



Genotyping maize varieties in Uganda

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Independent
Science and
Partnership
Council

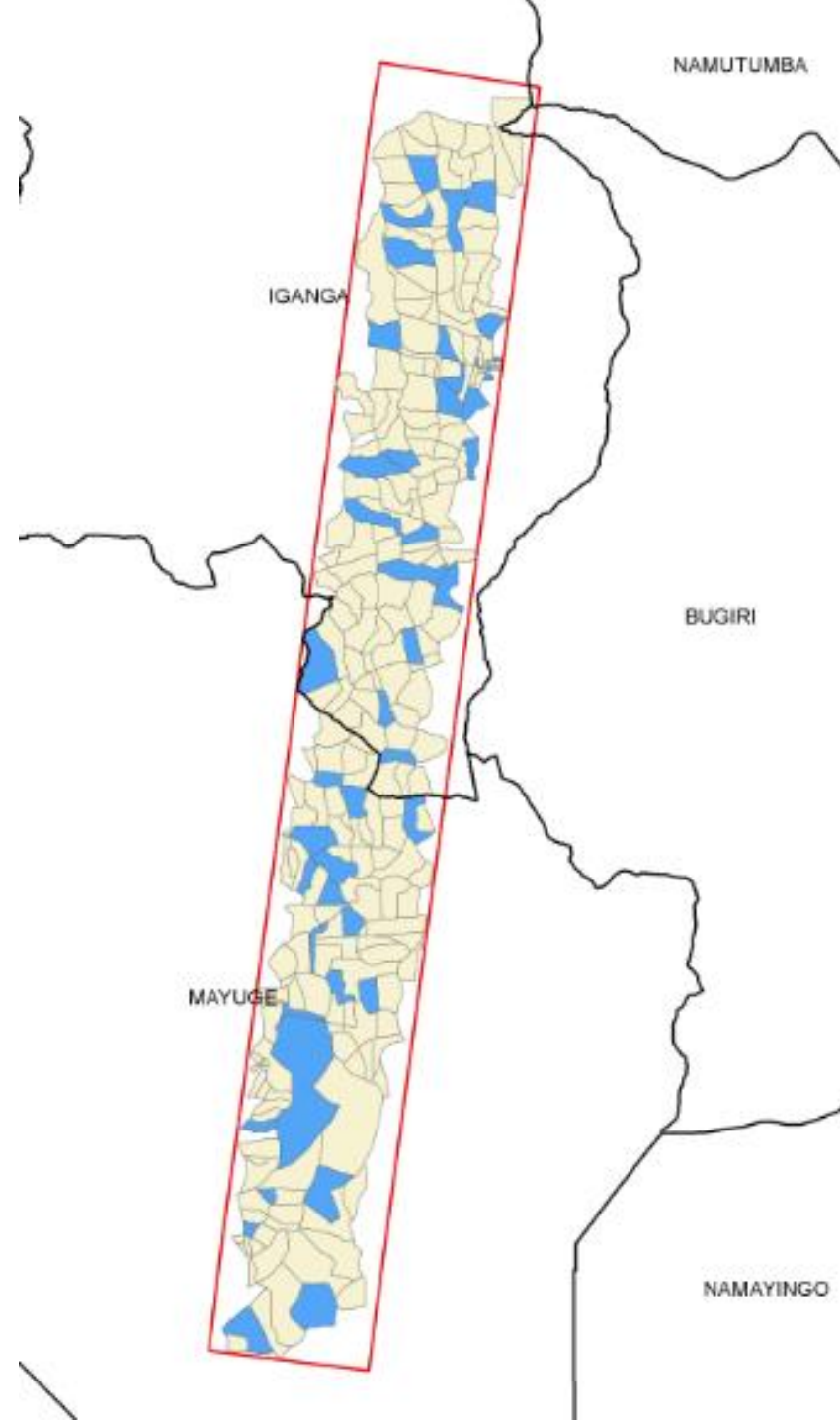
MAPS Sample

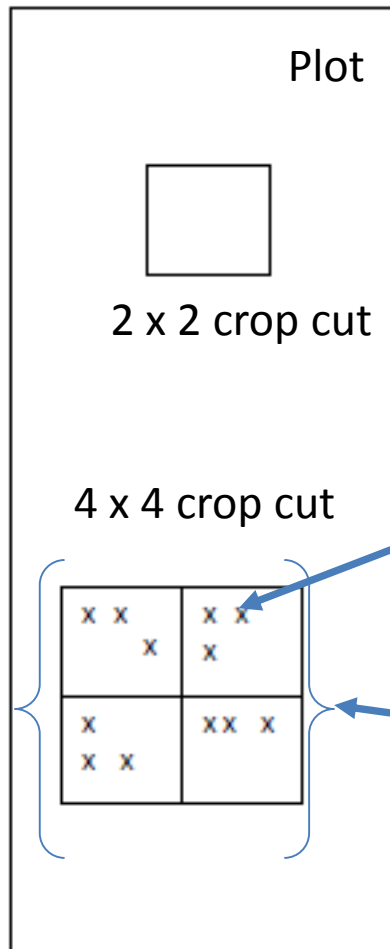
– EAs

75 EAs total

3 Strata in Eastern Uganda:

- Serere District (15 EAs)
- Sironko District (15 EAs)
- Portion of Iganga and Mayuge districts for which remote sensing imagery will be collected (45 EAs, shown at right)





Team spent 1 month training the enumerators for the survey as a whole
Mix of classroom exercises and field practice
A full week of training and practice on laying crop cuts, leaf sampling, and post-harvest grain sampling

