Genotyping maize varieties in Uganda

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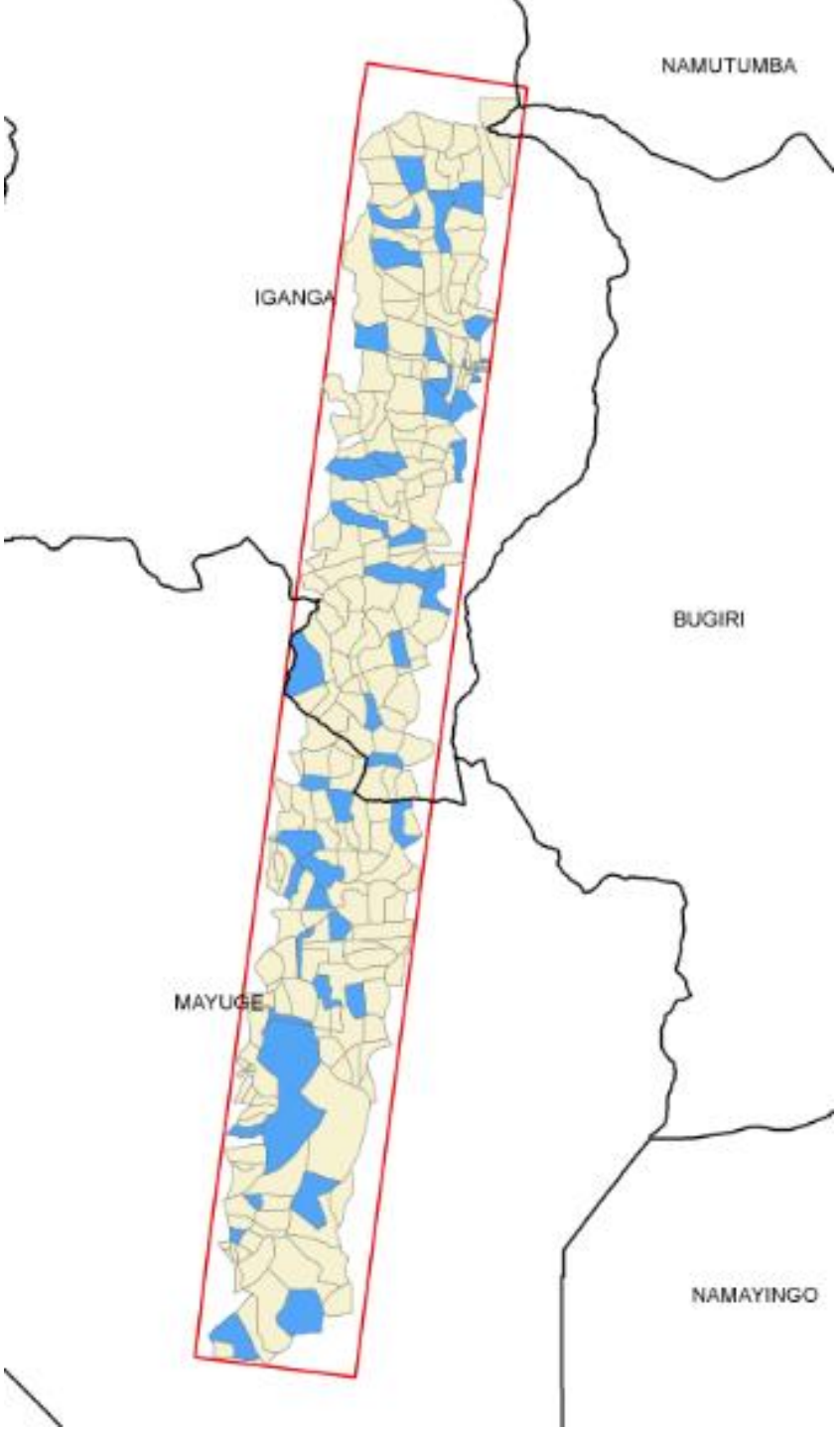
MAPS Sample – EAs

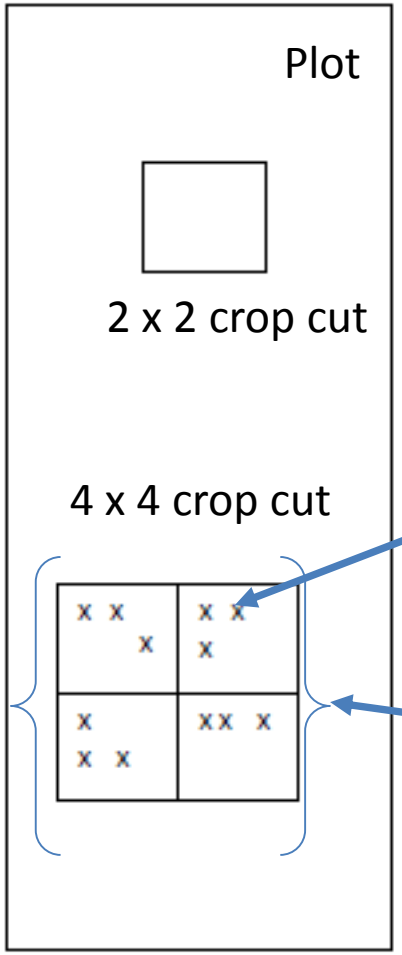
75 EAs total

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)



