

**GENETIC DIVERSITY OF THE SOYBEAN CULTIVARS BRED IN  
ZIMBABWE FROM 1940 TO 2010**

**MUSHORIWA H<sup>1,2\*</sup>, DERERA J<sup>2</sup>, SHANAHAHAN P<sup>2</sup>, NAIDOO R<sup>2</sup> & TICHAGWA J<sup>1</sup>**

<sup>1</sup>*Seed Co Ltd, P. O. Box CH142, Chisipite, Harare, Zimbabwe*

<sup>2</sup>*School of Agricultural, Earth and Environmental Sciences, University of KwaZulu-Natal  
P. Bag X01, Scottsville 3209, Pietermaritzburg, South Africa*

\*Email: [hapsonmushoriwa@rars.seedco.co.zw](mailto:hapsonmushoriwa@rars.seedco.co.zw)

Soybean [*Glycine max* (L.) Merr.] has food security, nutritional, medicinal and economic value with a high industrial potential which can be exploited by developing economies in sub-Saharan Africa. However, intensive selection may reduce the genetic base which has serious consequences for future breeding progress. Breeding strategies that emphasise the mating of elite strains can result in recombining genes contributed by a limited number of ancestral introductions leading to narrowing of the genetic base. Consequently, the germplasm becomes vulnerable to environmental challenges such as biotic and abiotic stresses. The other consequences are rapid occurrence of the yield plateau, genetic erosion and limited germplasm options. As a result of global climate change, there are bound to be more challenges that will impact soybean breeding progress unless a diversified germplasm is maintained.

The soybean programme in Zimbabwe is over 70 years old; therefore, we found it prudent to investigate the levels of diversity that is available within the germplasm pool. A representative sample of 42 soybean cultivars was evaluated in the field at five locations using a 6 x 7 rectangular lattice design with three replications in Zimbabwe, Malawi and Zambia, from 2010 to 2012. The phenotypic data was analysed using the Gebei Pattern Analysis Procedure of Cropstat version 7.2 that groups cultivars into clusters. The Powermaker Software was used to analyse molecular data.

The results revealed that the SSR markers were highly polymorphic, informative and more discriminatory than the phenotypic data. Both phenotypic and molecular analyses indicate wide genetic variation and reveal 9 and 15 clusters, respectively. The dendrograms from molecular data are consistent with the pedigree information while dendrograms from phenotypic data of four traits were generally divorced from pedigree data. Furthermore, grain yield ranged between 3.6 and 6.2 t ha<sup>-1</sup> for the 1966- and 2005-bred cultivars, respectively, indicating significant progress by the breeding programme in Zimbabwe, which has been achieved without compromising genetic diversity. Overall results support existence of wide genetic diversity and present a good opportunity for maximum utilization of the germplasm.



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# Genetic Diversity & Performance of Soybean Cultivars bred in Zimbabwe from 1940 to 2010

H. Mushoriwa, J. Derera, P. Shanahan, R. Naidoo & J.S. Tichagwa



EDGEWOOD CAMPUS



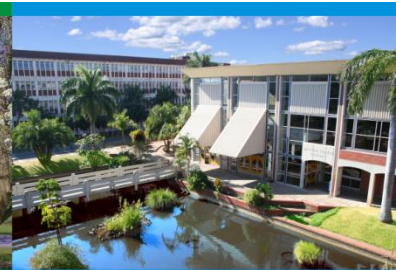
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INSPIRING GREATNESS

# Presentation Outline

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- ❖ Background & Introduction
- ❖ History of Soybean Breeding in Zimbabwe
- ❖ Significance of Genetic Diversity
- ❖ Materials and Methods
- ❖ Results and Discussion
- ❖ Implications for Breeding
- ❖ Conclusion: results represent a huge breeding gain that was made without compromising genetic diversity

# INTRODUCTION

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- ❖ Soybean has food security, nutritional, medicinal, economic value & high industrial potential that can be exploited globally
- ❖ The food & feed values as well as biodiesel volumes have generated a huge interest as well as enormous demand for energy, human & animal consumption
- ❖ SADLY, the current demand for soybean far outstrips supply
- ❖ Moreover, global protein demand is expected to increase in response to rising global population
- ❖ Scarcity results in higher prices, which hit the poorest of the poor the hardest since these people typically spend 50-70% of their income on food (FAO, 2009)

