

Supplementary Table S1. Regional maize genotypes and local cultivars evaluated across greenbelt and ironstone plateau zones over three years (2013-2015) in South Sudan

Entry	Germplasm	Category	Source	Entry	Genotype	Category	Source
E1	Check 1 (Local cultivar)	OPV	Farmer	E25	SC627	Hybrid	Seed CO. Ltd
E2	Check 2 (Longe5)	OPV	NaCRRI (Uganda)	E26	SC533	Hybrid	Seed CO. Ltd
E3	KDV1	OPV	KARI (Kenya)	E27	05C362	Hybrid	Seed CO. Ltd
E4	KDV4	OPV	KARI (Kenya)	E28	06C1400	Hybrid	Seed CO. Ltd
E5	SUD-KATEH2012-01	Hybrid	Pannar (Kenya)	E29	SC529	Hybrid	Seed CO. Ltd
E6	SUD-KATEH2012-02	Hybrid	Pannar (Kenya)	E30	SC719	Hybrid	Seed CO. Ltd
E7	SUD-KATEH2012-03	Hybrid	Pannar (Kenya)	E31	Longe 6H	Hybrid	NaCRRI (Uganda)
E8	SUD-KATEH2012-04	Hybrid	KARI (Kenya)	E32	Longe 7H	Hybrid	NaCRRI (Uganda)
E9	SUD-KATEH2012-05	Hybrid	KARI (Kenya)	E33	Longe 10	Hybrid	NaCRRI (Uganda)
E10	SUD-KATEH2012-06	Hybrid	KARI (Kenya)	E34	Longe 11	Hybrid	NaCRRI (Uganda)
E11	SUD-KATEH2012-07	Hybrid	KARI (Kenya)	E35	Pannar 67	Hybrid	Pannar (Kenya)
E12	SUD-KATEH2012-08	Hybrid	KARI (Kenya)	E36	KH500-21A	Hybrid	KARI (Kenya)
E13	SUD-KATEH2012-09	Hybrid	KARI (Kenya)	E37	KH500-22A	Hybrid	KARI (Kenya)
E14	SUD-KATEH2012-10	Hybrid	KARI (Kenya)	E38	KH500-31A	Hybrid	KARI (Kenya)
E15	MU03-123	Hybrid	KARI (Kenya)	E39	KH500-32A	Hybrid	KARI (Kenya)
E16	MU03-137	Hybrid	KARI (Kenya)	E40	KH500-33A	Hybrid	KARI (Kenya)
E17	MU06-024	Hybrid	KARI (Kenya)	E41	KH500-34A	Hybrid	KARI (Kenya)
E18	MU07-014	Hybrid	KARI (Kenya)	E42	KH500-35A	Hybrid	KARI (Kenya)
E19	MU08-006	Hybrid	KARI (Kenya)	E43	KH500-43A	Hybrid	KARI (Kenya)
E20	MU08-024	Hybrid	KARI (Kenya)	E44	KH500-44A	Hybrid	KARI (Kenya)
E21	ZM521	OPV	Seed CO. Ltd (Zimbabwe)	E45	KH500-45A	Hybrid	KARI (Kenya)
E22	ZM421	OPV	Seed CO. Ltd (Zimbabwe)	E46	KH500-46A	Hybrid	KARI (Kenya)
E23	SC0923	Hybrid	Seed CO. Ltd (Zimbabwe)	E47	KH500-47A	Hybrid	KARI (Kenya)
E24	SC403	Hybrid	Seed CO. Ltd (Zimbabwe)	E48	KH500-48A	Hybrid	KARI (Kenya)

Supplementary Table S2. Agronomic traits and major diseases recorded in multilocation trials in greenbelt and ironstone plateau zones of South Sudan during 2013 - 2015 cropping seasons.