Sampling



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
ical Experiment on Measuring Maize
tivity, Variety and Soil Fertility

THE WORLD BANK

orld Bank – World Agroforestry Centre – FAO SPIA

ENUMERATOR MANUAL

Post-Planting – Crop-Cutting

April 2015

DRAFT

Table of Contents

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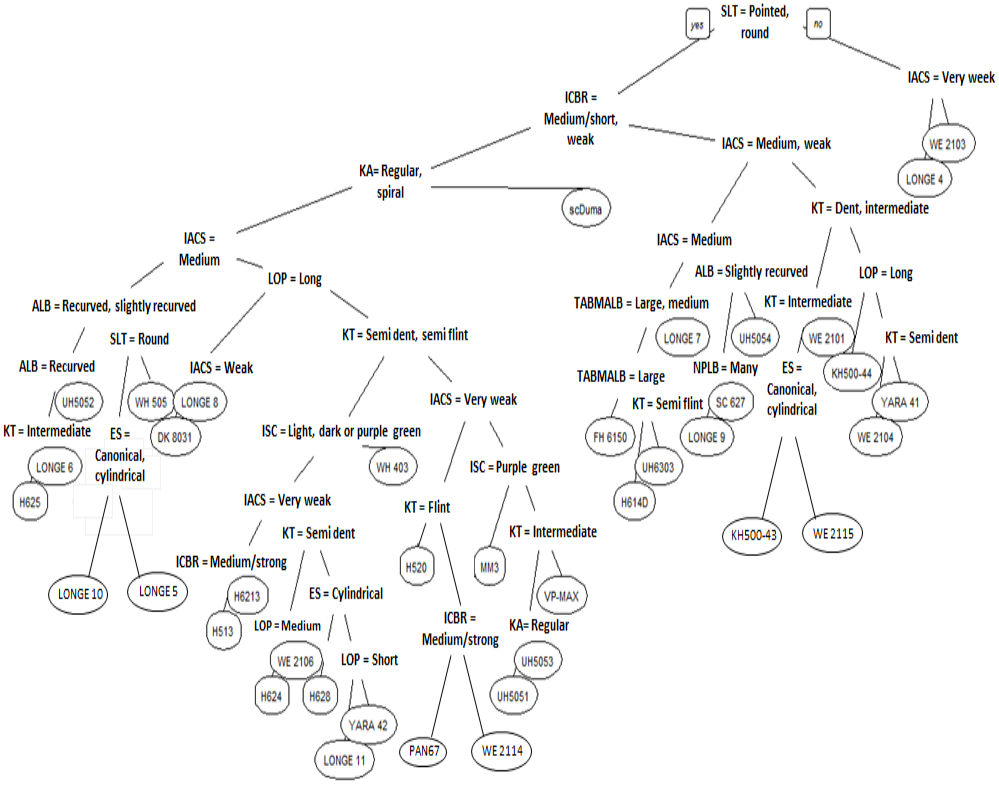
Recursive Partitioning & Classification Tree Analysis of Morphological Attributes of 38 Reference Library Samples

- 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 farmer responses on morphological attributes



LSMS
Living Standards Measurement Study

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	
	Freq.	*%*	*Freq.*	*%*	*Freq.*	*%*
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	

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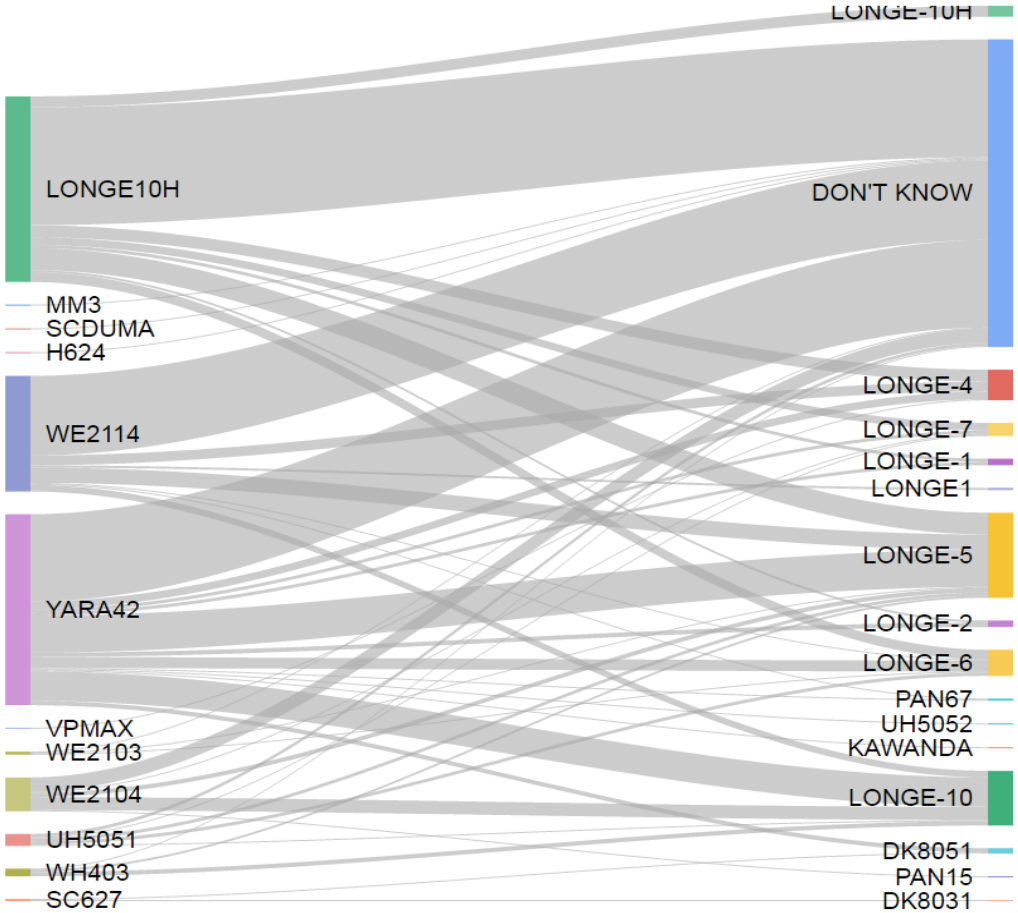
Results