# Challenge

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- Need to continue raising the grain yields per unit area
- Need to expand soybean production area (ha)
- **BUT** available farmland is limited by weak property rights, heightened sensitivities about the adoption of modern technologies, increased farmland loss for urbanisation and competition with other crops

# History of Soybean Breeding in Zimbabwe

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- ❖ Before the introduction of soybean in 1940, the govt used to import fish meal for feeding livestock
- ❖ However, the cost became unsustainable to carry
- ❖ At this point, the govt initiated soybean breeding
- ❖ Earlier efforts focused on breeding for fodder cultivars
- ❖ Full support to the program began in the early 60s-a team mandated to breed and develop soybean was engaged
- ❖ More resources were channelled to this program with a view to achieve self sufficiency

# Achievements of the Soybean Breeding Programme in Zimbabwe

Breeding Period	Decade	No. of Varieties Released
1940-1950	1	1
1950-1960	2	-
1960-1970	3	1
1970-1980	4	5
1980-1990	5	5
1990-2000	6	12
2000-2010	7	15
Total number of varieties released		39

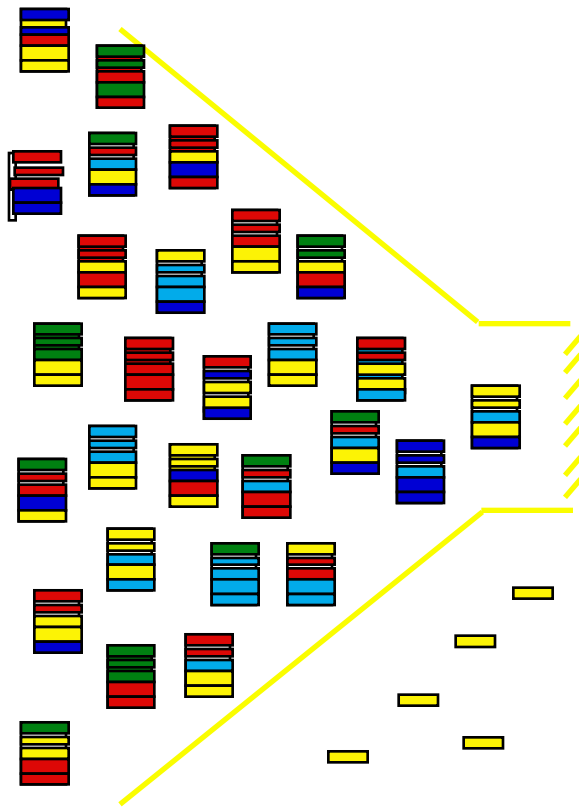
# Justification of the study

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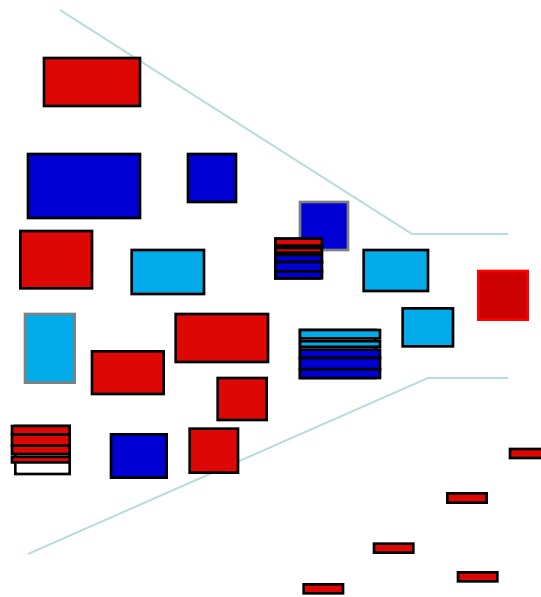
- ❖ Admittedly, the programme has made tremendous achievements over 70 years
- ❖ However, yield growth or improvement maybe affected by narrow genetic diversity due to;
  - ✓ contribution of a few parents to the primary gene pool.
  - ✓ repeated use of the same parents in the breeding program
- ❖ Consequences of reduced genetic diversity include;
  - exposure of the germplasm to genetic vulnerability
  - yield plateaus
  - genotypes may be exposed to ever changing environmental stresses they may not cope with.
  - climate change may demand new varieties
  - continued erosion of diversity



