



South African Sugarcane Research Institute

# SASRI Variety Development Strategies

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# History of sugarcane breeding in SA

- Sugarcane production in South Africa started by planting varieties imported from several countries,
- Imported cultivars were not adapted to local conditions and succumbed pests and diseases leading establishment of SASRI 1925 to import, test and release varieties,
  - Few imported varieties achieved short lived success,
- Only one out of several imported crosses (Co421 x Co312) imported from India in 1938 (NCo310 released 1945) and 1944 (NCo376 released 1955) produced successful varieties
  - Importing varieties/crosses was not a long-term solution for variety development for South Africa,
- Research on pollen survival and seed development led to the establishment of Glasshouse (1966) and photoperiod house (1971) marking the beginning of modern sugarcane breeding.



## SUGARCANE AREAS AND RESEARCH STATIONS



- Irrigated: Pongola
  - 12 months age
  - Early, Mid, Late
  - Smut, YSA, rusts
  - Variable soils
- Coastal: Empangeni & Gingindlovu
  - 12 to 18 months
  - High and average yield potential
  - Eldana, smut, rusts
  - Terrain, variable soils
- Midlands – Bruyns Hill
  - 18 to 24 months
  - Rusts, Mosaic
  - Humic & sand soils

# Objectives of sugarcane breeding

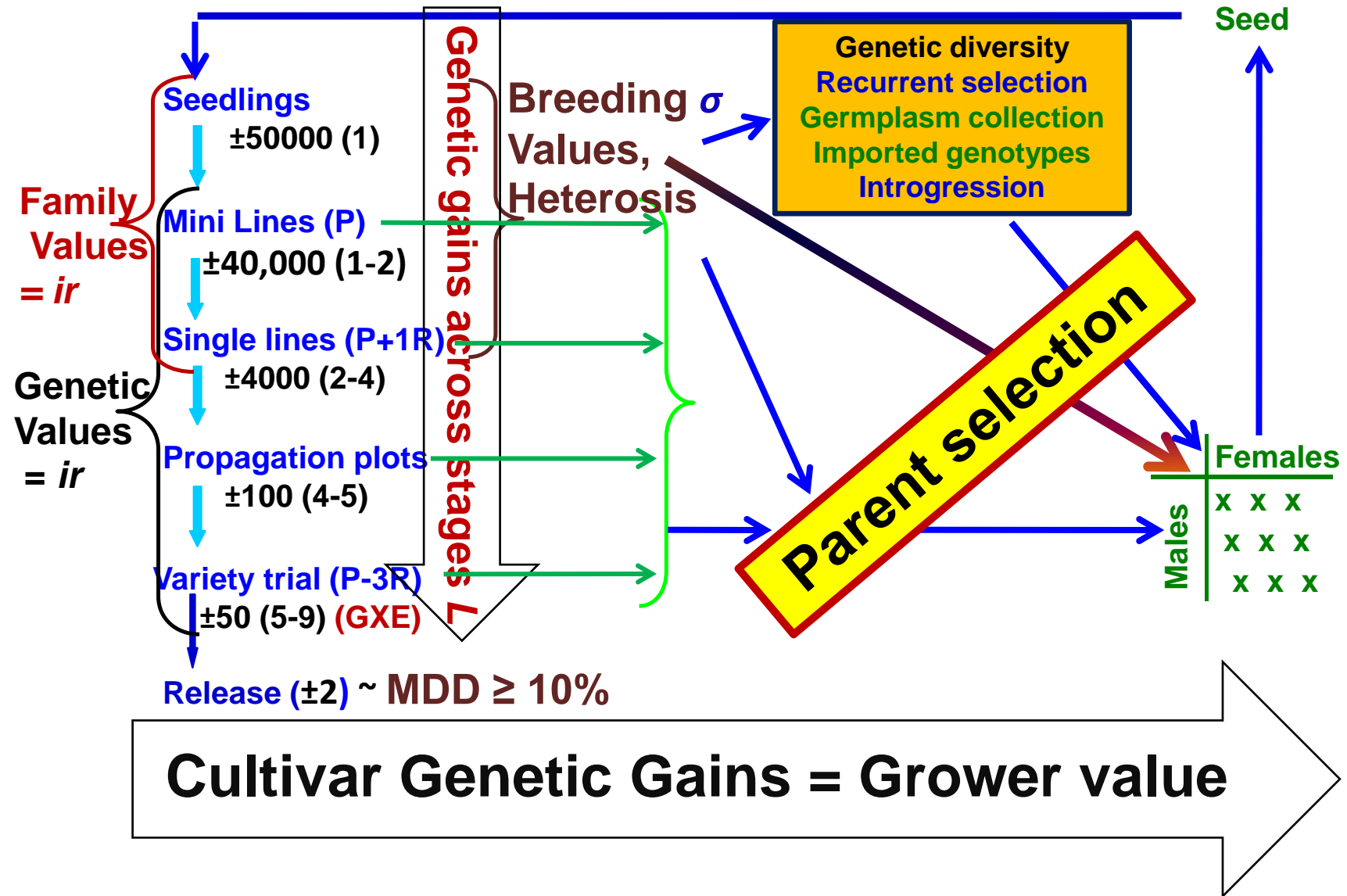
- Sugar yield (TRV) = TCH x RV%,
- Adaptability
  - Early (M, A, M) and Late season (O, N, D)
  - Soil types (Humic, Sandy soils)
  - Age at harvest = 12, 18, 24 months
- Ratooning ability,
- Agronomic characters
  - Lodging, flowering, straight stalks, canopy,
- Pest & disease resistance
  - Pests – Eldana, YSA, thrips
  - Diseases – Smut, rusts, mosaic



