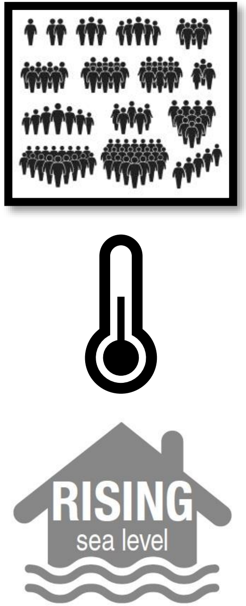
AGRICULTURE VICTORIA

Sowing the Future: Predictions, Simulations & Speed Breeding for Legumes

Dr Sukhjiwan Kaur
Agriculture Victoria
Melbourne, Australia

GRDC GRAINS RESEARCH & DEVELOPMENT CORPORATION

Climate Change and Global Agrifood Volatility



9.8 billion

+1.5°C

↑ 30 cm

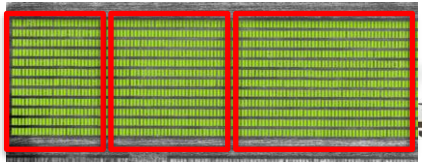
"The amount of food produced in the last 12,000 years is the same amount of food we will need to produce in the next 40 years"

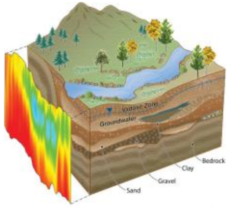
Source: https://www.youtube.com/watch?v=2jF2IsicDC4

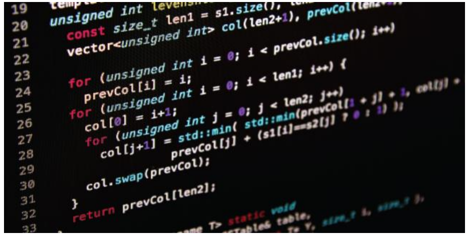
Link from Australian Seed Federation website

By 2050, pulse production should be doubled

Omics in Today's World



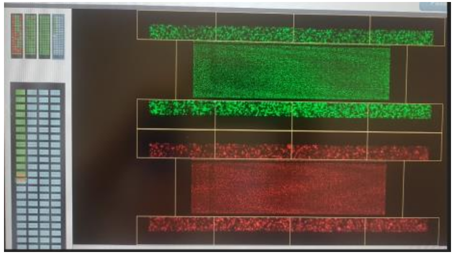


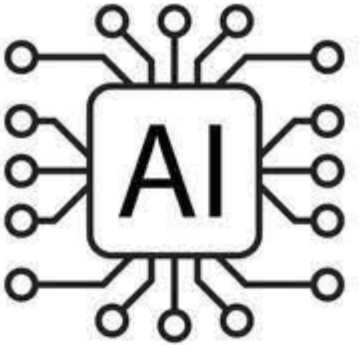


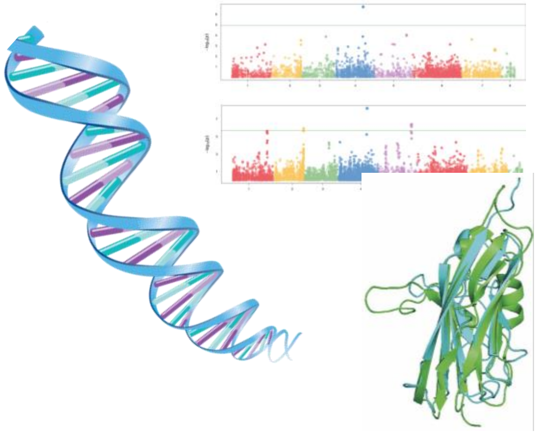
```
unsigned int
  const size_t len1 = s1.size(),
  vector<unsigned int> col(len2+1), prevCol(

  for (unsigned int i = 0; i < prevCol.size(); i++)
    prevCol[i] = i;
  for (unsigned int i = 0; i < len1; i++) {
    col[0] = i+1;
    for (unsigned int j = 0; j < len2; j++)
      col[j+1] = std::min( std::min(prevCol[1 + j] + 1, col[j] +
                      prevCol[j] + (s1[i]==s2[j] ? 0 : 1) );

    col.swap(prevCol);
  }
  return prevCol[len2];
```