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%

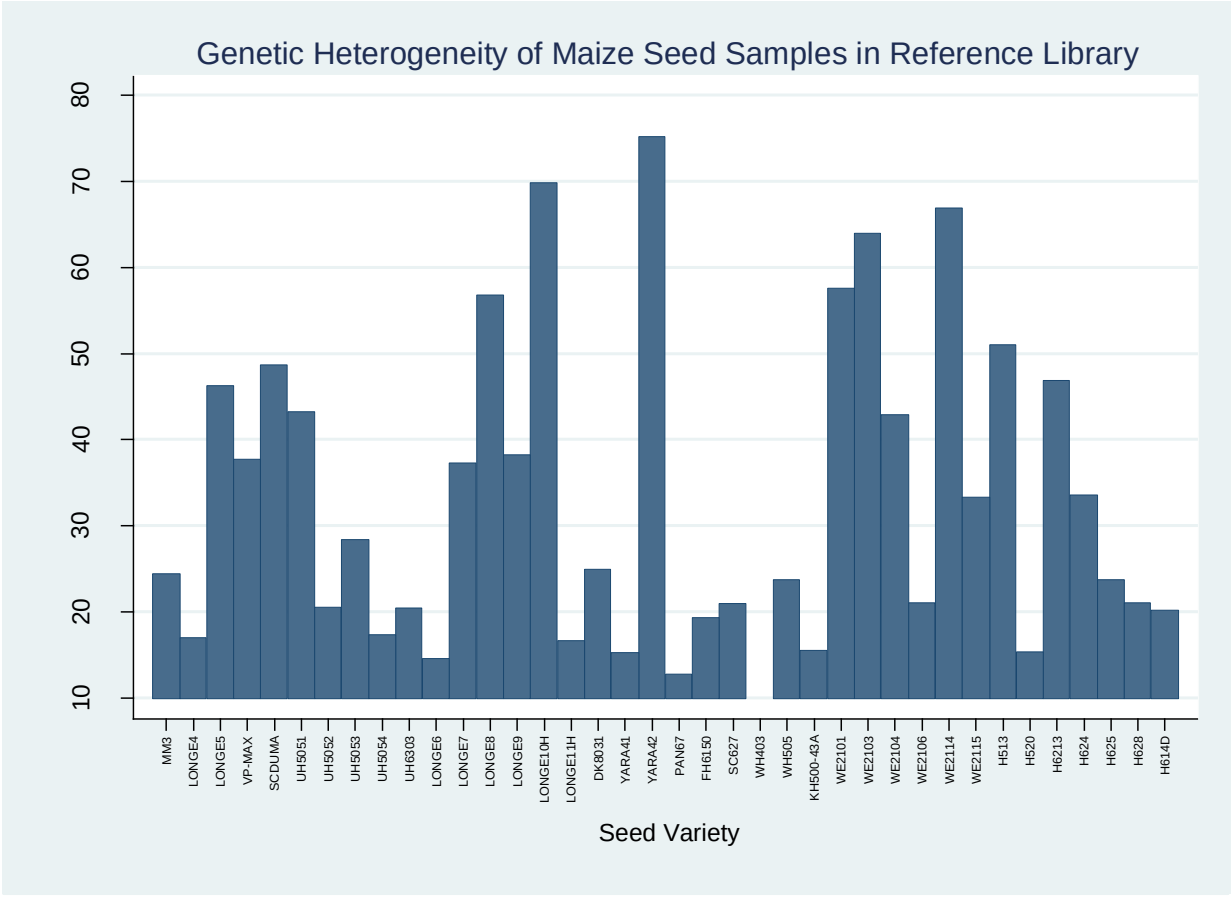
Phenotypic protocol doesn't work

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%

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