# Breeders' equation = breeding efficiency

- **Genetic gain =  $ir\sigma/L$** 
  - $i$  = selection intensity
  - $r$  = selection accuracy
  - $\sigma$  = genetic variability
  - $L$  = generation interval
- Any disruptions to the breeding cycle affects the breeders' equation negatively,
- Assuming additive gene action and single genes
  - Total progenies to combine traits =  $4^n$ 
    - $n$  = number of traits
  - Number of total genotypes to combine 17 traits =  $4^{17} = 17,179,869,184$  seedlings = 85899 times!!
  - Actual evaluated = 200,000 seedlings!!
  - **Combine traits in progenies = efficient crossing,**
  - **Identify the progenies = accurate selection,**
  - **Plant Breeding strategy = increase success.**

# Plant Breeding strategy





- **Combining traits among populations**

- Germplasm evaluation
- Parent selection
- Crossing

**Generating  
populations =  $\sigma$**

- **Identifying genotypes from populations**

- Replicated families
- Replicated genotypes

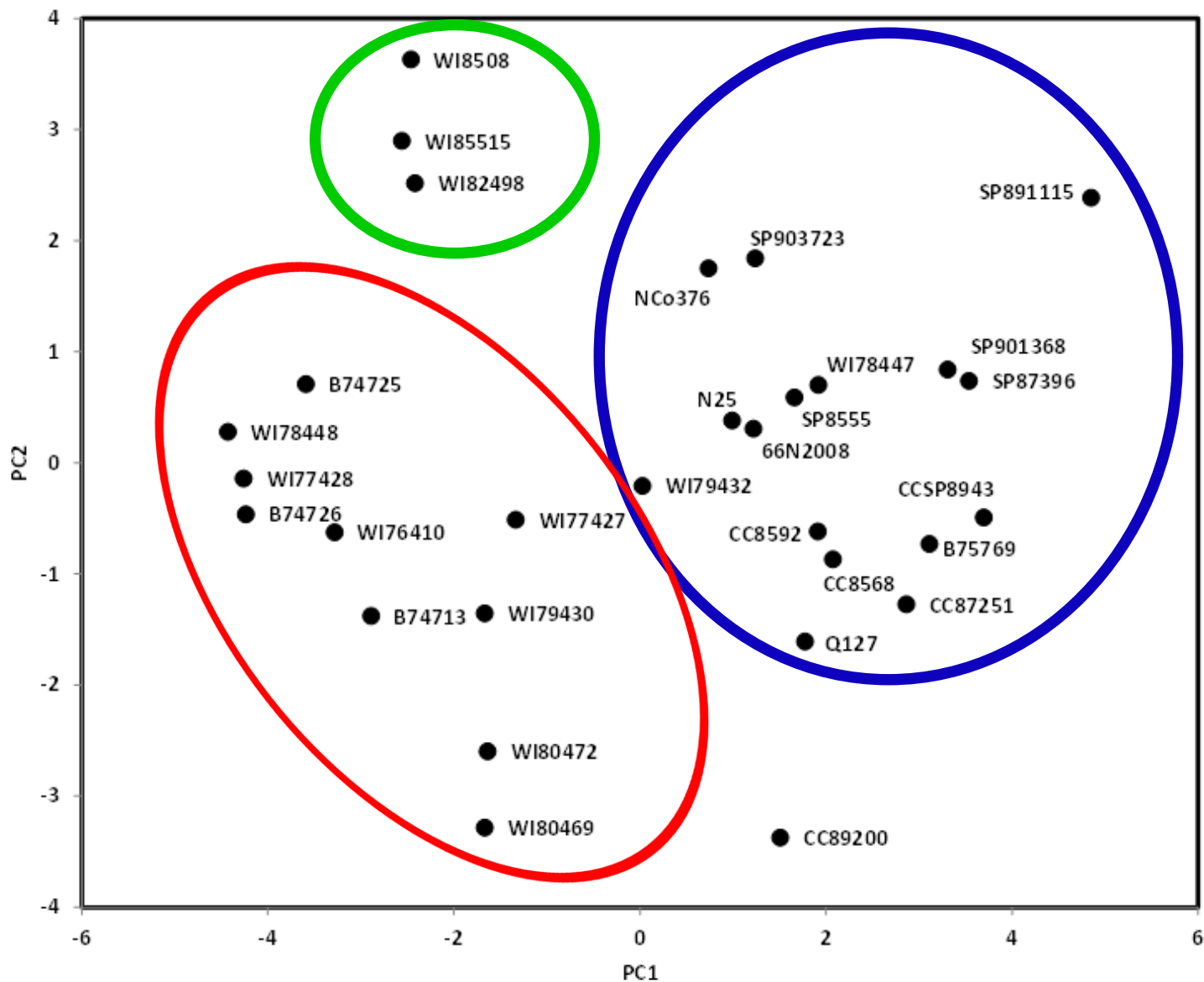
**Evaluating  
populations =  $i, r$**

# Parent selection and Crossing = $\sigma$

- **Genetic values**
  - Value of genes to itself
  - Mean performance of genotypes
- **Breeding values**
  - Additive genes = easier to breed
  - Value of genes passed to progenies
- **Heterosis**
  - Non-additive genes
  - Genetic interactions among parents
  - Dominance, epistasis, hybrid vigour
  - Genetic distance/diversity
  - Utilised in maize breeding