Leaf: 4 discs punched from each of 12 individual plants distributed across 4 x 4m quadrant

Grain: Entire 4 x 4m area harvested and weighed; random sample of approx. 300 grains dried; ground into flour in Uganda; shipped to lab in Australia

Leaf sampling kits are difficult to use in survey fieldwork settings



MAPS 2015
 cal Experiment on Measuring Maize
 tivity, Variety and Soil Fertility
 World Bank – World Agroforestry Centre – FAO SPLA

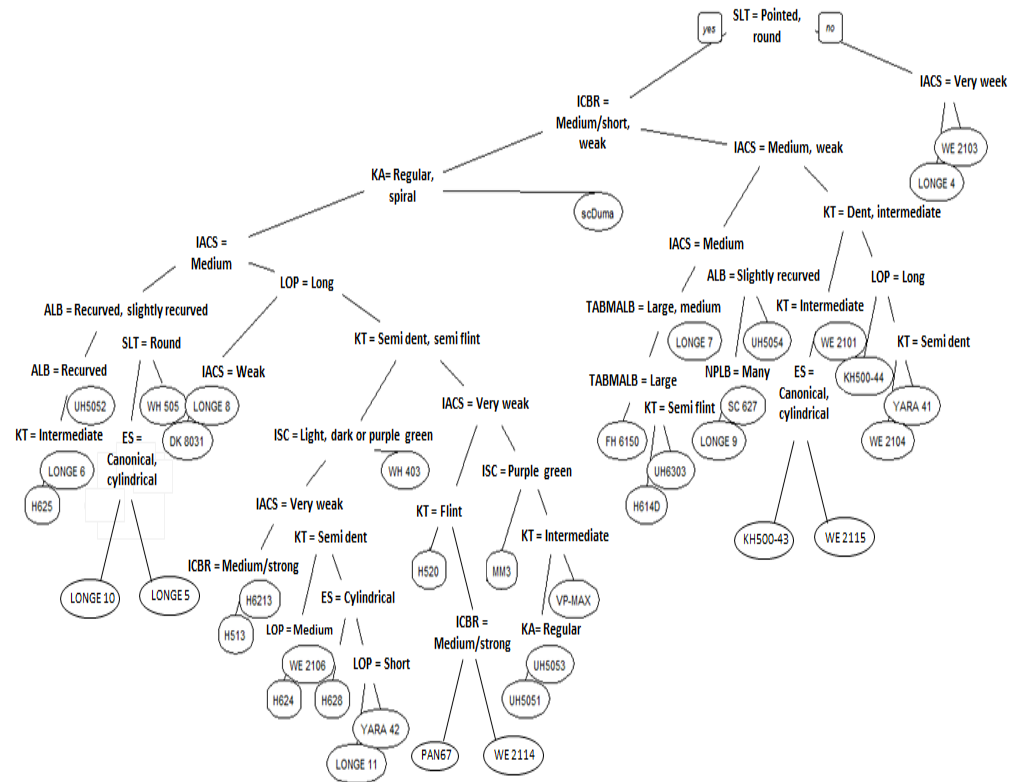


ENUMERATOR MANUAL
 Post-Planting – Crop-Cutting
 April 2015

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Recursive Partitioning & Classification Tree Analysis of Morphological Attributes of 38 Reference Library Samples

