

# Trait Variation in a Banana Training Population for Genomic Selection

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## Introduction

Conventional crossbreeding is the main approach used in banana improvement. However, the method requires up to two decades of crossing and field evaluation to develop a new hybrid. This is because selection is carried out at different levels (Fig 1). At every level, plants are evaluated after three crop cycles, each taking about a year. Yield traits can only be scored at harvest while organoleptic traits are recorded after harvesting, making the selection process slow, expensive and labour intensive. Molecular tools with the potential to improve banana breeding efficiency are being investigated. These include genomic selection (GS), which will benefit breeding through increased genetic gain per unit time (Meuwissen et al. 2001; Nakaya and Isobe 2009). Understanding trait variation and the correlation among economically important traits is an essential first step in the development of GS models. In this study we tested the hypothesis that trait variations in bananas are not affected by cross combination, cycle, field management and their interaction with genotype.

Black Sigatoka-related traits were not affected by crop cycle. These could be measured in the first cycle thus reducing on phenotyping burden. Growth traits such as plant height and girth were the least affected by field input management. Conversely, yield-related traits such as bunch weight, number of hands and number of fingers were significantly affected by both crop cycle and field input management. The variation in traits observed suggest that different genomic selection models should be tested. For traits affected by cycle and field management, models that account for non-additive genetic effect are likely to have better predictive ability on them. Integration of genomic selection in crossbreeding allows simultaneous prediction and selection of best hybrids. This is likely to reduce the selection cycle and increase genetic gain per unit time.

**Table 1: Pearson's correlation coefficients of traits under high input field management**

	Pant height	Plant girth	Index of non-spotted leaf	Bunch weight	Number of hands	Number of fruits	Fruit length	Fruit circumference	Fruit diameter
Plant girth	0.77*								
Index of non-spotted leaf	0.21	0.27							
Bunch weight	0.37*	0.62*	-0.13						
Number of hands	0.22	0.42*	0.10	0.52*					
Number of fingers	0.37*	0.58*	0.19	0.57*	0.84*				
Fruit length	0.20	0.44*	-0.15	0.83*	0.28*	0.27*			
Fruit circumference	0.33*	0.45*	-0.15	0.81*	0.15	0.15	0.85*		
Fruit diameter	0.39*	0.48*	-0.16	0.79*	0.16	0.18	0.80*	0.97*	
Pulp diameter	0.39*	0.45*	-0.16	0.74*	0.11	0.13	0.76*	0.94*	0.99*

\* Significant correlation with P-value < 0.05

**Table 2: Effect of genotype and genotype interaction with cycle and field management on the traits**

Trait	Indep. variable	Sum Sq	Df	F value	P value
Plant height	Genotype	2222889	306	3.77	<0.0001
	Genotype x Field	432297	284	0.79	0.995
	Genotype x Cycle	332846	299	1.05	0.266
Plant girth	Genotype	73176	306	4.30	<0.0001
	Genotype x Field	12061	284	0.76	0.998
	Genotype x Cycle	13057	299	1.51	<0.0001
Index of non-spotted leaf	Genotype	116602	306	2.44	<0.0001
	Genotype x Field	58584	284	1.32	0.0005
	Genotype x Cycle	51026	299	0.95	0.695
Bunch weight*	Genotype	1214	303	12.55	<0.0001
	Genotype x Field	127	269	1.48	<0.0001
	Genotype x Cycle	109	276	1.49	<0.0001
Number of hands	Genotype	3334	303	8.67	<0.0001
	Genotype x Field	570	269	1.67	<0.0001
	Genotype x Cycle	429	276	1.26	0.005
Number of fruits	Genotype	1380509	303	5.46	<0.0001
	Genotype x Field	333081	269	1.49	<0.0001
	Genotype x Cycle	262981	276	1.23	0.009

\* Original data square root transformed

## Conclusions and Recommendations

Genomic selection as a form of marker assisted selection is a non-stand alone approach but if integrated into conventional crossbreeding it has the potential to accelerate the breeding process. The effectiveness of genomic selection in banana will greatly depend on the prediction accuracy of the genomic selection models.