Genetic distance = higher heterosis =  $\sigma$





UNLOCKING THE POTENTIAL OF SUGARCANE

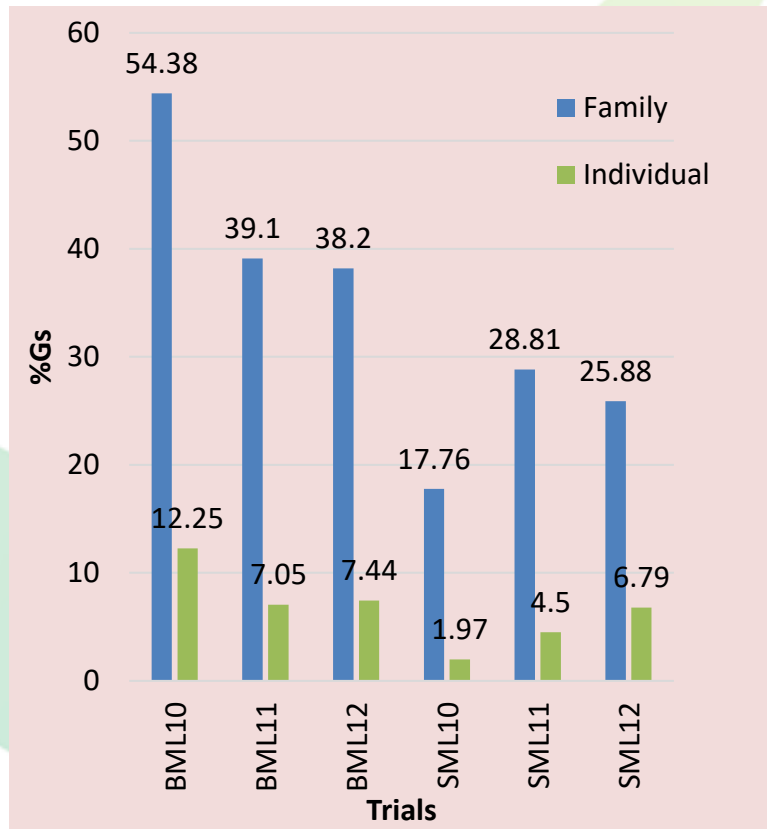
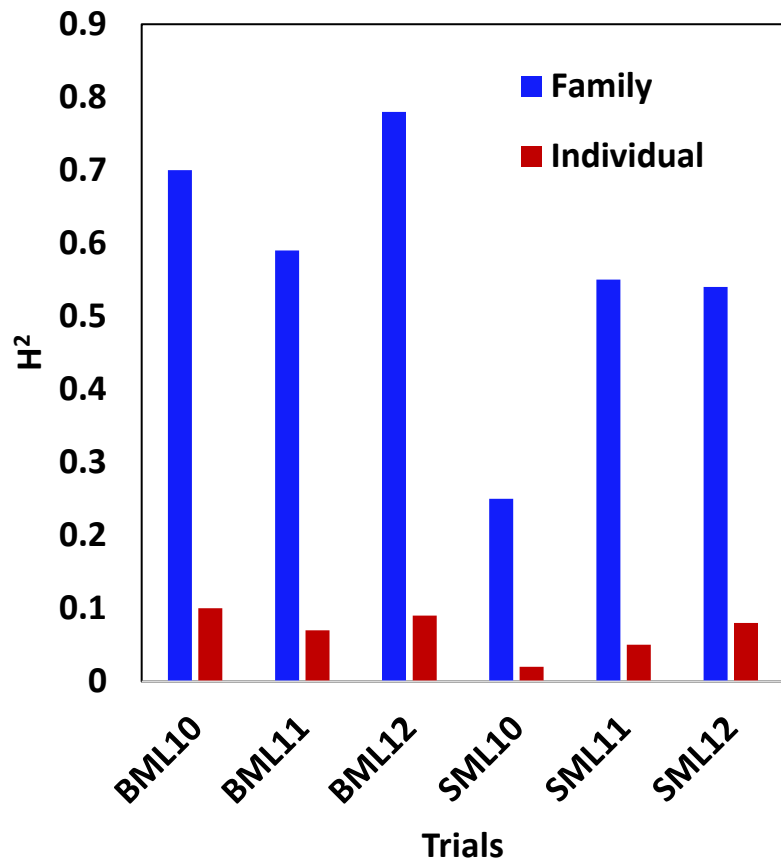


# Optimising field selection = $i, r$

## Family evaluation and selection

- Families are planted in replicated plots made up of individual genotypes,
  - Yield, quality, P & D data collected in family plots,
  - The family values are used to select elite families,
  - Genotypes with optimum trait combinations selected from elite families,
  - Family data is used to estimate breeding values of parents and heterosis of parent combinations of crosses.
- 
- Zhou & Lichakane, 2012; Zhou et al. 2013a,b; Zhou, 2014, 2016; Zhou & Mokwele, 2015; Mbuma et al. 2017, 2018a,b; 2020a,b,c.