- Morphological attributes for the reference library: Obtained by planting out the 38 varieties in NaCCRI fields.
- **Results:** Varieties are uniquely identified using 11 attributes.
- Identification of the varieties in the field: Using these attributes, varieties that the farmers plant were identified based on farmer responses on morphological attributes



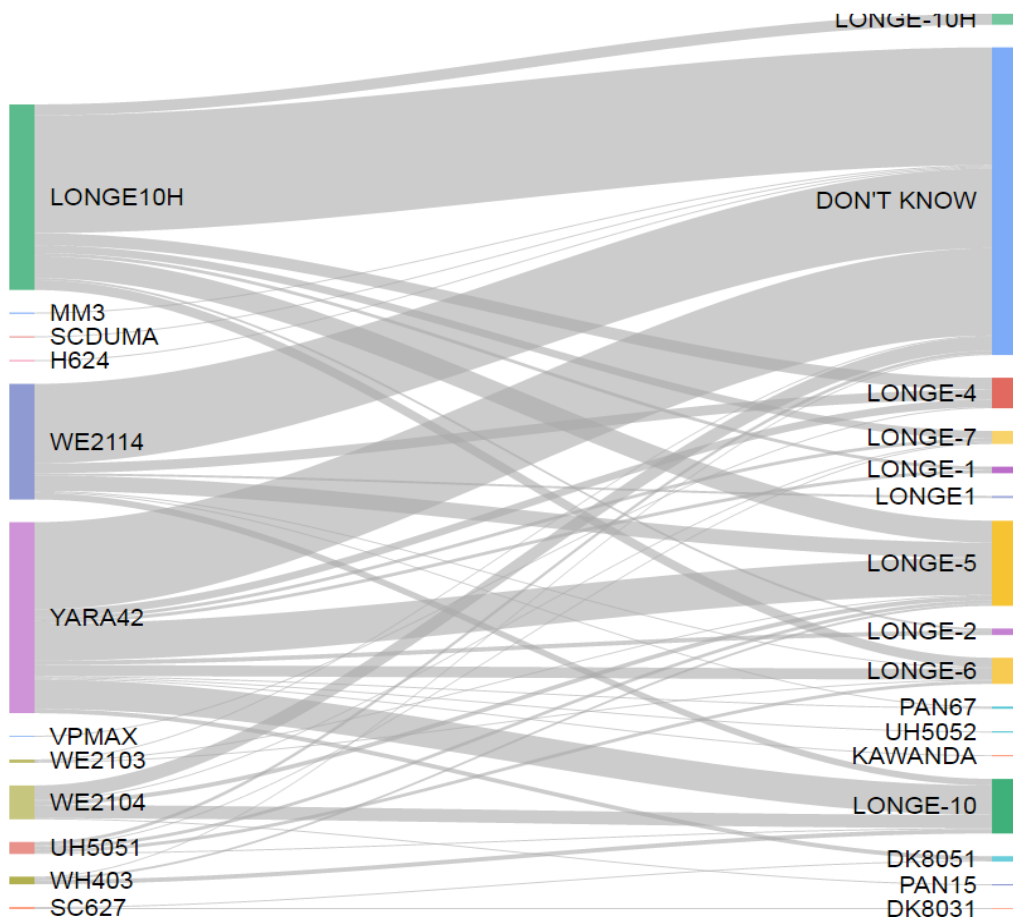
How Do Different Methods Perform in Unique Identification of Maize Varieties?

- 55 percent of farmers could not state the variety they have planted
- Farmer-reported morph. attributes does not uniquely identify varieties
- DNA fingerprinting performs the best for **unique** varietal identification

	Farmer Elicitation (FE)		Strict Morph. Protocol (SP)		DNA Fingerprinting	
	<i>Freq.</i>	<i>%</i>	<i>Freq.</i>	<i>%</i>	<i>Freq.</i>	<i>%</i>
Don't Know	283	55	448	88	0	0
Uniquely identified	227	45	62	12	510	100
TOTAL	510	100	510	100	510	100
Number of Varieties	13		16		12	

Results

<http://impact.cgiar.org/>



2% of sample of 510 farmers able to correctly identify variety name

Mean reference library heterogeneity level is 33% - genetic lines not been well maintained?

