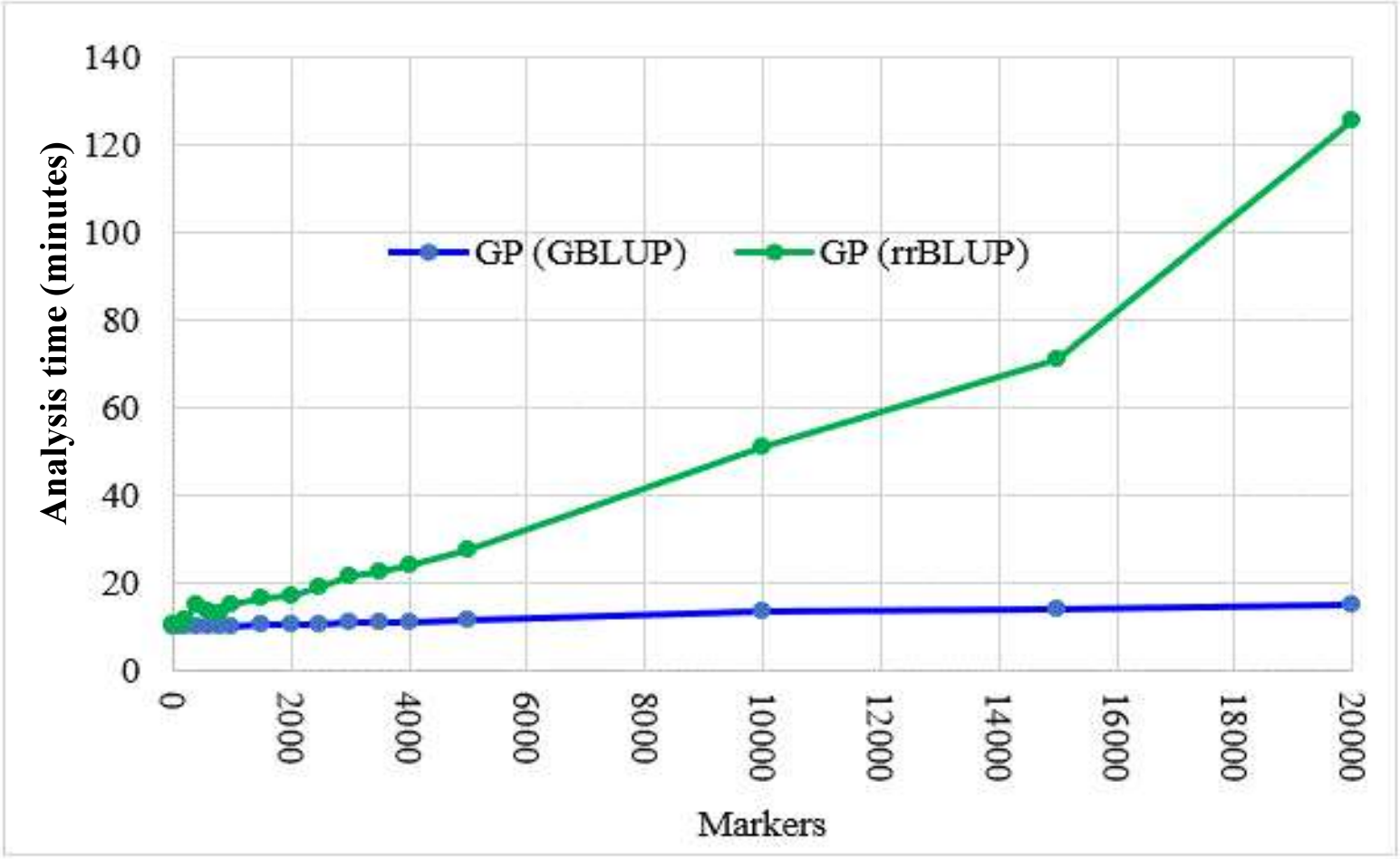
GP Model	Predictive ability in different Environments					
	E1 (20 Osn)	E2 (20 Far)	E3 (20 Car)	E4 (21 Car)	E5 (21 GH)	Average
BayesA	0.32	0.36	0.35	0.37	0.49	0.38
BayesB	0.33	0.36	0.35	0.37	0.48	0.38
BayesC	0.33	0.36	0.34	0.37	0.49	0.38
BL	0.33	0.36	0.34	0.38	0.49	0.38
BRR	0.34	0.35	0.34	0.38	0.48	0.38
EN	0.21	0.35	0.27	0.36	0.42	0.32
EGBLUP	0.32	0.36	0.36	0.35	0.49	0.38
GBLUP	0.32	0.34	0.34	0.36	0.47	0.37
LASSO	0.18	0.33	0.23	0.37	0.40	0.30
MKRKHS	0.32	0.35	0.34	0.34	0.50	0.37
RKHS	0.33	0.35	0.35	0.34	0.49	0.37
RF	0.33	0.38	0.38	0.37	0.50	0.39
RRBLUP	0.35	0.33	0.36	0.36	0.49	0.38