# Family vs individual $H^2$ & predicted genetic gains



# Using Logistic regression in selection

$$\pi(x_{i1}, x_{i2}, x_{i3}, x_{i4}, x_{i5}, x_{i6}) \text{ probability of selection}$$
$$= \frac{e^{-32+0.05x_{i1}+6.5x_{i2}+5.8x_{i3}+0.07x_{i4}+0.17x_{i5}-0.42x_{i6}}}{1 + e^{-32+0.05x_{i1}+6.5x_{i2}+5.8x_{i3}+0.07x_{i4}+0.17x_{i5}-0.42x_{i6}}}$$

Zhou et al. 2011,  
2014; Zhou, 2013,  
2018a,b;

Plug in values of traits in model  
to calculate probability of selection = genotypes  
with the best combination of traits

## SAS Code for logistic regression analysis

```
proc Logistic data=one Descending covout outest=FSL11;  
model Select = Stalks Height Diameter ERC Fibre Eldana;  
output out=predict p=ph_hat lower=LCL upper=UCL; run;  
Proc print data=predict; run; Proc print data=FSL11; run;
```



Parameter	BSL13	$\chi^2$	SSL13	$\chi^2$
Intercept	-32.63	21.05***	-34.62	16.06***
Stalks	0.05	18.87***	0.05	16.34***
Height	6.45	21.25***	6.44	15.36***
Diameter	5.79	20.88***	6.89	16.30***
ERC%	0.07	0.12ns	0.34	0.74ns
Fibre%	0.17	0.55ns	0.10	0.10ns
Eldana	-0.42	14.78***	-0.80	16.70***

**Positive and negative coefficients**

Line	Female	Male	Stalks	Ht	Dm	Fibre	ERC	TCH	EBS	Prb
1	71L0416	MO	168	1.1	2.3	12.3	10.4	64	6	0.00142
2	71L0416	MO	154	1.0	1.9	11.8	9.1	51	2	0.00004
3	94H0031	99B1439	145	1.3	2.0	12.4	11.4	78	3	0.00070
4	94H0031	99B1439	145	1.5	1.8	12.6	11.4	72	4	0.00055
5	94H0031	99B1439	141	1.5	1.6	13.0	9.4	63	6	0.00002
6	94H0031	99B1439	118	1.4	1.9	12.1	8.4	38	10	0.00001
7	94H0031	99B1439	154	1.8	1.7	13.3	9.0	61	4	0.01384
8	<b>N19</b>	<b>98G0115</b>	<b>214</b>	<b>1.9</b>	<b>2.5</b>	<b>10.9</b>	<b>9.7</b>	<b>111</b>	<b>3</b>	<b>0.51556</b>
9	95L0828	MO	114	1.3	1.9	13.0	10.9	35	3	0.00004
10	95L0828	MO	118	1.0	2.4	11.1	8.6	45	5	0.00013
11	<b>95L0828</b>	<b>MO</b>	<b>141</b>	<b>2.1</b>	<b>2.7</b>	<b>8.8</b>	<b>8.6</b>	<b>152</b>	<b>4</b>	<b>0.82103</b>
12	95L0828	MO	154	1.6	2.3	10.8	9.5	78	7	0.03813
13	97B0707	MO	118	1.1	2.3	13.6	9.5	57	12	0.00001
14	97B0707	MO	168	1.3	2.6	14.4	12.2	78	10	0.02785
15	00B1741	MO	177	1.3	2.1	10.5	8.7	79	7	0.00150
16	86H0437	95H0059	150	0.9	2.3	10.7	8.9	65	9	0.00002
17	94H0031	97B0107	145	1.4	2.2	14.8	10.9	50	7	0.00234

# Selected vs discarded

BSL13	Stalks	Height	Diamtr	ERC%	Fibre%	TCH	TSH	Eldana
Selected	184	1.70	2.61	8.8	12.1	137	12.1	6.0
Discarded	151	1.41	2.37	8.9	11.9	87	7.9	7.0
Mean	156	1.45	2.41	8.9	11.9	104	9.4	6.9
S%D	<b>122</b>	<b>121</b>	<b>110</b>	<b>98</b>	<b>101</b>	<b>158</b>	<b>153</b>	<b>86</b>

SSL13	Stalks	Height	Diamtr	ERC%	Fibre%	TCH	TSH	Eldana
Selected	169	1.65	2.36	10.5	14.2	118	12.4	4.7
Discarded	141	1.34	2.20	10.1	13.8	71	7.2	7.6
Mean	144	1.37	2.22	10.1	13.9	76	7.8	7.2
S%D	<b>120</b>	<b>123</b>	<b>107</b>	<b>104</b>	<b>103</b>	<b>166</b>	<b>172</b>	<b>63</b>

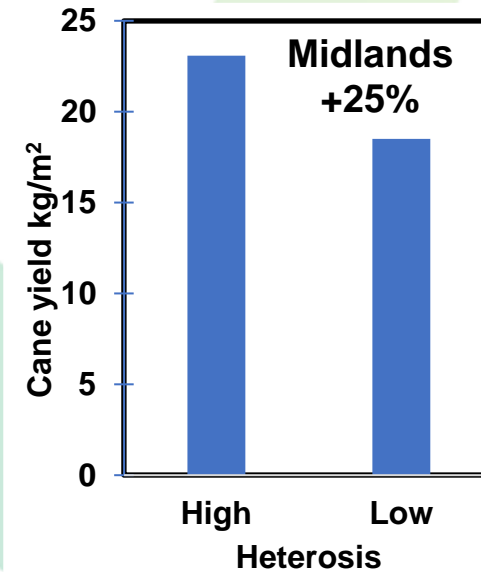
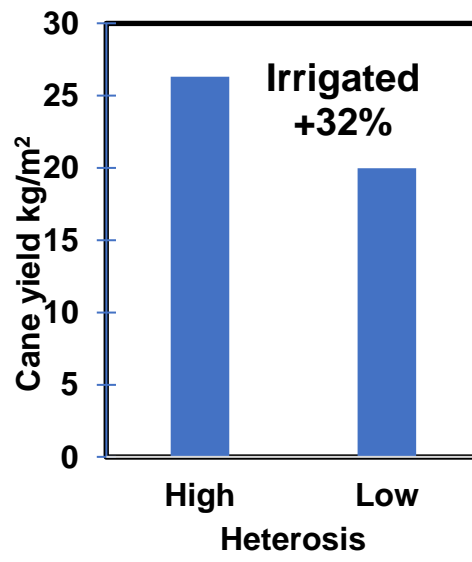
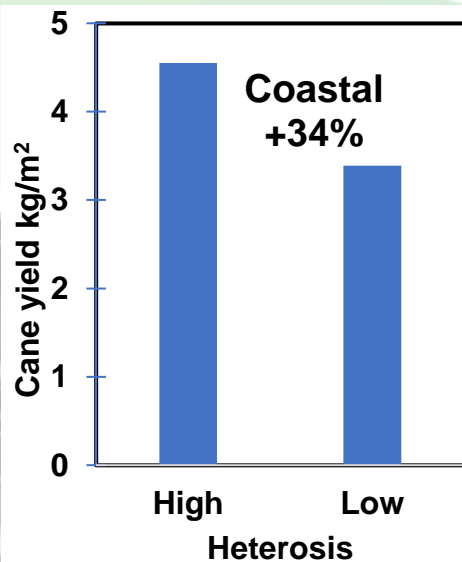
# Plant ideotypes – trait combinations (Zhou, 2018)

