

The New Zealand Institute for Plant & Food Research Limited

Plant & Food  
**RESEARCH**

RANGAHAU AHUMĀRA KAI



# Development of the NZ Apple Breeding and Genetics Programme: A synthesis of results

**Satish Kumar**

# Outline

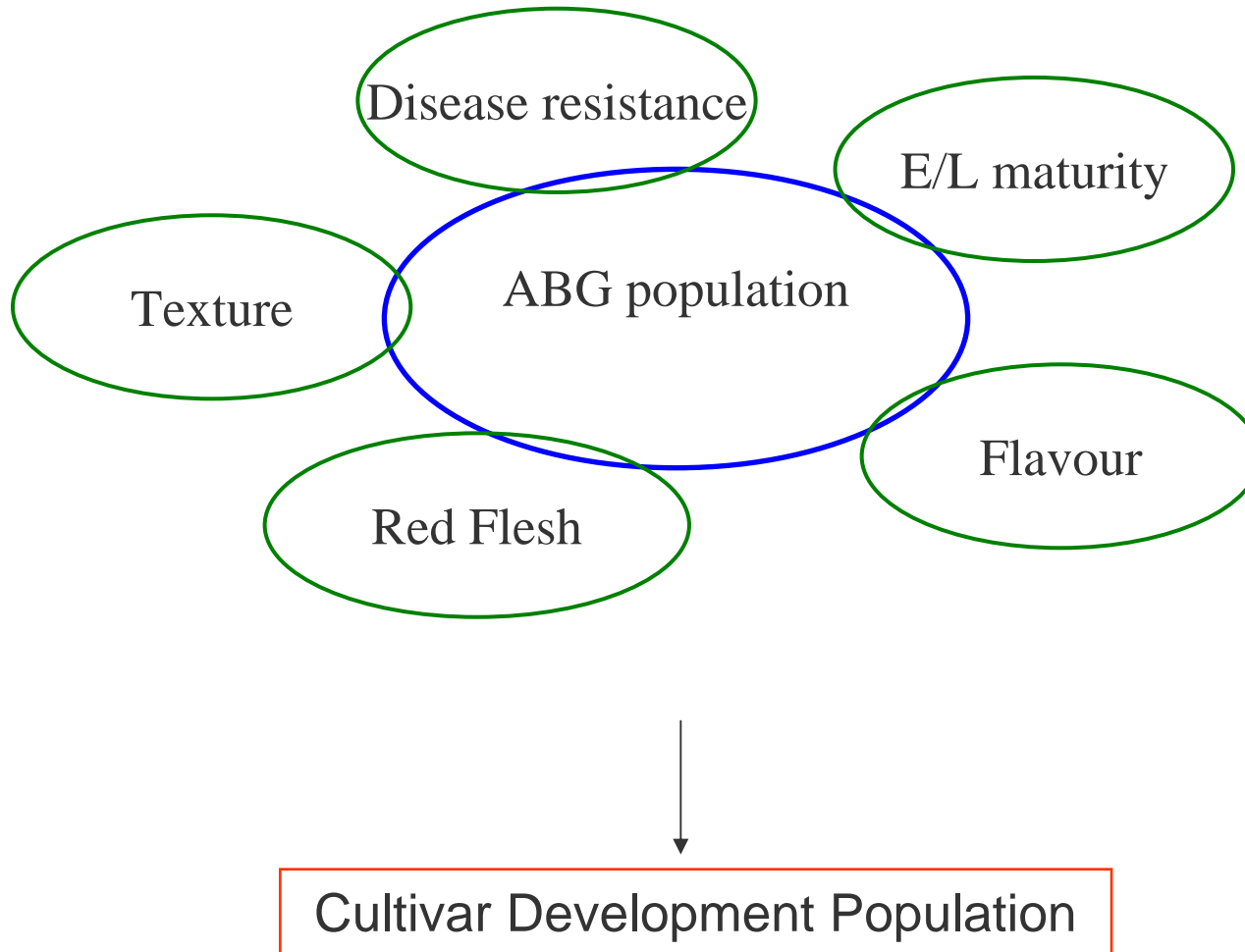
- Apple Breeding and Genetics (ABG) programme
- Elite Populations
- Future Plan

# ABG: Rationale / Objective

- Small effective population size of cultivar development programme
- Discover and preserve novel traits
- Provide new genotypes for the Elite

Niotoon and Shelbourne (1992)