What is the Optimal Number of Markers Required for Genomic Prediction?

Canola



Time Required for Genomic Prediction Analysis



Time requirement by different models - Flax

CCAST= Center for Computationally Assisted Science and Technology

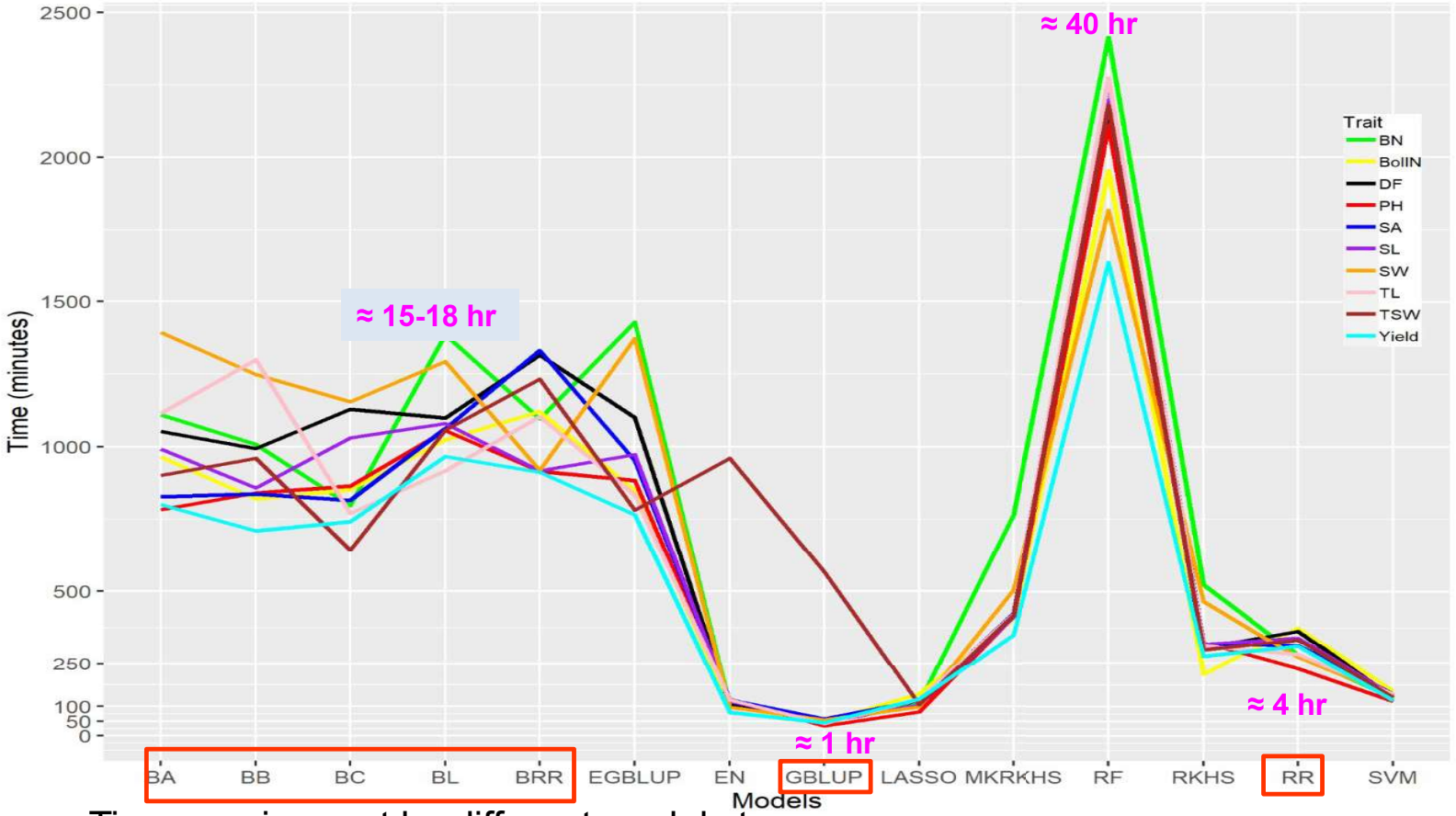