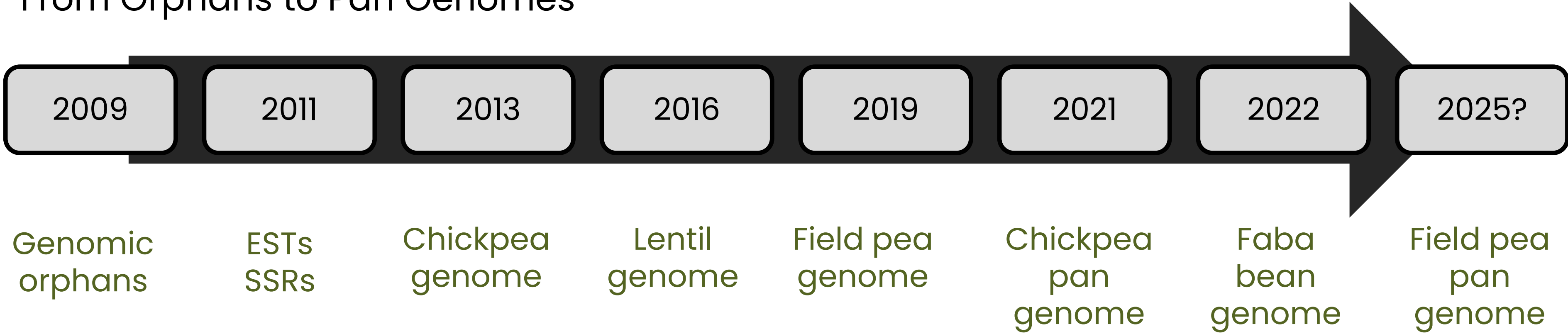






Genomic Resources Over Time

From Orphans to Pan Genomes

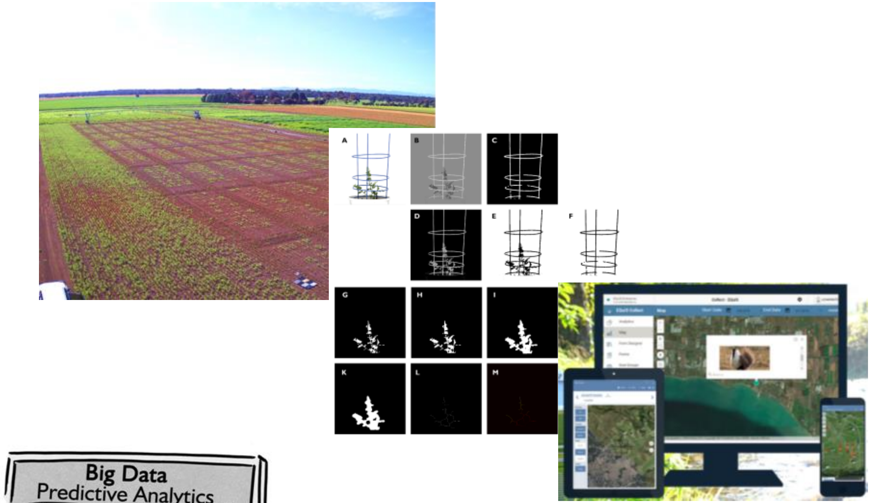


2009	2011	2013	2016	2019	2021	2022	2025?
Genomic orphans	ESTs SSRs	Chickpea genome	Lentil genome	Field pea genome	Chickpea pan genome	Faba bean genome	Field pea pan genome

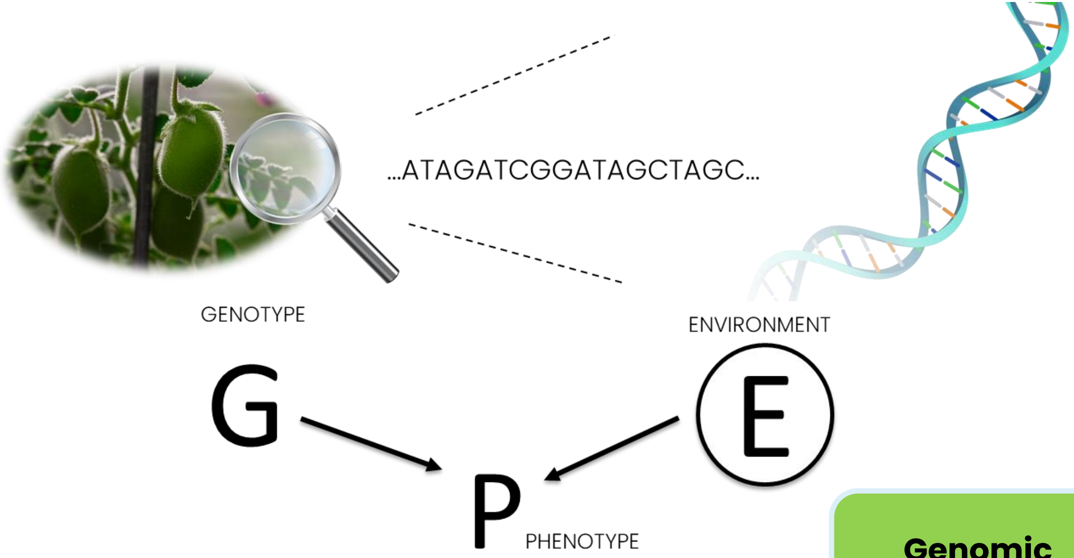
- Genetic linkage maps
- Transcriptome Atlas
- QTL mapping and GWAS studies for trait dissection
- Functional genomic studies

A Data Driven World

From Breeder's eye to Drone's eye



An Integrated Approach



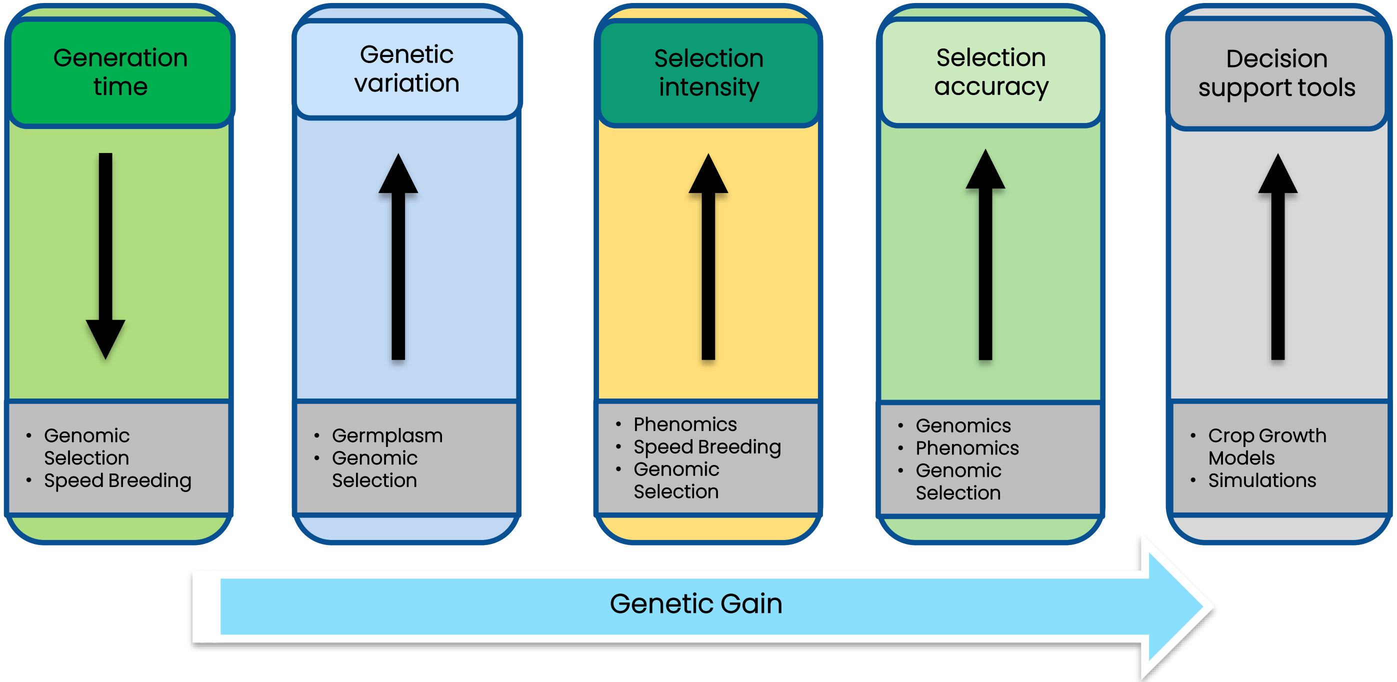
Genomic Predictions + **Future-state climatic models** + **Biophysical crop models**