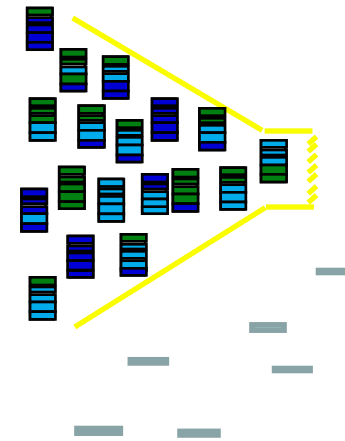
# Spectrum of allelic variation



Wild species



Early Domesticates



Modern varieties

## Justification of the study (cont.)

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- ❖ Given regional & global expansion initiatives, we felt that there was a need to audit the existing germplasm
  
- ❖ In addition, the need to maintain continued genetic progress or gains also warranted us to assess genetic diversity

# Objectives of the Study

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- ❖ To determine genetic diversity among Zimbabwean soybean cultivars
- ❖ To ascertain the genetic relatedness among the 42 cultivars.
- ❖ To compare the relationship between estimates of genetic diversity measured by SSR markers and phenotypic traits.

# Approaches used to estimate genetic diversity

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Two methods were employed;

- a) Phenotypic Characterisation
- b) Molecular Characterisation

# Phenotypic Characterisation

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- ❖ 42 soybean cultivars were planted at 5 sites in Zimbabwe, Malawi and Zambia
- ❖ The experiment was laid out as 6 x 7 rectangular lattice design
- ❖ 3 replications were used
- ❖ Out of the 42 varieties 3 were Plant Introductions and 39 developed in Zimbabwe
- ❖ Gross plot: 13.5 m<sup>2</sup>
- ❖ Nett plot: 7.92m<sup>2</sup>

# Phenotypic Characterisation

- Best practices of management were applied
- Basal fertilizer (Cottonfert) applied at 300-400kg/ha
  - Supplying:
    - 15kg-28N,
    - 51-68kg P<sub>2</sub>O<sub>5</sub> and
    - 30-40kg/ha K<sub>2</sub>O<sub>5</sub>
- The seed was inoculated with *Bradyrhizobium japonicum* Grasslands strain 1491.
- Herbicides were used to control the weeds
- ANOVA was performed in Cropstat Version 7.2

# Data Collected

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- Percentage lodged plants at maturity
- Days from planting to 50% flowering
- Days from planting to 95% pod maturity
- Days from 95% pod maturity to first pod shattering
- Seed mass
- Seed yield in kilograms per hectare
- Percentage crude protein
- Percentage oil content

# Molecular Characterisation

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- ❖ 42 cultivars were grown in pots in the green house
- ❖ Each pot had 4 plants
- ❖ Fresh leaf tissues were harvested at trifoliate stage
- ❖ Harvested leaf discs were loaded into 96-well block or plate
- ❖ The entire block was then sealed with air pore tap & placed into a plastic containing silica gel for 48 hours.
- ❖ This was done to dehydrate the leaf discs, thereafter, the block was couriered to DNA Landmarks for genotyping
- ❖ 30 SSR markers were used for genotyping



# Molecular Characterisation

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- ❖ Genetic similarities between the cultivars were determined using NTSYS v2.1 software programme
- ❖ Pair-wise comparisons were made between the cultivars based on DICE similarity coefficient (Dice, 1945)
- ❖ A Dendrogram was generated using un-weighted pair-group method with an arithmetic average (UPGMA) sub-programme of NYSTS (Rohlf, 1998)
- ❖ PIC values were generated using Powermarker V3.0 (Lui et al., 2005)