Purity (% of major genotype representing constituent of genetic material present in plot) is average of only 63%

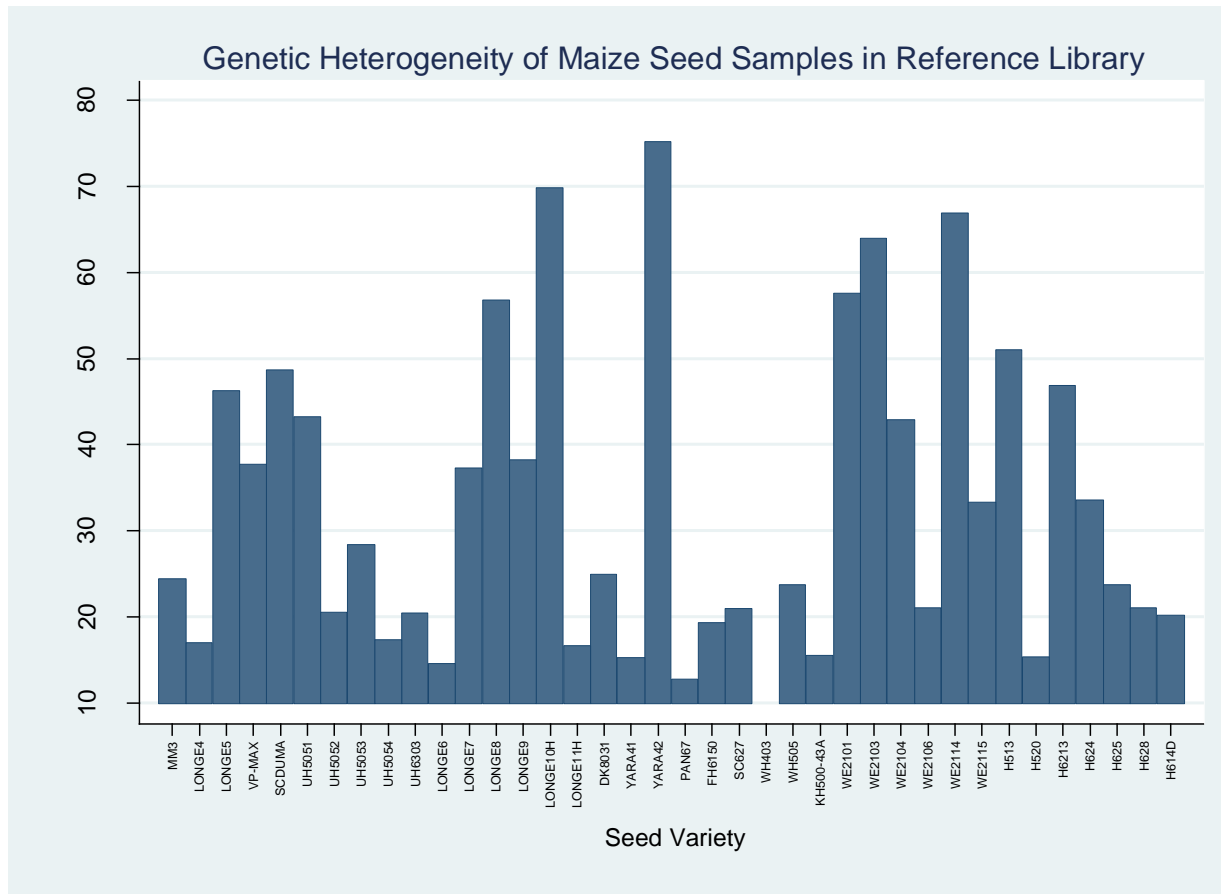
Phenotypic protocol doesn't work

GENOTYPE (Method E)

Farmer elicited variety name (Method A)

(Unacceptable Levels of) Heterogeneity in Reference Library Samples

- Acceptable level of heterogeneity of the samples is 15% (0.15) but our results show that most of the hybrids are above the threshold.



Mean	32.9%
Median	24.6%
Min	9.8%
Max	75.2%