+ + +

Advanced Statistics + **Speed Breeding** + **High-throughput Phenomics**

An Integrated Approach – Rate of Genetic Gain

$$\frac{\textbf{Genetic Variation X Selection Intensity X Selection Accuracy}}{\textbf{Generation time (Cross-Cross)}}$$



Generation time

- Genomic Selection
- Speed Breeding

Genetic variation

- Germplasm
- Genomic Selection

Selection intensity

- Phenomics
- Speed Breeding
- Genomic Selection

Selection accuracy

- Genomics
- Phenomics
- Genomic Selection

Decision support tools

- Crop Growth Models
- Simulations

Genetic Gain

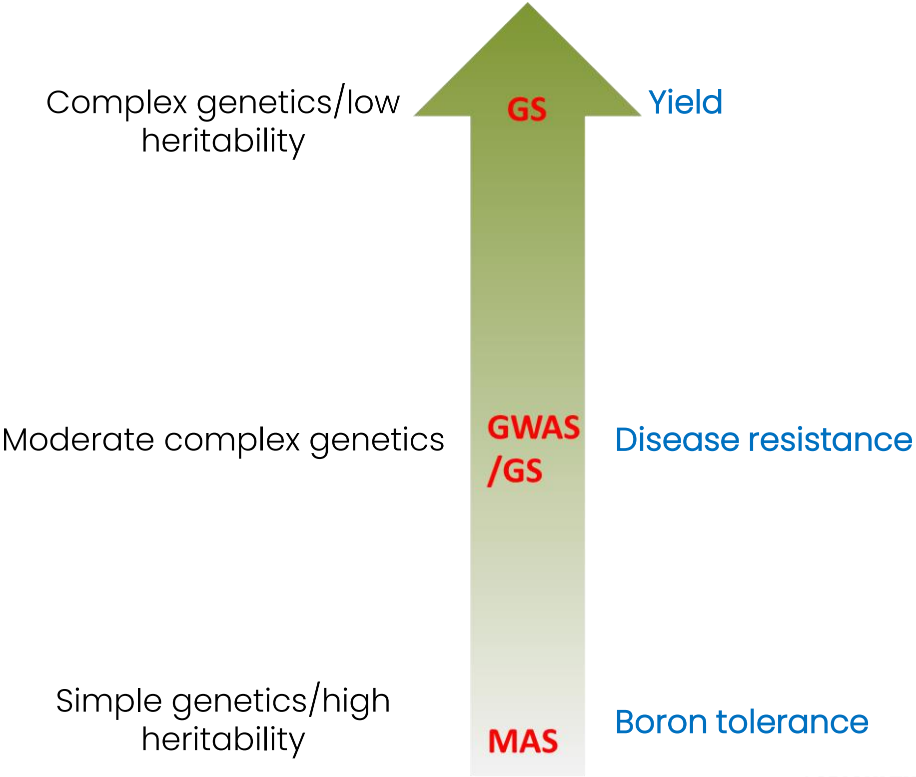
Drivers

- Genomics
- Genomic Selection
- Simulations/Modelling
- High-throughput Phenomics
- Speed Breeding

Last six decades – rate of genetic gain ~1.23% per annum

Target Traits for Lentil and Field pea Breeding

- **Yield (tonnes/ha)**
- **Biotic and Abiotic Stresses**
  - **I. Biotic traits**
    1. **Ascochyta blight (AB)**
    2. **Botrytis grey mould (BGM)- lentil**
    3. **Bacterial blight (BB)- field pea**
    4. **Downy mildew (DM) - field pea**
  - **II. Abiotic traits**
    1. **Salinity toxicity**
    2. **Boron toxicity**
- **Agronomic traits**
  1. **Flowering time**
  2. **Maturity time**
- **Quality Traits**
  1. **Grain weight - 100 seeds (GWT)**
  2. **Protein content**
  3. **Seed Size Index (SSI)**
  4. **Plumpness**



Complex genetics/low heritability — **GS** — Yield

Moderate complex genetics — **GWAS /GS** — Disease resistance

Simple genetics/high heritability — **MAS** — Boron tolerance

Implementation of Genomic Selection

- **Training population**
  - Advanced breeding lines
  - Genotyping – Infinium SNP chip
  - 60,000 – 70,000 genome wide markers
  - Phenotypes (2010-onwards)

- **GS models**
  - Bayesian and GBLUP approaches
  - Annual update of training population

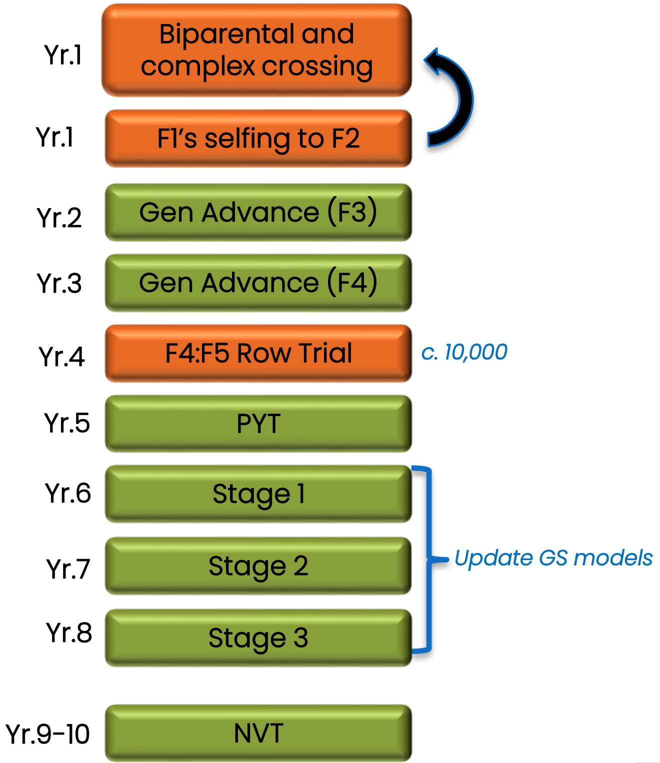
Moderate to High prediction accuracies

Trait	Lentil	Field pea
Yield	0.41	0.42
AB resistance	0.56	0.25
BGM resistance	0.49	–
BB resistance	–	0.36
DM resistance	–	0.35
Bean leaf roll virus res	–	0.50
Seed borne Mosaic virus res	–	0.60
Salinity toxicity	0.47	0.47
Boron toxicity	0.65	0.78
Days to flowering	0.61	0.65
Days to Maturity	0.24	0.35
Early Vigour	–	0.42
Grain weight - 100	0.83	0.49
Protein content	0.50	0.49
Seed size index	0.75	0.47
Seed Plumpness	0.66	–