Trait	BSL12	SSL12	KSL12	GSL12	USL12	TSL12	FSL13
Stalks	33.4	19.6	67.8	33.6	20.7	53.5	34.1
Height	20.2	14.8	32.0	26.3	16.1	40.7	9.8
Diameter	34.5	17.6	58.1	22.6	23.4	76.3	45.6

- Good growing environments
- Midlands Humic = Diameter>Stalks>Height
- Irrigated = Diameter>Stalks>Height
- Coastal short High = Diameter>Stalks>Height
- Coastal short average = Diameter>Stalks>Height
- Average growing environments
- Midlands Sandy = Stalks>Diameter>Height
- Coastal Long High = Stalks>Diameter>Height
- Coastal Long average = Stalks>Height>Diameter

# Heterosis in sugarcane breeding = $\sigma$

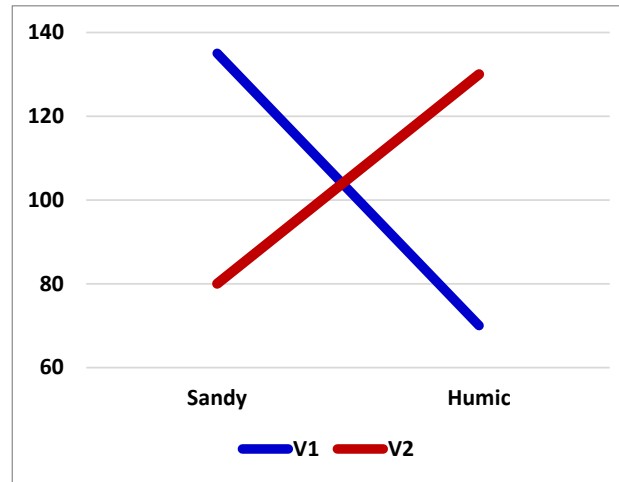
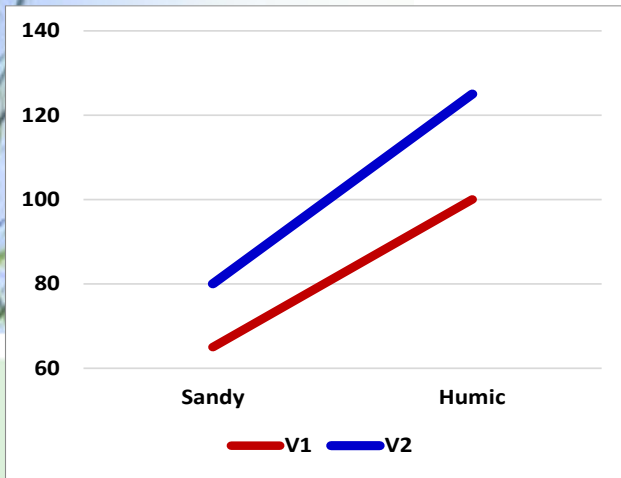
Significant in 34 out 35 populations  
Genetic distance = higher heterosis  
1. Different genetic backgrounds  
2. Different generations



Zhou 2019, 2020a,b, 2023



# Genotype by Environment interactions



F-values	CSCHP	CSCAP	CLCAP	CLCHP
Environment	3.52	1.41	2.10	2.02
Genotype	8.88*	4.41*	12.71*	15.48*
GxE	3.09*	1.88*	2.54*	3.28*
Crop-year	122.30*	89.86*	49.32*	94.17*
ExCY	57.29*	37.94*	15.91*	48.13*
GxCY	3.90*	1.86*	3.56*	2.61*
GxExCY	2.74*	1.45*	1.23	2.15*
Mean	70.6±14.2	52.6±13.9	66.9±19.5	84.9±17.0
R <sup>2</sup>	0.77	0.65	0.64	0.84
CV%	20.1	26.4	29.2	20.1