# Breeding Population



# ABG Programme: Progeny Testing

	<b>1<sup>st</sup> Gen.</b>	<b>2<sup>nd</sup> Gen.</b>	<b>3<sup>rd</sup> Gen.</b>
<b>No. of Parents</b>	530	310	250
<b>Mating design</b>	Open-pollinated (OP)	OP (16%), CP (64%)	CP (60% DPM)
<b>Field design</b>	Single Tree Plot, IBD	Row plot, IBD	-
<b>Family size</b>	20	10	-
<b>Traits</b>	Tree, Disease, Quality	Tree, Disease, Quality	-
<b>Selection method</b>	Two-stage, Single-trait neutral selection except for disease	Two-stage, Single-trait selection* except for disease	-

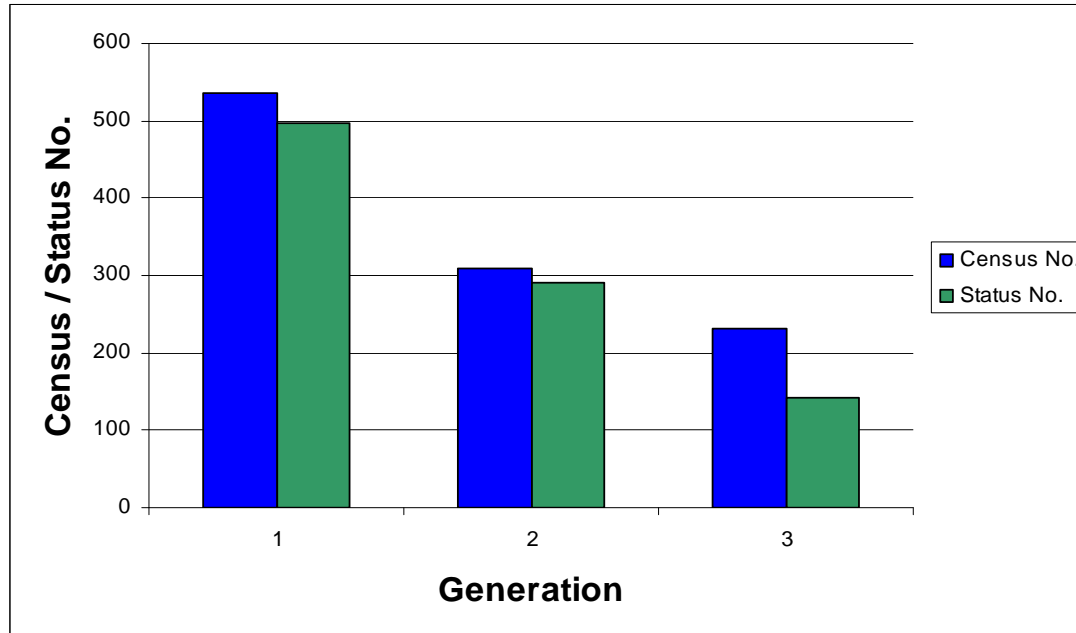
# Results: Heritability

Trait	Heritability ( $h^2$ )
Powdery mildew	0.15
Scab	0.31
Fireblight	0.33
Tree Habit	0.32
Harvest date	0.76
Fruit weight	0.78
Russet	0.36
Firmness	0.50
Crispness	0.32
Acidity	0.22
Sweetness	0.37
Juiciness	0.24
Astringency	0.48

# Results: Genetic gain

<b>Trait</b>	<b>1<sup>st</sup> Gen. (Obs. Mean)</b>	<b>2<sup>nd</sup> Gen. (Obs. Mean)</b>	<b>3<sup>rd</sup> Gen. (Pred. Mean)</b>
Powdery mildew (0-9)	2.83	2.13	2.09
Fruit weight (g)	104.5	98.1	107.9
Firmness (0-9)	7.28	7.00	7.47
Soluble solids (%)	13.04	13.35	13.39
Crispness (0-9)	4.49	3.64	3.87
Juiciness (0-9)	4.12	3.56	3.75