Figure: Time requirement by different models to run

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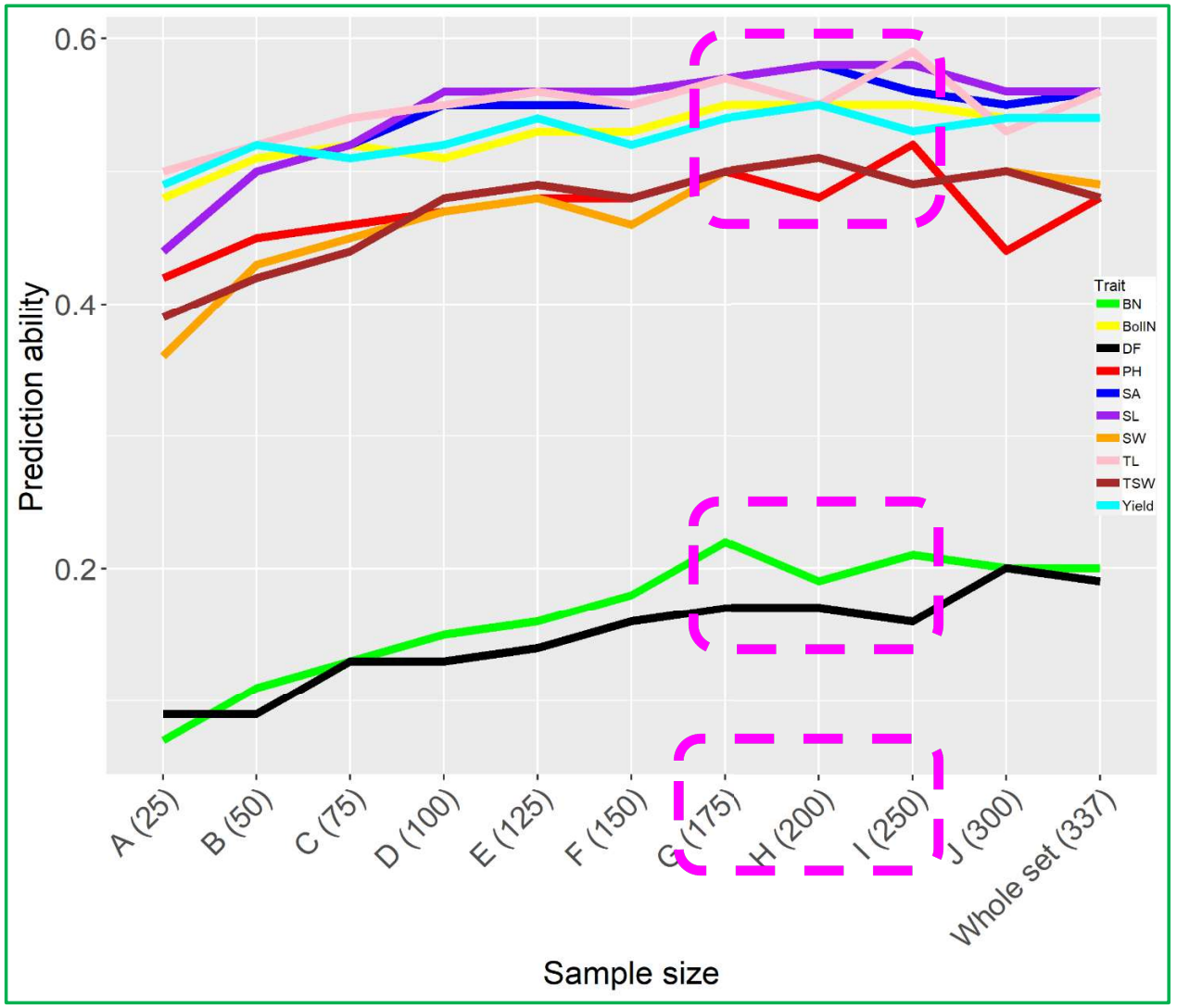
What is the Required Number of Genotypes for the Training Population? - Flax



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