# RESULTS

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a) Phenotypic data

b) Molecular data

# Phenotypic data

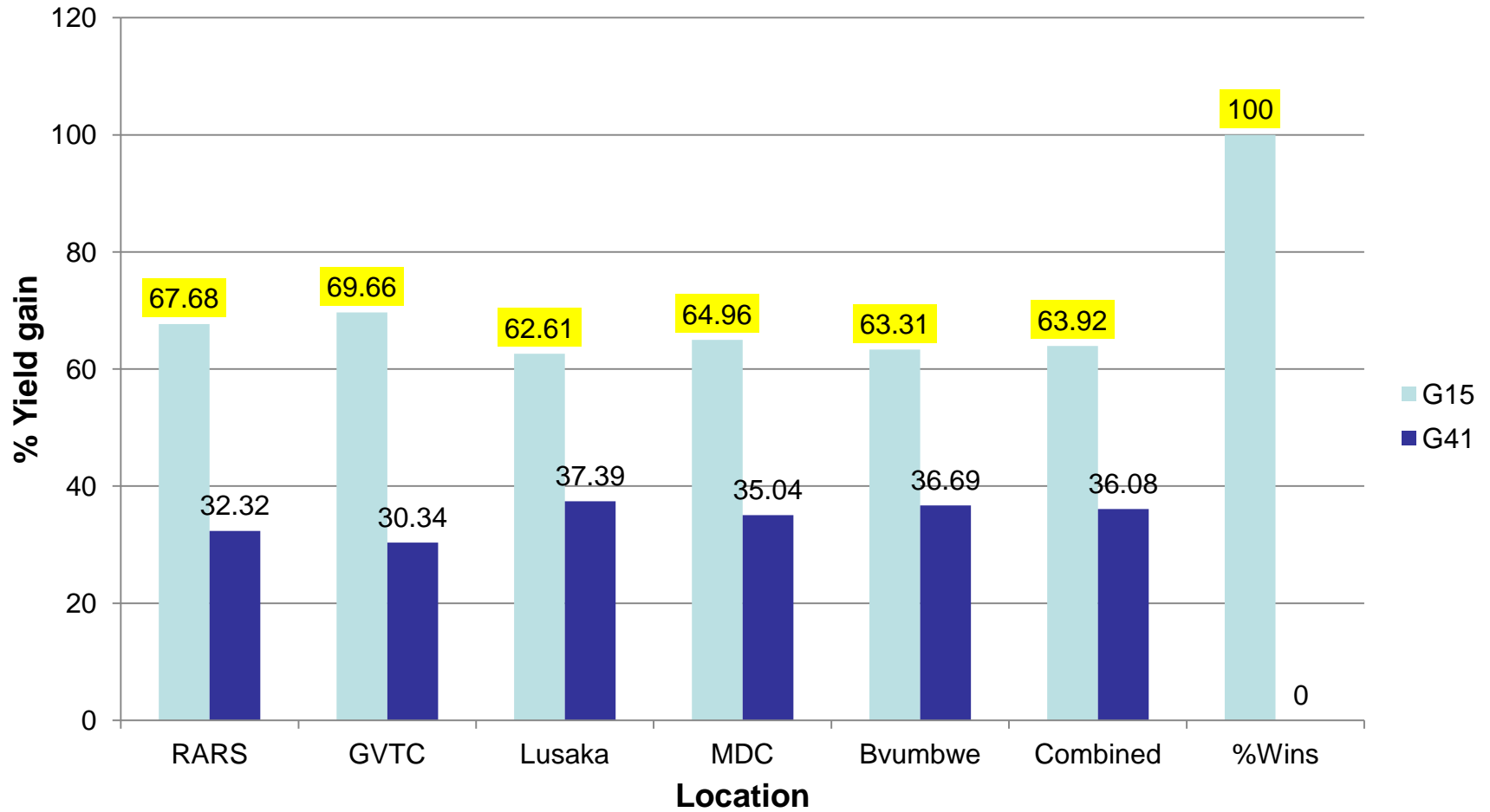
Trait	2010-11		2011-12	
	Range	Mean	Range	Mean
%LODG	0-33	2	0-30	2
DFL (days)	50-64	53	47-63	52
DSH (days)	23-40	33	18-38	27
Maturity (days)	106-129	122	114-135	126
% Crude Protein	39-45	41	37-41	40
% Crude oil	16-19	18	16-19	18.0
Seed Mass (g)	14-25	18	19-32	24
Seed yield (kg/ha)	3697-6232	5293	2363-4807	4095