Implementation of Genomic Selection

Application of Genomic Estimated Breeding Values for

- Early parental selection
  - As early as F_2 progenies
- Multiparent crossing designs
  - Shuffling genetics
- Progeny selection at F4:F5 stage
- Selection of advanced germplasm for national variety trials – QA/QC



Yr.1 Biparental and complex crossing

Yr.1 F1's selfing to F2

Yr.2 Gen Advance (F3)

Yr.3 Gen Advance (F4)

Yr.4 F4:F5 Row Trial *c. 10,000*

Yr.5 PYT

Yr.6 Stage 1

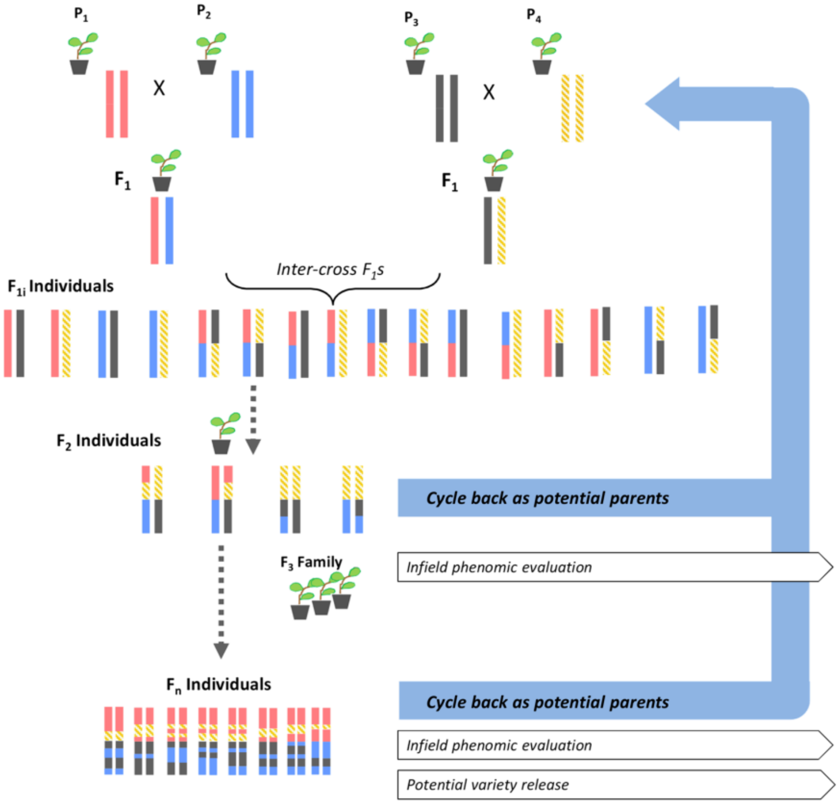
Yr.7 Stage 2

Yr.8 Stage 3

Update GS models

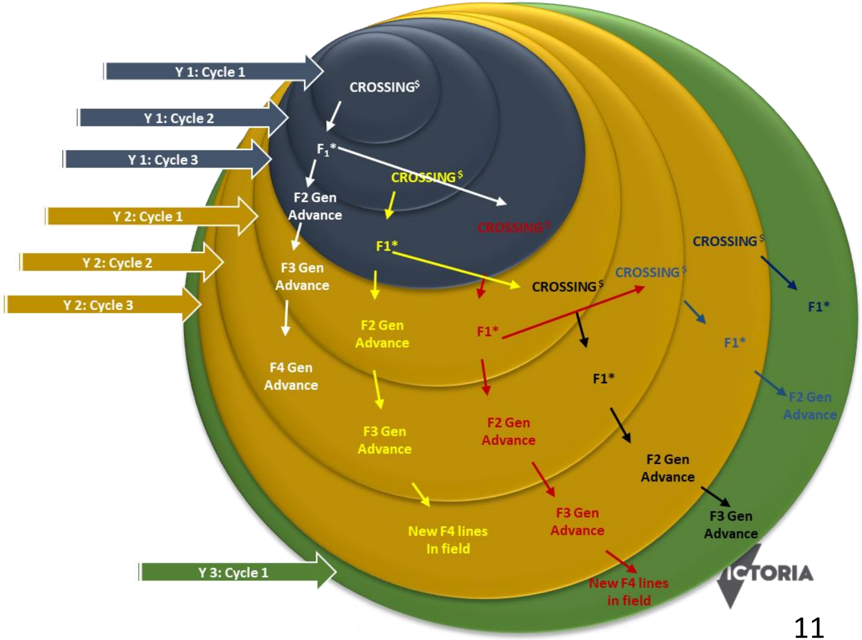
Yr.9–10 NVT

Implementation of Simulations- Parental Selection



- Simulation modelling
  - Greater than 1 million theoretical crosses; diversity
  - Application of selection indices

- Continuous crossing cycle



Implementation of Speed Breeding

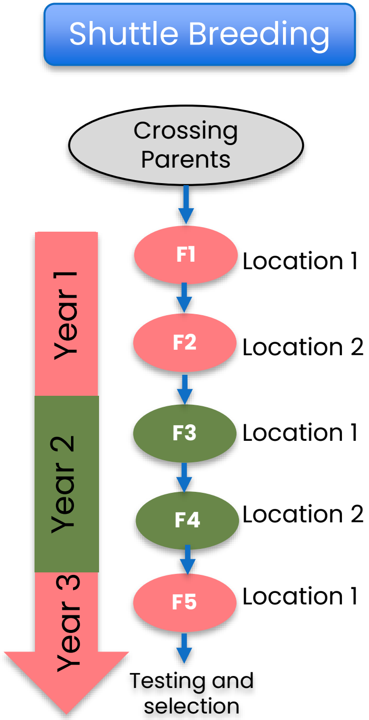
4-5 Generations per year – Accelerated gen advance