# Genetic Diversity

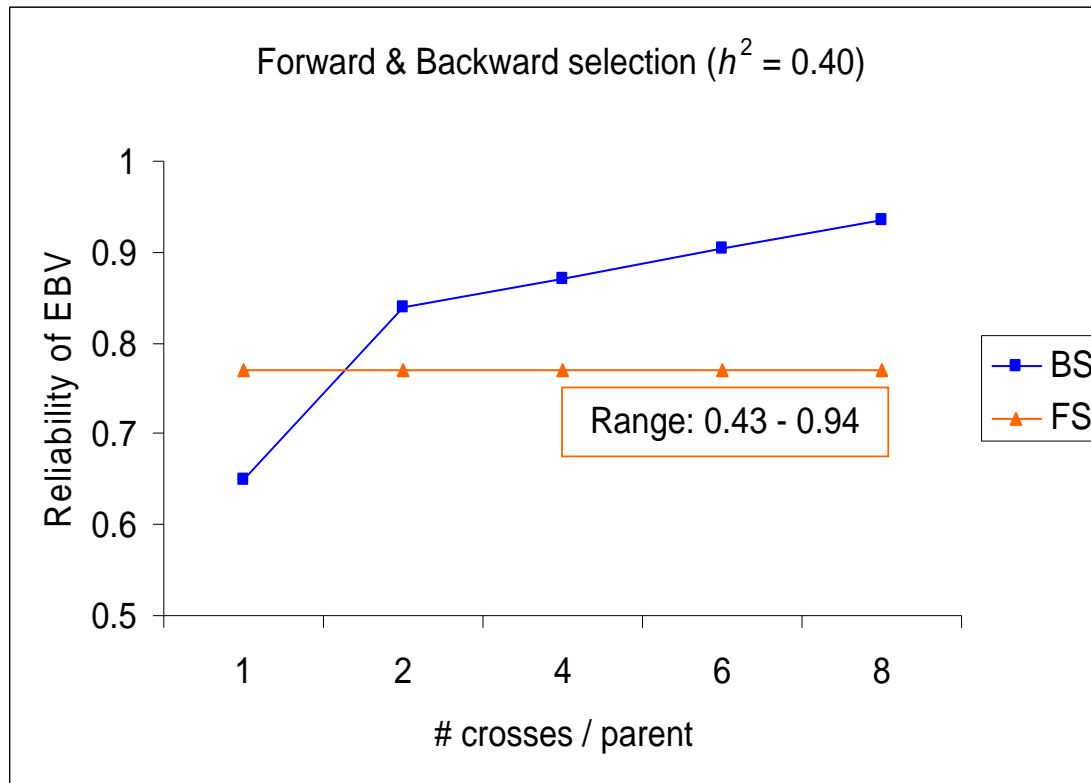


Status Number =  $0.5 / \Theta$  (Lindgren et al. 1996)