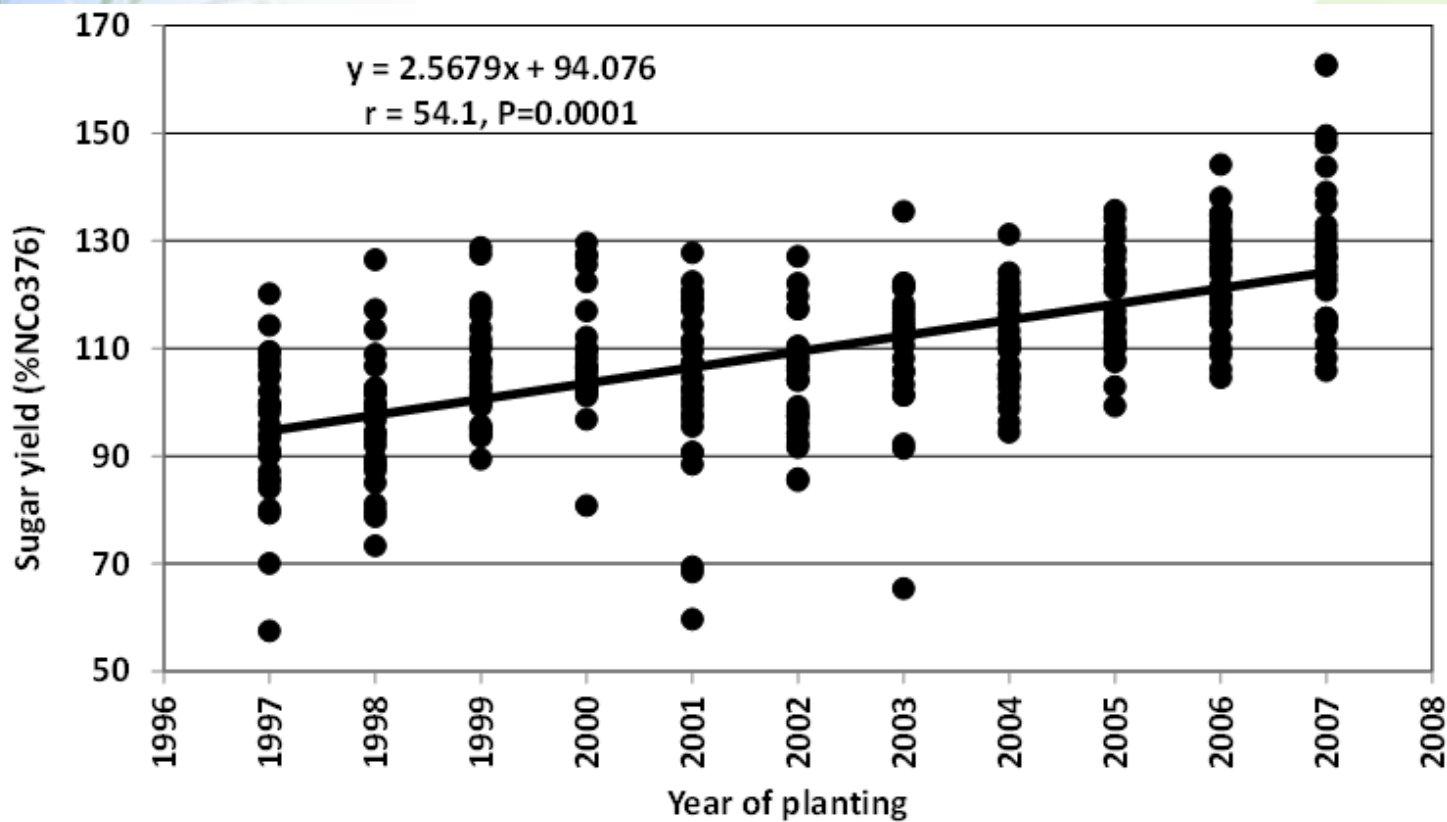
Variety adaptation is environment specific

Variety yield fluctuates across ratoons

Variety ratooning is environment specific\*\*

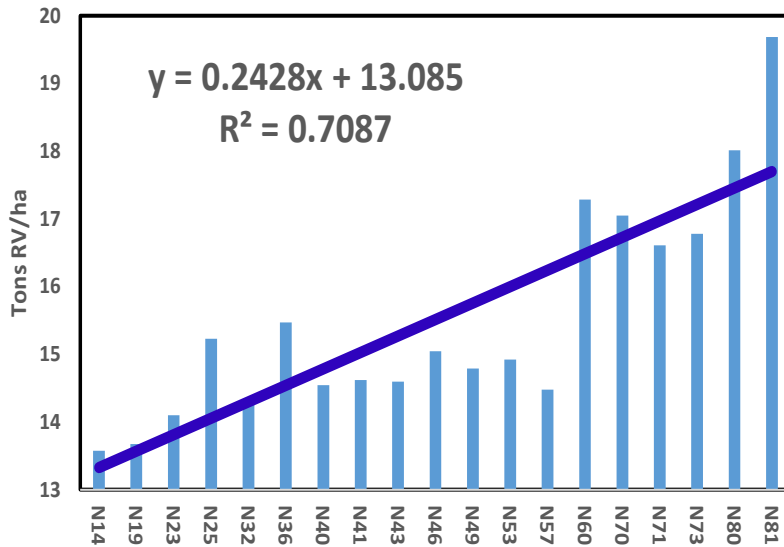
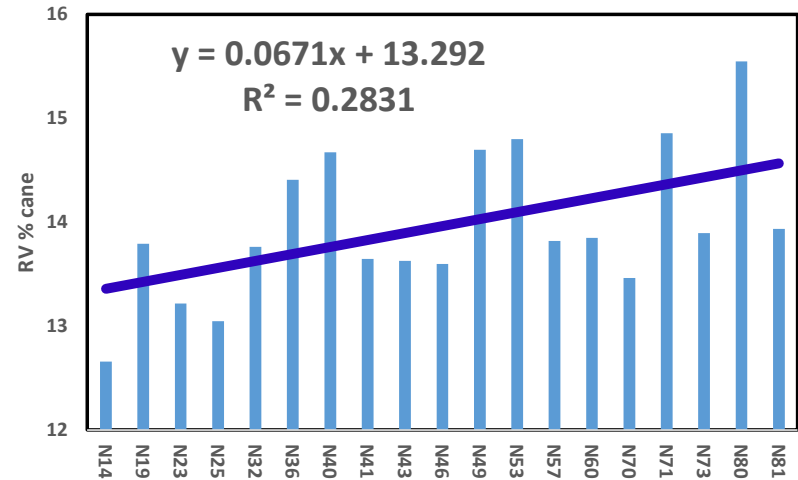
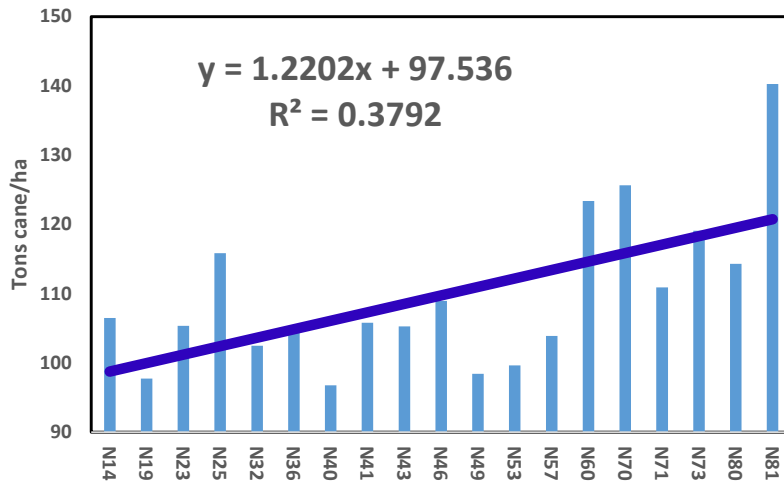
Ramburan et al. 2011, 2012a,b; Zhou et al. 2012a,b, 2013; Zhou and Gwata, 2015; Sengwayo et al. 2018a,b,c; Zhou, 2015, 2019, 2021, 2022.