Yr.1	Biparental and complex crossing
Yr.1	F1's selfing to F2
Yr.2	Gen Advance (F3)
Yr.3	Gen Advance (F4)
Yr.4	F4:F5 Row Trial
Yr.5	PYT
Yr.6	Stage 1
Yr.7	Stage 2
Yr.8	Stage 3
Yr.9-10	NVT

Yr.1	Biparental and complex crossing
Yr.1-2	F1-F4
Yr.3	F4:F5 Row Trial
Yr.4	PYT
Yr.5	Stage 1
Yr.6	Stage 2
Yr.7	Stage 3
Yr.8-9	NVT

Production	**500,000 t**
Value	$350 million
1% genetic gain	$3.5 million
2% genetic gain	$7 million
4% genetic gain	$14 million

Are We on the Right Path to Feed the World?



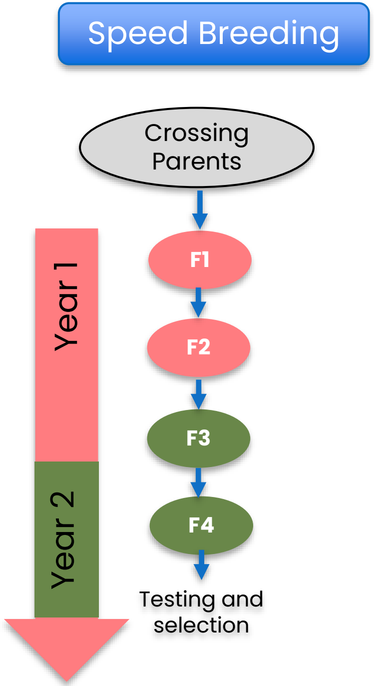
Shuttle Breeding

Crossing Parents

- Year 1
  - F1 Location 1
  - F2 Location 2
- Year 2
  - F3 Location 1
  - F4 Location 2
- Year 3
  - F5 Location 1

Testing and selection

3.5 years



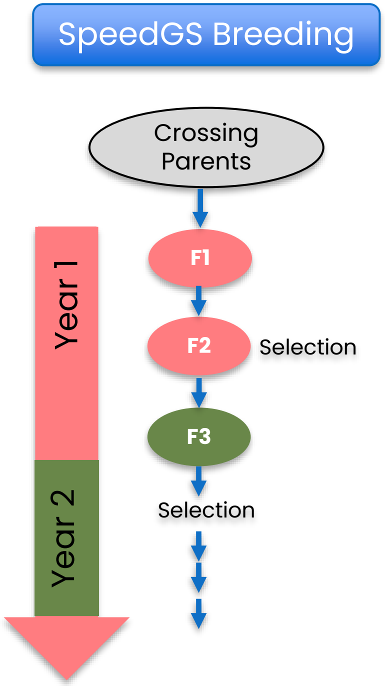
Speed Breeding

Crossing Parents

- Year 1
  - F1
  - F2
  - F3
- Year 2
  - F4

Testing and selection

2-2.5 years



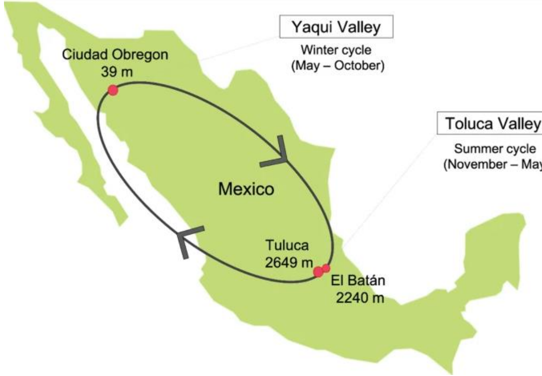
SpeedGS Breeding

Crossing Parents

- Year 1
  - F1
  - F2 Selection
  - F3
- Year 2

Selection

1-1.5 years



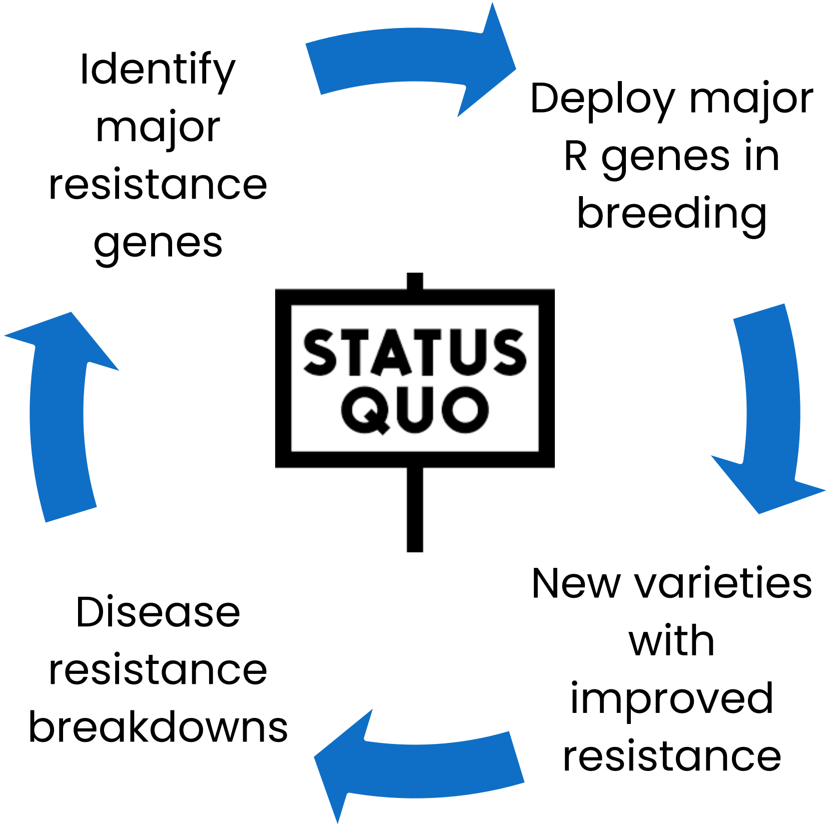
Impact

	Genetic Variation	Selection Intensity	Selection Accuracy	Years/Cycle
Genomic Selection	✓	✓	✓	✓
Simulations	✓	✓		✓
Speed Breeding		✓		✓