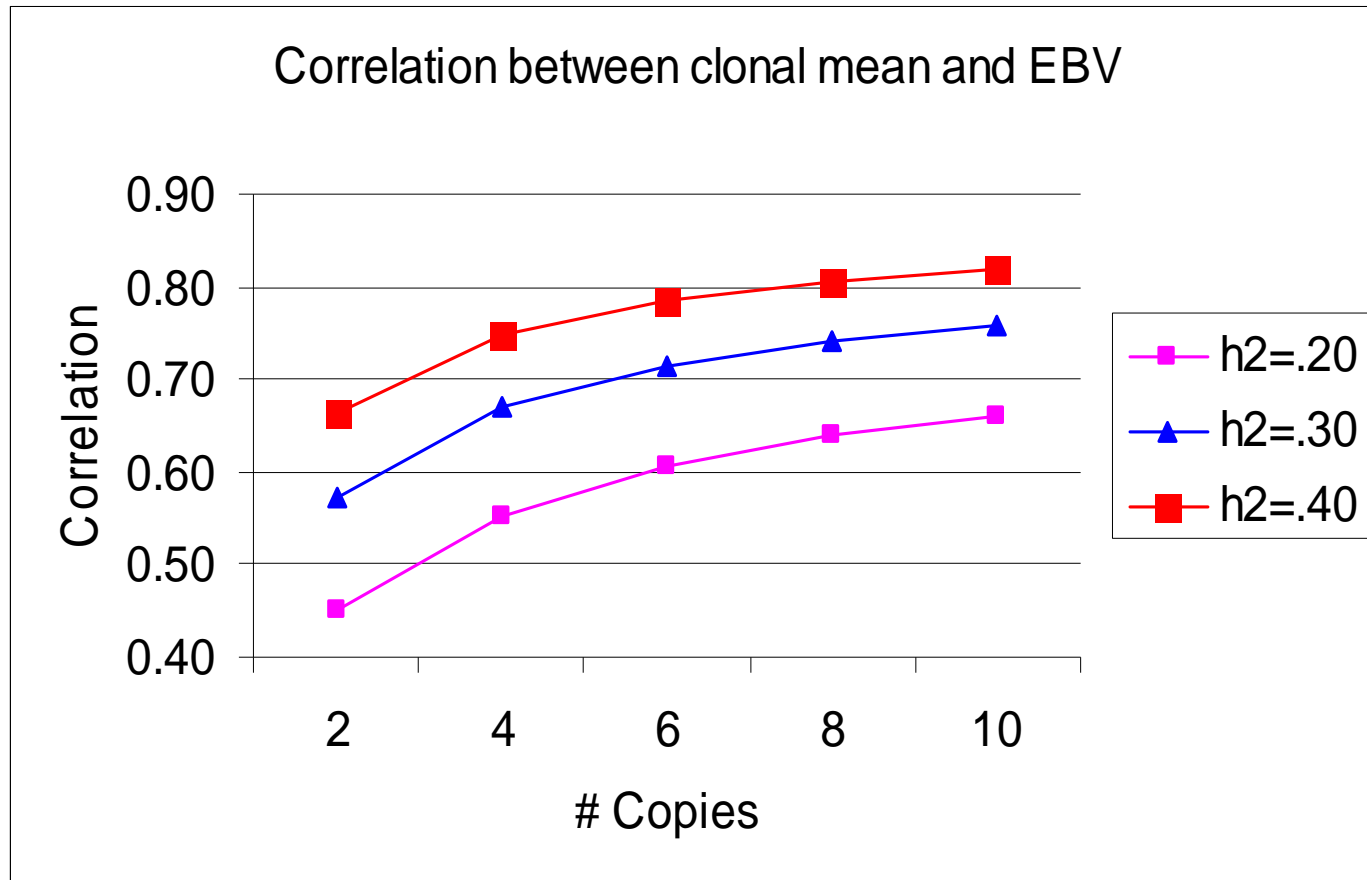
# Elite Population

# Elite Population: Function & Structure

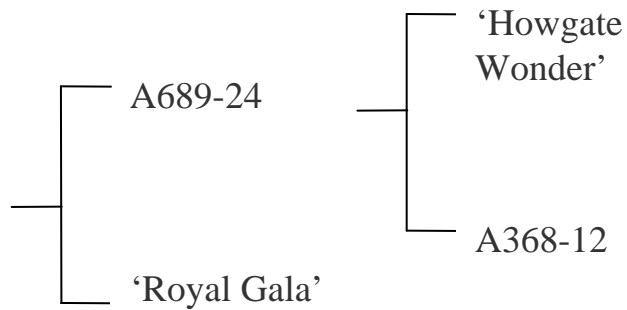
- Major source of parents for cultivar breeding
- About 20 parents, variable no. of crosses per parent
- Backward and Forward selection



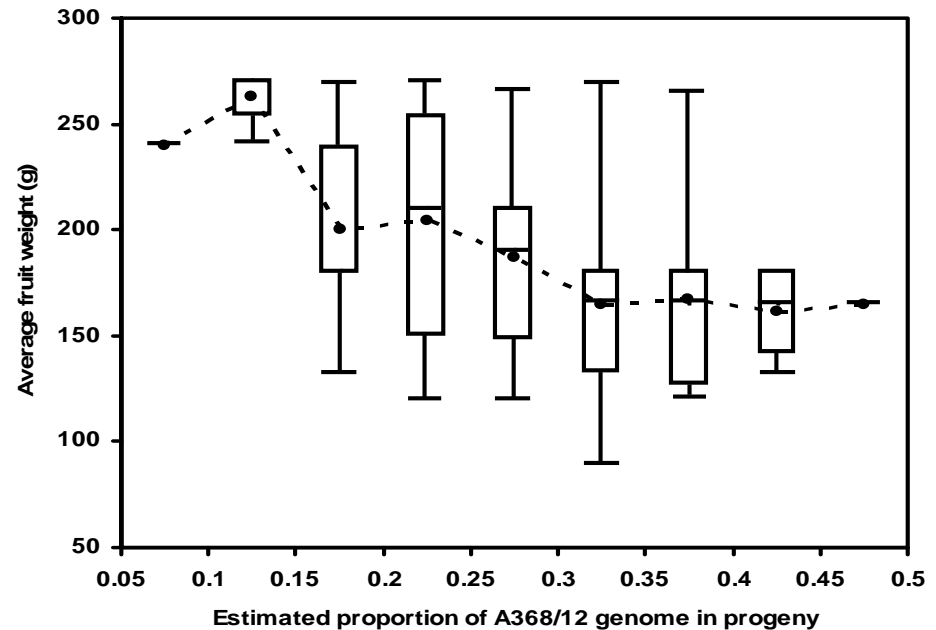
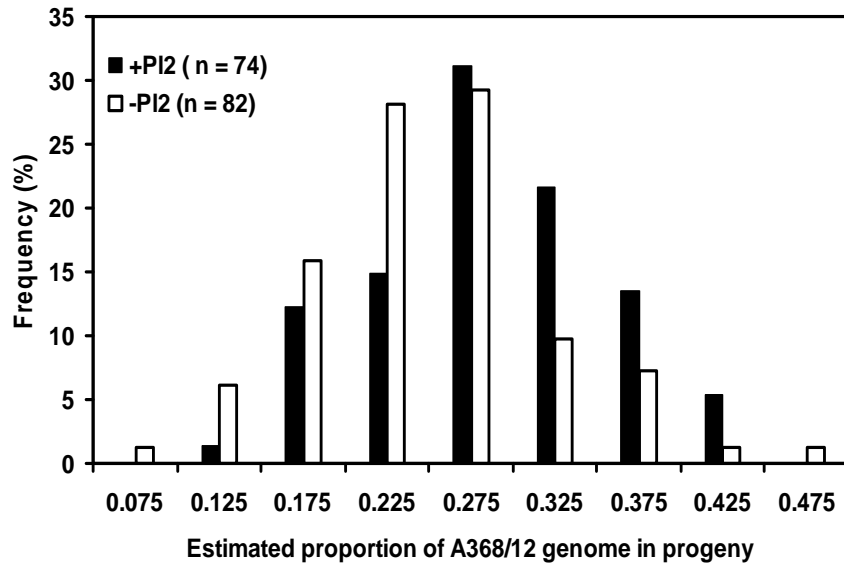
# Improving efficiency of FS