% LODG = Percentage lodged plants at maturity, Days from planting to 50% flowering, DSH = Days from maturity to first pod shattering

# Head to Head Analysis for yield (t/ha)

	2010-2011					2011-2012				
	Sites					Sites				
Var.	1	2	3	4	5	1	2	3	4	5
G15	3.6	4.1	5.8	7.3	6.9	5.3	4.1	4.3	3.1	4.9
G41	1.8	2.0	3.7	3.2	4.7	2.4	1.5	1.9	2.5	1.8
G41 = founder variety;					G15 = Recent variety (2008)					

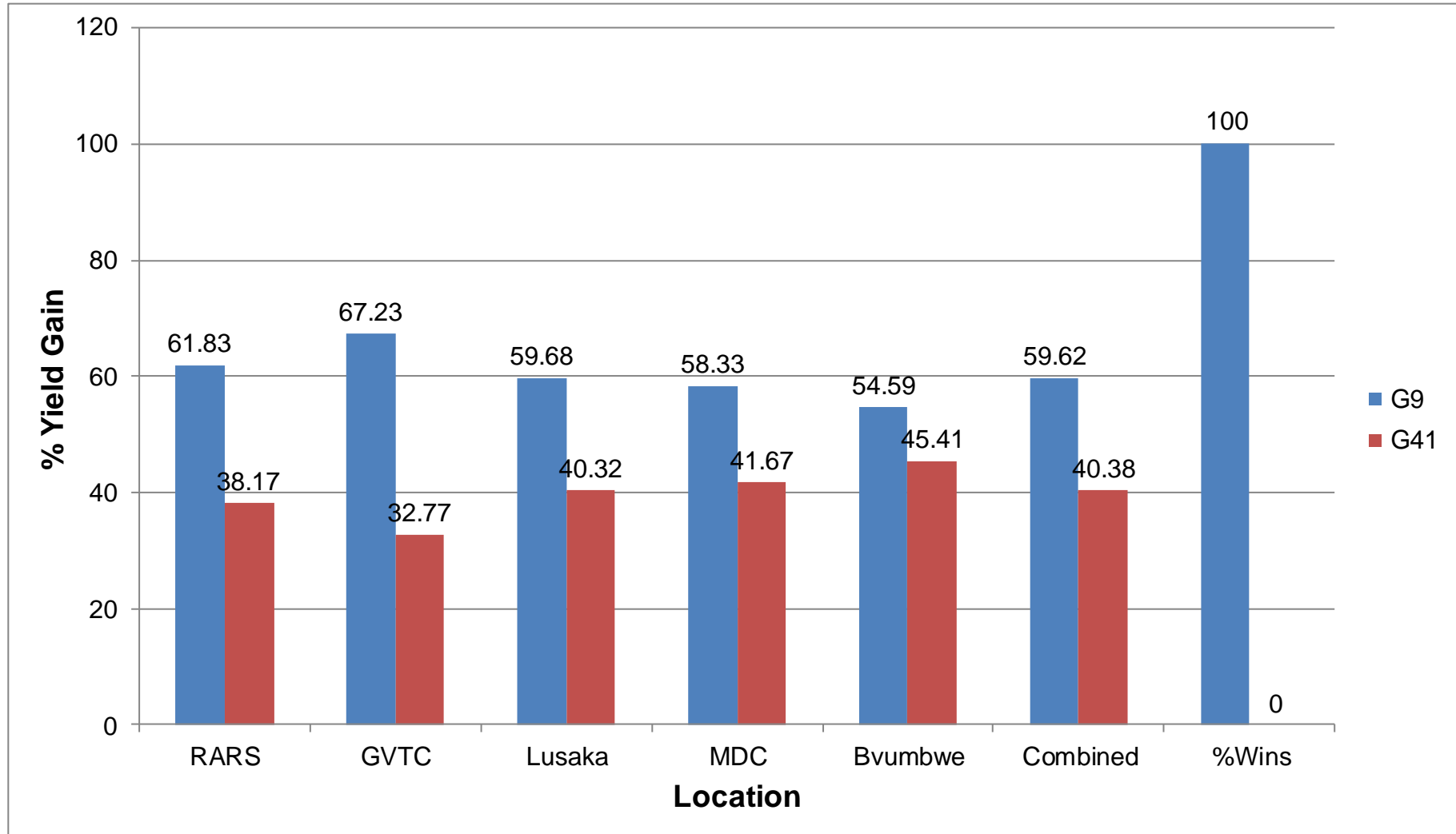
# Head to Head Analysis:G15 vs G41 (10 sites)