Greater genetic gain

$$\frac{\text{Genetic Variation X Selection Intensity X Selection Accuracy}}{\text{Generation time (Cross-Cross)}}$$

Breeding for Improved and Durable Disease Resistance



Identify major resistance genes

Deploy major R genes in breeding

New varieties with improved resistance

Disease resistance breakdowns

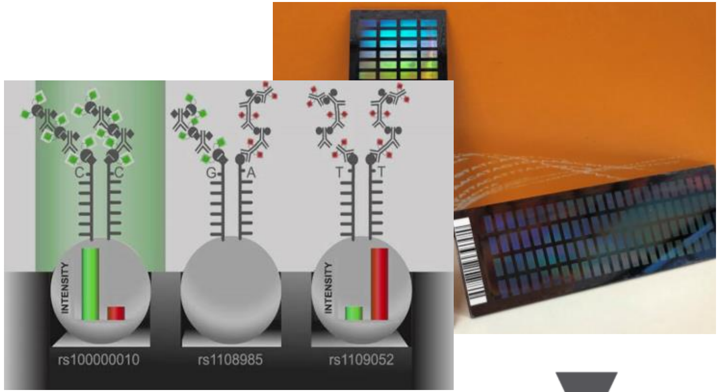
Ascochyta Blight in Chickpea

- Field
  - Field trials in 2020-2022 (n= 2,790)
    - Infected in stubble with a mixture of AB isolates

- Terrace
  - Screened with 7 different isolates from 2016-2022

- Genotyping - Infinium SNP chip
  - c. 23 K genome wide SNPs

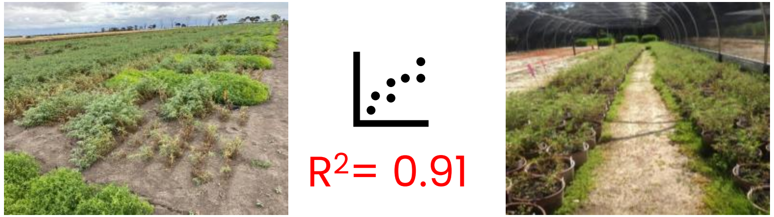
Collection	**Type**	**N**
CBA	Breeding	396
CCDM	Wild Introgressions	443
FLIP	Pre-breeding	1212
HT	Herbicide mutants	7
UC Davis	Wild Introgressions	193
UWA	Advanced lines	15
Vavilov	Pre-breeding	524
Total		**2,790**



Implementation of Genomic Selection

High correlation between field and terrace screens implies opportunity to scale phenotyping using field disease nursery

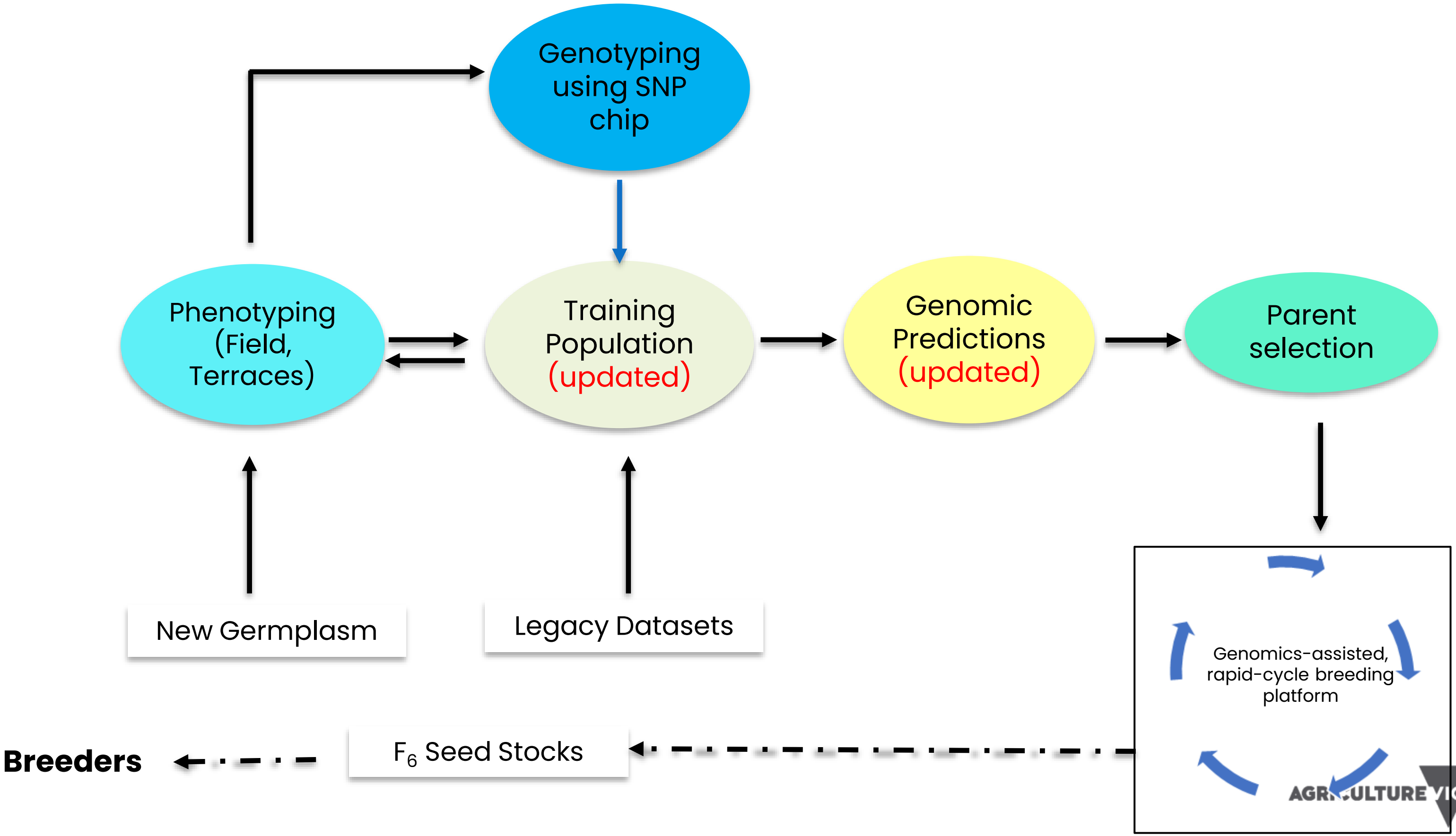
- Bivariate analysis
  - Trait 1: Field BLUEs
  - Trait 2: Mean scores across isolates in terraces