## References

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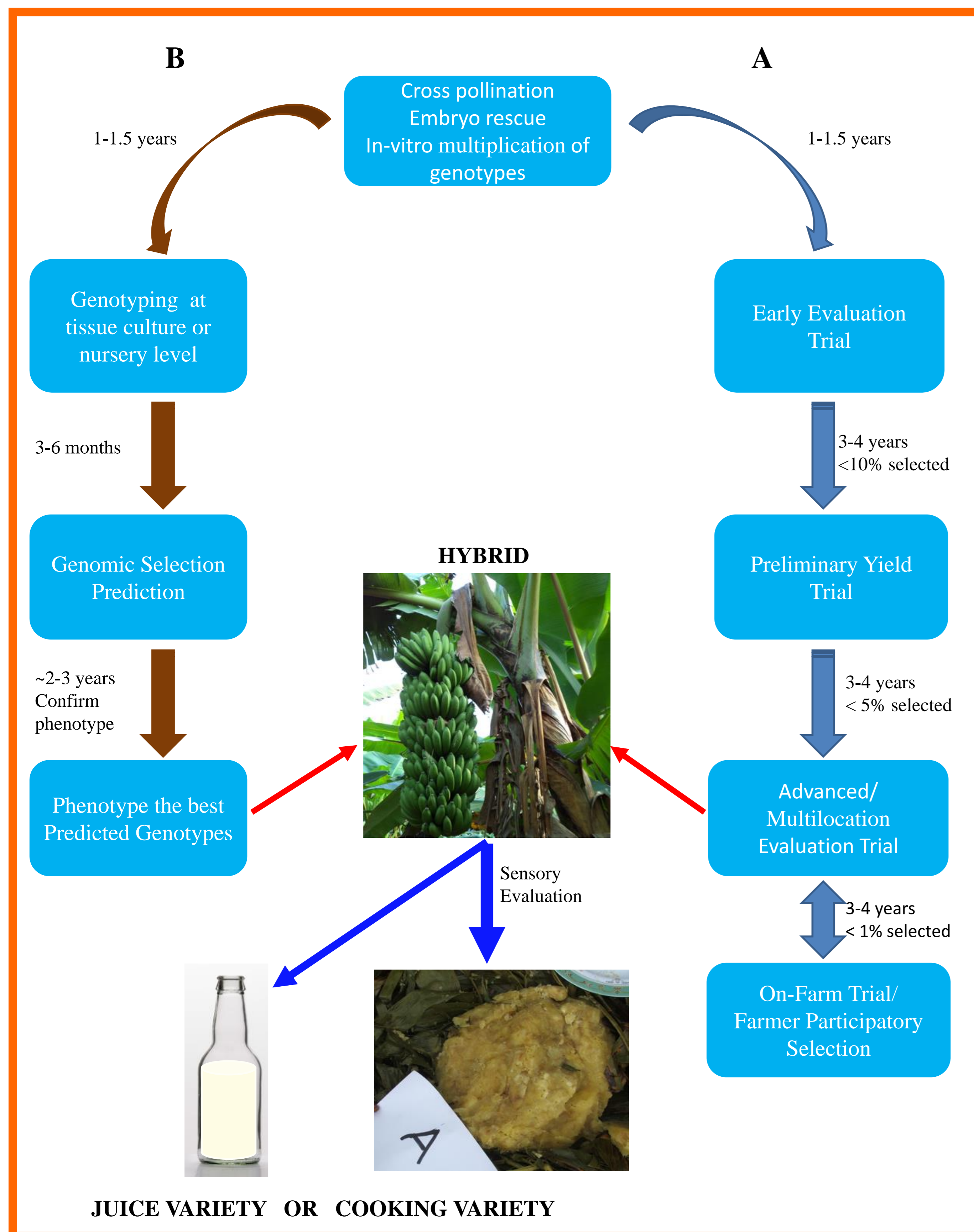


Fig 1: Approaches to hybrid selection in banana breeding program. (A) the classical phenotypic selection of banana hybrids and (B) integrated genomic selection and phenotypic selection approach being investigated.

## Materials and Methods

The training population consists of 307 genotypes that include parents and the resulting hybrids. The population was phenotyped under low (no mulch and NPK fertilizer) and high (mulch + NPK) field input management at Namulonge research station. Data collected on two crop cycles were analysed using R statistical software. The correlations and significance of correlations were determined using R package Hmisc. Analysis of variance was performed to understand the effect of genotype and the interaction between genotype and cycle, and genotype and field management on trait variation.

## Results and Discussion

A high level of correlation among vegetative and yield related traits was observed (Table 1). This could mean that the predictive ability of traits that are difficult to phenotype will be similar to less difficult traits they are highly correlated with. Therefore, genomic selection models could be developed for traits that are easily measured. Table 2 summarizes the genotypic effects and the interaction between genotype and cycle and genotype and field management on the traits.