# Head to Head Analysis G9 vs G41 (10 Sites)

Variety	2010-2011					2011-2012				
	Sites					Sites				
	1	2	3	4	5	1	2	3	4	5
G9	2.7	3.3	4.2	5.8	4.9	4.2	4.1	4.6	3.2	3.1
G41	1.8	2.0	3.7	3.2	4.67	2.4	1.5	1.9	2.4	1.8
G41 = Founder Variety					G9 = Recent Rust Tolerant Variety					

# Head to Head Analysis: G9 vs G41 (10 Sites)



# Head to head analysis: by Group Means

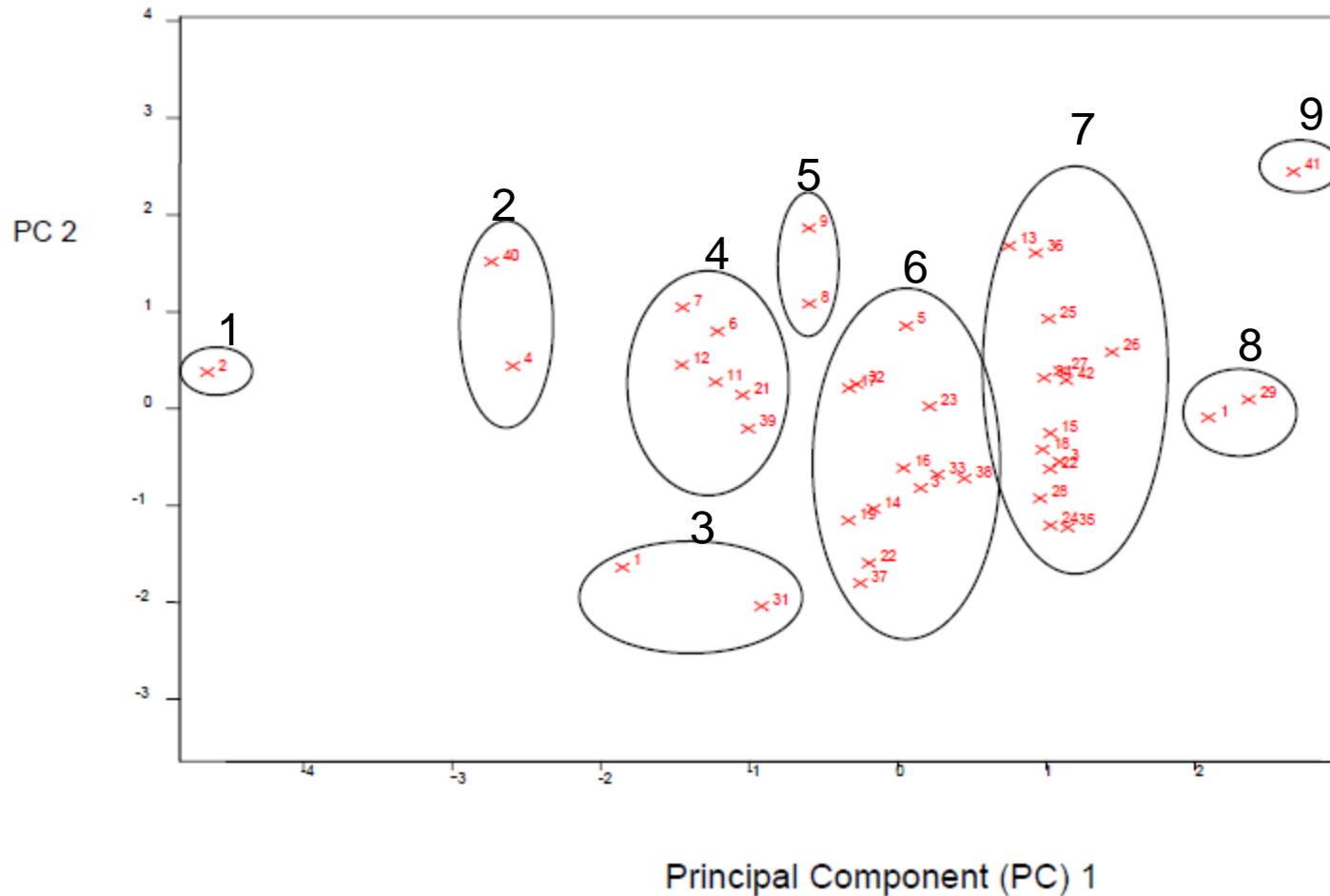
Group	2010-11	2011-12	Overall
Rust Tolerant Varieties	4091	3809	3950
Plant Introductions	4445	4003	4224
Fodder Varieties	3625	3633	3629