$R^2= 0.91$

- Genetic correlation
  - $r_g = 0.91 \pm 0.02$
- Genomic Predictions
  - Training using field BLUE to predict terrace data
    - Accuracy is 0.63
  - Training using terrace to predict field BLUEs
    - Accuracy is 0.81

Delivering Improved Seed Stocks to Breeders



Genotyping using SNP chip

Phenotyping (Field, Terraces)

Training Population (updated)

Genomic Predictions (updated)

Parent selection

Genomics-assisted, rapid-cycle breeding platform

New Germplasm

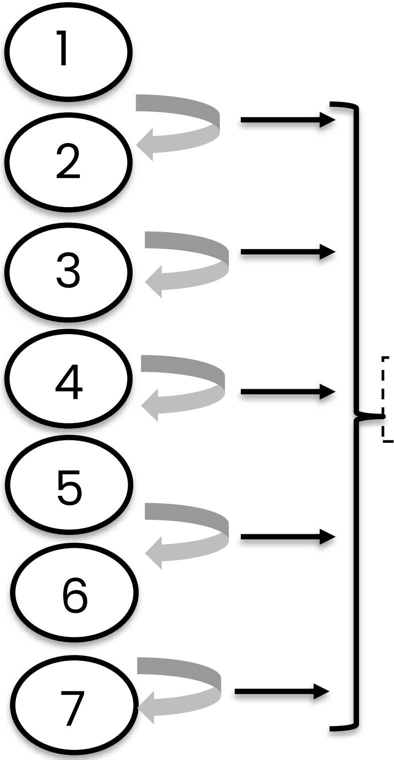
Legacy Datasets

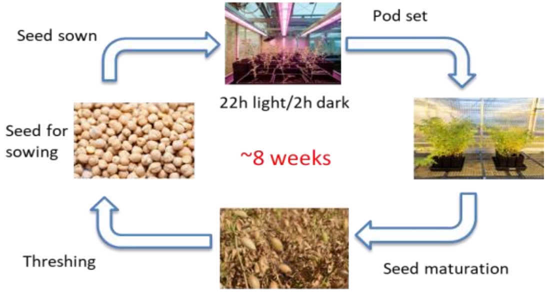
F_6 Seed Stocks

Breeders

Allele Enrichment through Speed Breeding

Implementation of Genomic Selection and Simulation





Rapid Cycle Breeding – Chickpea

- Crossed buds
- Uncrossed buds

- Next crossing cycle
- Single Seed Descent

Phenotypic assessment

Genomic Prediction Update

- In silico per cycle to guide cross selection
  - Generate all possible crosses, e.g. 387 F_1 in cycle2 = 74,691 crosses
  - Simulate all crosses till F_8
- Evaluate crosses by GEBVs of F_8
- Select crosses to maximize genetic gain

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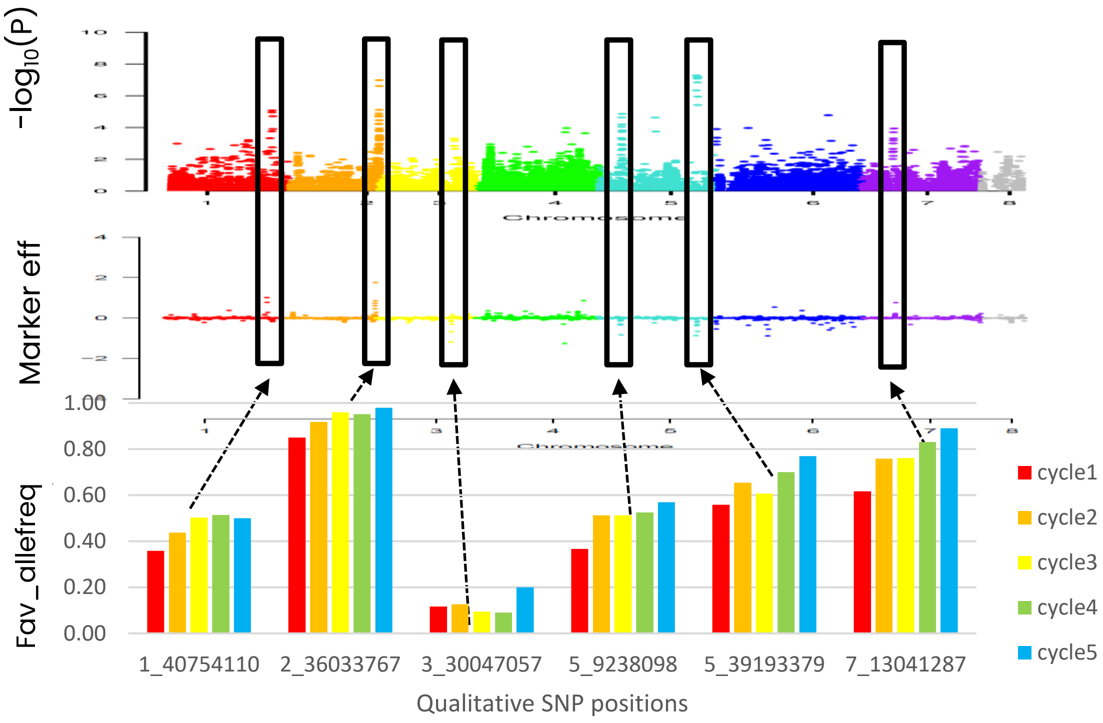
Breeding for Resistance in Speed Breeding Program