# Population genetic gains measure of breeding efficiency



Zhou, 2013

# Cultivar Genetic gains = quality of varieties



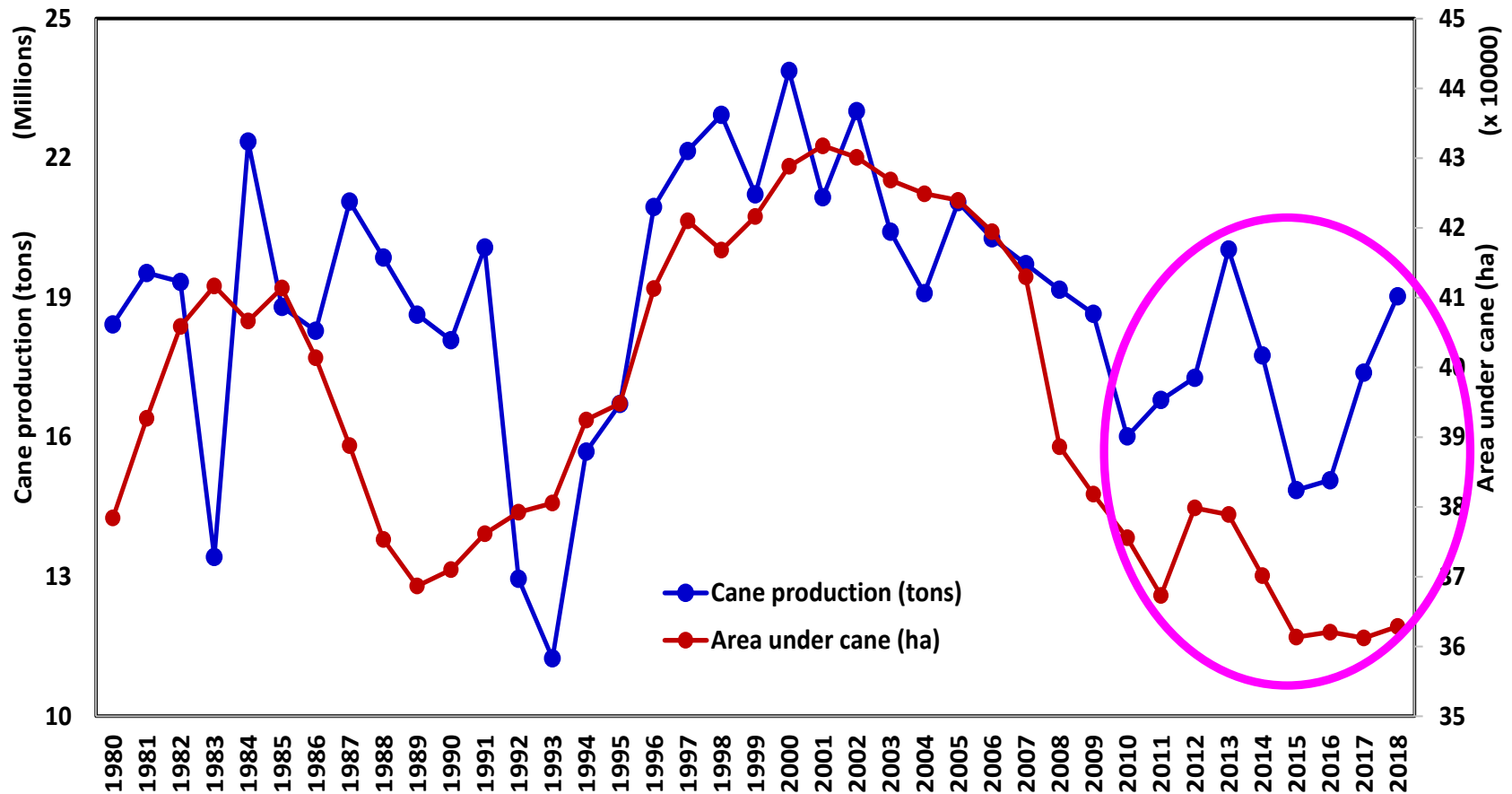
Coast	%
CLCHP	122*
CLCAP	122*
CSCAP	108
CSCHP	110*