# Head to head analysis: by decade

Decade		2010-11	2011-12	Overall
Number	Year	Kg/ha		
1	1940-1950	-	-	-
2	1950-1960	-	-	-
3	1960-1970	2897	2363	2630
4	1970-1980	4200	3725	3963
5	1980-1990	4667	3913	4290
6	1990-2000	5063	4053	4558
7	2000-2010	5340	4168	4754

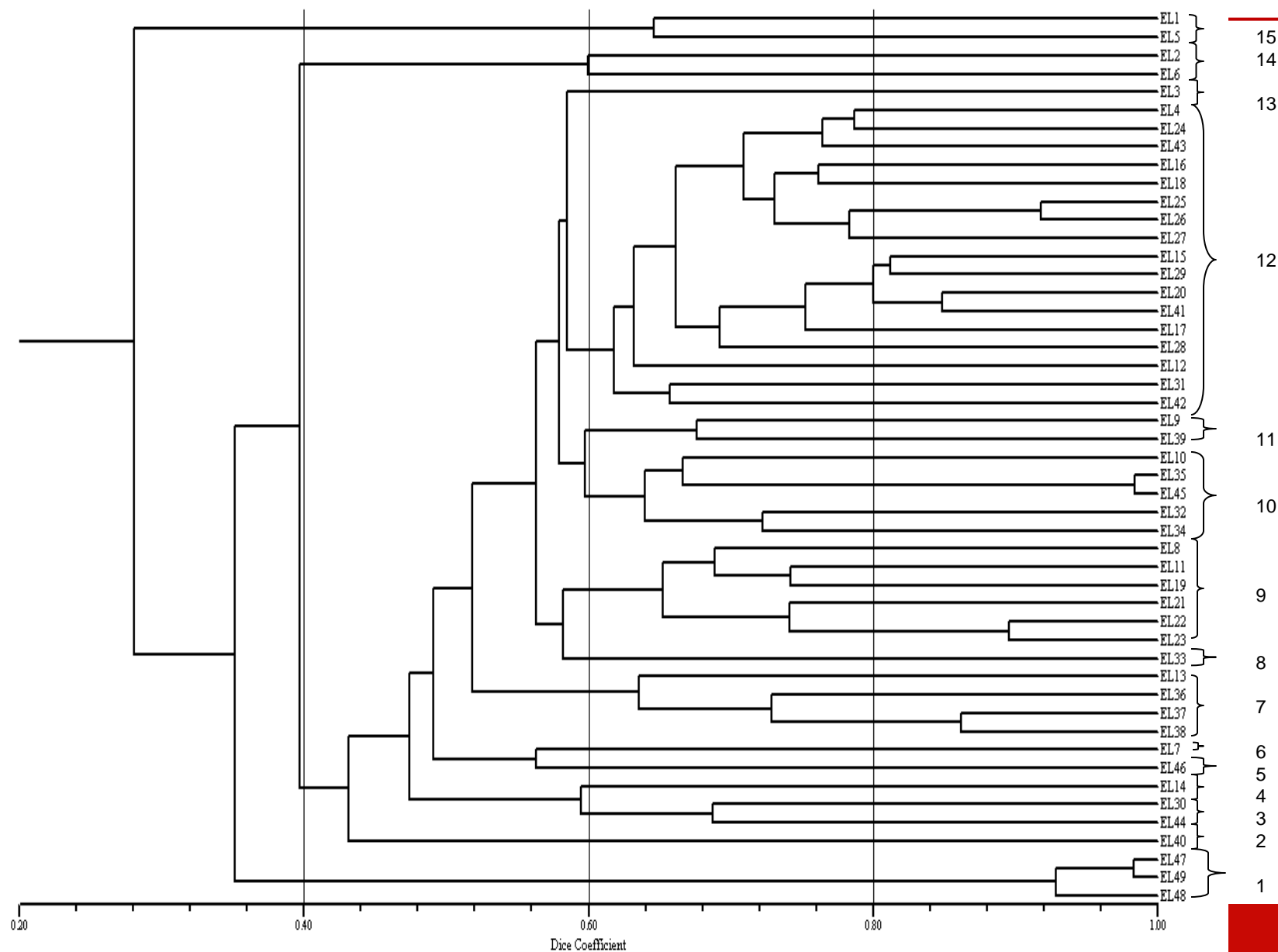
# Clustering pattern: By Seed yield & Maturity