- Enrichment of qualitative resistance QTL across cycles



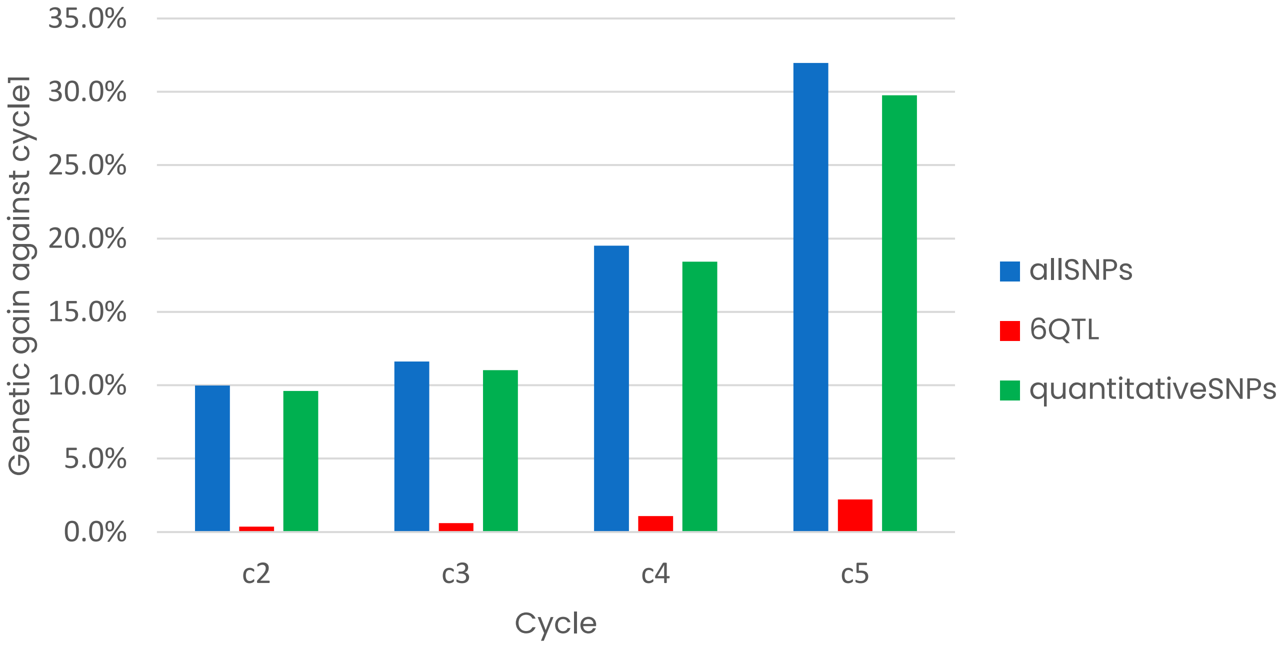
33% gVar explained by qualitative SNPs

Genetic gain over cycles using qualitative SNPs

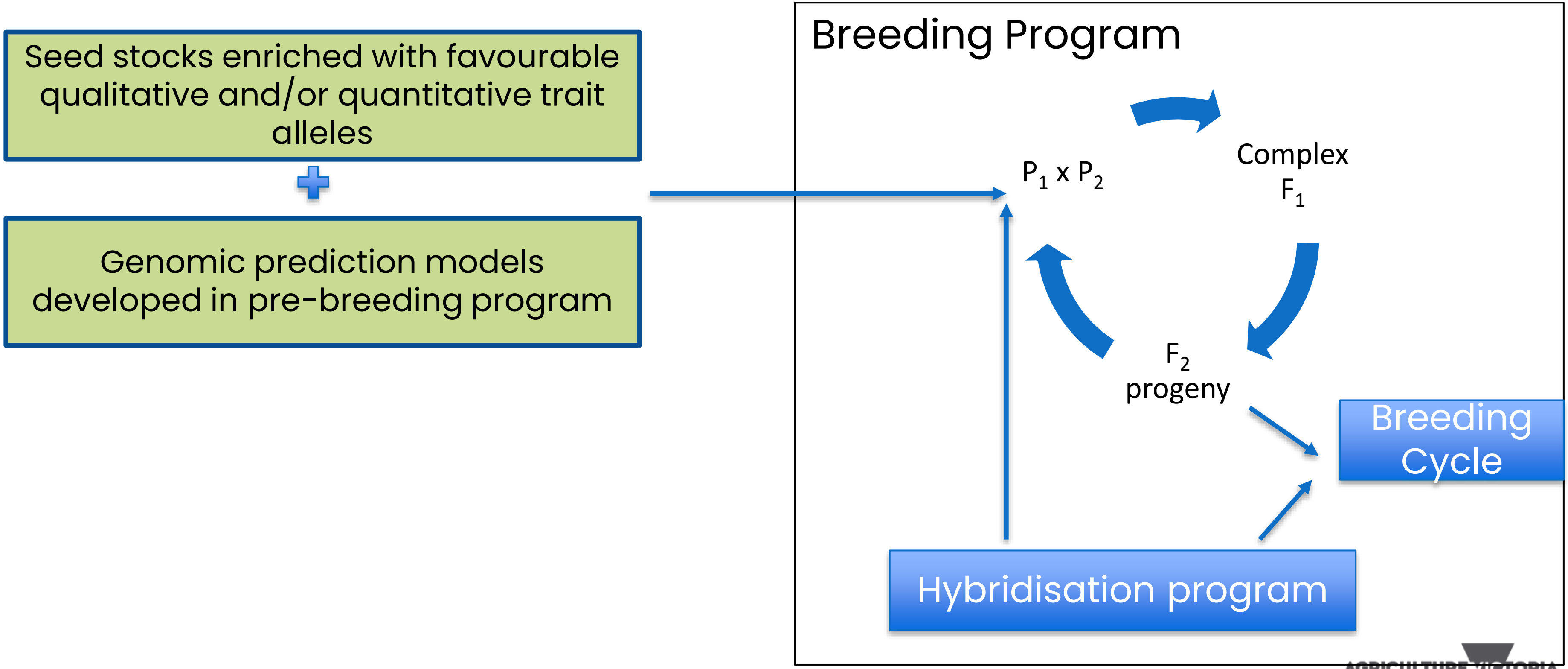
Breeding for Resistance in Speed Breeding Program

- Enrichment of quantitative resistance QTL across cycles

- 67% gVar explained by the quantitative SNPs
- 10x more genetic gain observed using quantitative SNPs



Bridging the Gap between Research and Breeding



Seed stocks enriched with favourable qualitative and/or quantitative trait alleles

+

Genomic prediction models developed in pre-breeding program

Breeding Program

P_1 x P_2

Complex F_1

F_2 progeny

Breeding Cycle

Hybridisation program

Points to Think About

- A Holistic Approach
- Bridge the gap between research and breeding
- Open communications among researchers, breeders and growers

Acknowledgements

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Technical and
Glasshouse teams

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Judith Atieno
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Janine Croser
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