# Whole Genome Selection: Current Approach



- 173 offspring screened for 108 SSR loci
- Estimate proportion of grandparents genome
- Early screen for *PI2* resistant seedlings
- Select ones with low proportion of donor g.p.
- Fast-forward for reproduction traits

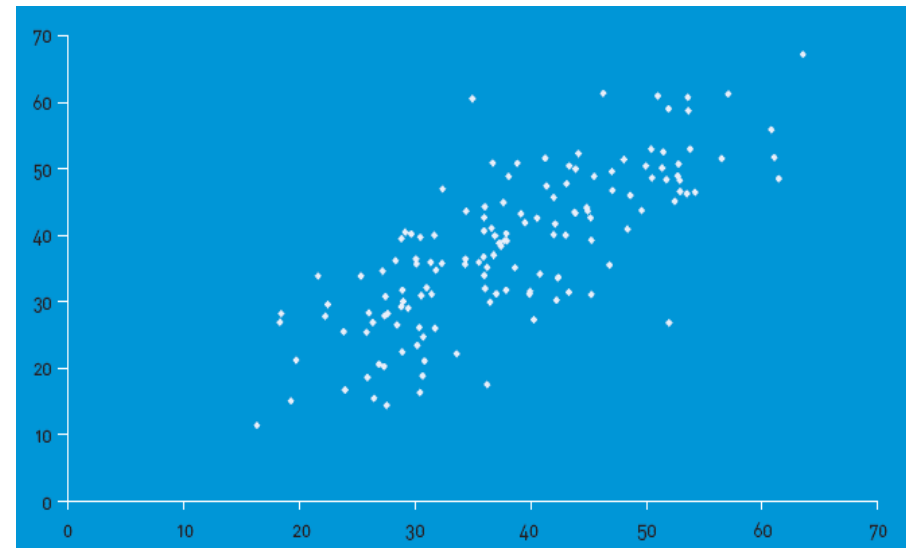


Volz et al. (2009) Acta Hort. (ISHS) 814:163-168

# Whole Genome Selection: Long Term Goal

- » Genomic EBV
- » Training Model development
- » Validation (Conventional BLUP *versus* GEBV)

Genotype	Texture	SS	Disease	
Locus 1	+0.05			
Locus 2	0			
Locus 3	-0.02			
...				
Locus 10,000	+1.2			
<b>Sum (GEBV)</b>	+0.06			<b>Index</b>



# Future Plan

- Better understanding of QG of breeding objective traits
- Better parental selection for CDP
  - » Clonal performance
  - » Molecular markers
- Association Genetics
- Genomic EBV

# Acknowledgements

- Peter Alspach
- Vincent Bus
- David Chagné
- Susan Gardiner
- Erik Rikkerink
- Richard Volz
- Allan White

- Plant & Food Research
- FRST
- Prevar™



**Thanks**





## Quantitative Genetics

- BSc (Agriculture)
- MSc (Applied Statistics)
- PhD (Forest Genetics & Breeding)



- Breeding strategy
- Genetic evaluation methods
- Genetic parameter estimation
- QTL mapping
- Association genetics
- Simulation studies