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# Results on Molecular Characterisation

# Dendrogram of 42 varieties using 30 SSR primers



# Results

- Cultivars were grouped into 15 clusters at 60% similarity
  - Clusters 2, 4, 5, 6, 8 and 13 were composed of 1 cultivar
  - Interestingly, 3 varieties from China fell in the same cluster (Cluster 1)
  - Cluster 12 was the largest and comprised of 17 varieties
  - Clusters 3, 11, 14 and 15 had two members
  - Clusters 9 & 10 contained 6 and 5 varieties respectively
  - **Good correspondence between clustering patterns and pedigree data**
- e.g. G25 and G26 were clustered together with the highest similarity (91.8%)

# Genotyping: Summary statistics

Attribute	Range	Mean Value
PIC	0.09-0.77	0.56
No. of Alleles	2.0-9.0	4.57
Gene diversity	0.09-0.79	0.50
Heterozygosity	0-0.19	0.11
Major Allele Frequency	0.34-0.91	0.63

PIC = Polymorphic Information Content

## Discussion: Genotypic characterisation

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- ❖ The mean number of alleles were consistent with previous studies. Tantasawat et al., 2011 found 4.82 alleles per locus among 25 cultivars
- ❖ Gene diversity was also in agreement with studies of Narvel et al., who reported an mean of 0.5
- ❖ Majority of the SSR markers (25/30) had PIC values  $\geq 0.3$ , the value commonly used to assess usefulness of RLFP, RAPD & AFLP (Tantasawat et al., 2011)
- ❖ The primers used were highly polymorphic. Hudcovicova, et al., 2003 demonstrated PIC values ranging from 0.14-0.89 among 67 cultivars
- ❖ The results reveal diversity among the cultivars

# Implications for breeding

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Both the Classical and molecular characterisation support observation of good genetic diversity

- ❖ The duo were able to reveal genetic variation among the soybean germplasm in Zimbabwe
- ❖ SSR markers were highly polymorphic, informative & more discriminatory than the phenotypic data (15 clusters vs 9)



# Implications for breeding

## Breeding progress:

- ❖ First grain soybean release was in 1966
- ❖ Last release for non rust tolerant varieties was in 2008
- ❖ Age difference = 44 years
- ❖ Average yield for G15 over 2 seasons = 5370kg/ha
- ❖ Average yield for G41 over 2 seasons = 3030 kg/ha
- ❖ Yield gain =  $5370 - 3030 = 2340$ kg/ha
- ❖ Yield gain = 77% over 44 years

**Representing 1.75 % gain per annum**

# Implications for breeding

- ❖ Annual gain for the rust tolerant varieties of 1.1% The rust program is relatively young (12 yrs)
- ❖ Annual gain of 1.75% for non-rust resistant program using classical tools is above 1.27% average in the USA where technology is widely used
- Further breeding progress can be accelerated by use of technology
- Available germplasm can be utilized for further genetic improvement

**Although genetic diversity exists, it will be prudent to continue enriching it by bringing foreign germplasm**

# Acknowledgement

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Thank You !