Irrigated	%
Early	103
Late	116*

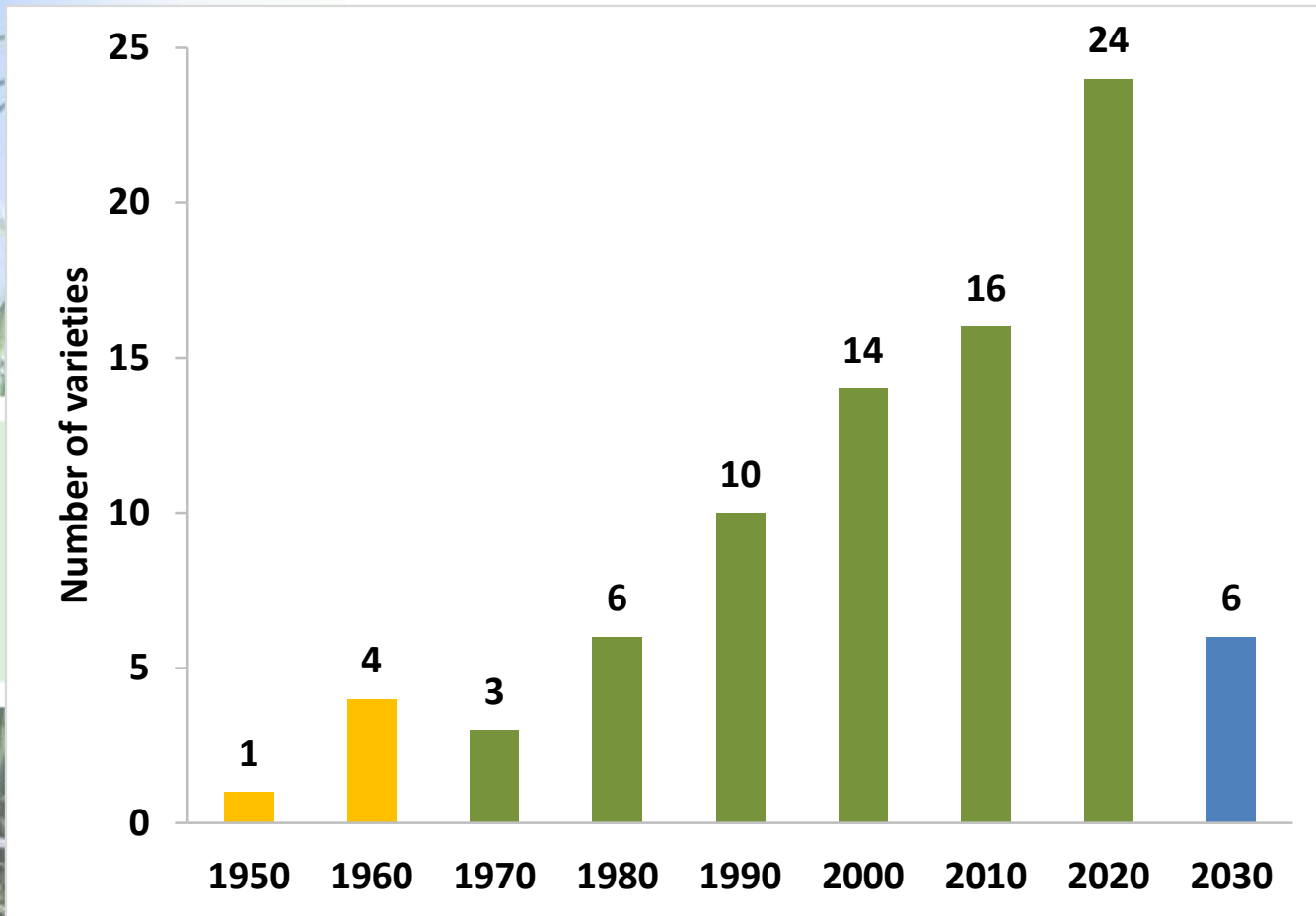
Midlands	%
Humics	114*
Sands	117*

Zhou & Gwata, 2016; Zhou, 2017, 2023

# Cultivar genetic gains and cane production



**Grower testimony = higher cultivar yield maintained cane production after reduction in cane area from diversification**



**81 N varieties released by SASRI**



# Summary

- Establishing SASRI breeding – visionary investment = 81 N varieties produced to date,
- Plant breeding strategy,
  - Breeding values + Heterosis for crossing = **higher genetic variability**
  - Family + Individual selection = **higher selection intensity and accuracy**
  - GxE = **optimizing variety positioning**
  - Population genetic gains = **breeding efficiency**
  - Cultivar genetic gains = **value to industry**
    - up to 22% higher sugar yield (New %old cultivars).

# THE FUTURE

- Evaluating heterosis across breeding populations and creating heterotic groups to maximize utilization of heterosis = **the future of sugarcane breeding**,
- Determining genetic control of eldana, smut, YSA, rusts infection to increase efficiency of breeding for P&D resistance,
- Utilizing GxE to optimize variety positioning in commercial production = **benefits for the grower**,
- **\*Opportunities for Post Graduate students.**

11F1245 = N80







**Many thanks to selection and field services staff who assist with implementing the Plant Breeding strategy.**