Trait recorded	Description
Anthesis date (AD)	Number of days after planting when 50 % of the plants per plot shed pollen.
Silking date (SD)	Number of days after planting when 50 % of the plants per plot show pollen.
ASI	Anthesis silking interval (in day) computed as the difference between anthesis and silking dates.
Plant height (PH)	Measured (cm) from the base of a plant to the insertion of the first tassel branch of the same plant.
Ear height (EH)	Measured (cm) from the base of a plant to the insertion of the top ear of the same plant.
Plant aspect (PA)	Scored at scale of 1-5 where 1= plants with uniform plant and ear heights, 5=non-uniform
Ear aspect (EA)	Scored at scale of 1-5 where 1= large, clean and uniform cobs, 5=small and poor cobs.
No. plant harvested (NPH)	Taken as number of plants harvested per plot excluding 1 plant from each end of a row.
Root lodging (SL)	Measured as % of fallen plants before harvest.
No. ear harvested (NEH)	Total number of ears per plot counted after harvest.
Number of ears (NE)	No. of ears (with at least 1 developed grain) per plot divided by number of harvested plants per plot.
Field weight (FW)	Weight (kg) of total number of ears per plot.
Moist. Cont. (MC)	Measured as total moisture available in the grain.
Grain yield (GY)	Total grain weight (t/ha) measured per plot.
Husk cover (HC)	Number of ear with open tip recorded per plot
<i>Turcicum</i> leaf blight (TLB)	Measured in scale of 1-5 where 1=leaves with no symptom and 5=all leaves affected
Maize streak virus (MSV)	Measured in scale of 1-5 where 1=clean l with no symptom and 5=all leaves affected
Gray leaf spot (GLS)	Measured in scale of 1-5 where 1=clean with no symptom and 5=all leaves affected
Stem borer (STB)	No. of ears per plot showing rotten grain(s)

Supplementary Table S3. Complete format for analysis of variance (ANOVA) and genotypic components combined across locations and seasons. Genotypes are fixed, locations, years and replications are random effects.

Source of variation	Df	Mean Square	Expectations of Mean Squares
Location (e)	(e-1)	M9	$\sigma^2_\epsilon + g\sigma^2_{rey} + r\sigma^2_{gey} + rg\sigma^2_{ey} + ry\sigma^2_{ge} + rgy\sigma^2_\epsilon$
Year (y)	(y-1)	M8	$\sigma^2_\epsilon + g\sigma^2_{rey} + r\sigma^2_{gey} + rg\sigma^2_{ey} + re\sigma^2_{gy} + rgl\sigma^2_y$
Location x Year	(e-1)(y-1)	M7	$\sigma^2_\epsilon + g\sigma^2_{rey} + r\sigma^2_{gey} + rg\sigma^2_{ey}$
Replication within location	(r-1)e	M6	$\sigma^2_\epsilon + g\sigma^2_{rey}$
Genotype (g)	(g-1)	M5	$\sigma^2_\epsilon + r\sigma^2_{gey} + re\sigma^2_{gy} + ry\sigma^2_{ge} + rey\sigma^2_g$
GxE	(g-1)(e-1)	M4	$\sigma^2_\epsilon + r\sigma^2_{gey} + ry\sigma^2_{ge}$
GxY	(y-1)(g-1)	M3	$\sigma^2_\epsilon + r\sigma^2_{gey} + re\sigma^2_{gy}$
GxLxY	y(g-1)(e-1)	M2	$\sigma^2_\epsilon + r\sigma^2_{gey}$
Error (ε)	ye(g-1)(r-1)	M1	$\sigma^2_\epsilon$
Total	(gery- 1)		
$\sigma^2_g$		=	(M4 - M3)/rey
$\sigma^2_{ge}$		=	(M3 - M2)/ry
$\sigma^2_{gey}$		=	(M2 - M1)/r
$\sigma^2_E$		=	M1
H <sup>2</sup> (Broad-sense heritability)		=	$\sigma^2_g/(\sigma^2_g + \sigma^2_{gey}/er + \sigma^2_\epsilon/re)$
h <sup>2</sup> (Narrow-sense heritability)		=	$\sigma^2_g/[\sigma^2_g + \sigma^2_{gey} + \sigma^2_\epsilon]$
SE $\sigma^2_g$		=	$[2/C^2 \{ \sum (MS_i^2)/(Df_i + 2) \}]^{1/2}$
SEH <sup>2</sup>		=	$SE\sigma^2_g/[(\sigma^2_g) + (\sigma^2_{gey})/er + (\sigma^2_\epsilon)/re]$
SEh <sup>2</sup>		=	$SE\sigma^2_g/[\sigma^2_g + \sigma^2_{gey} + \sigma^2_\epsilon]$

Supplementary Table S4. Format for AMMI analysis across environments

Source of variation	Df	SS	MS	Total variation (%)	GxE explained (%)
Treatment	(ge-1)	SSTrt	M9		
Replication	(r-1)	SSr	M8	(SSr/SSTrt)*100	....
Genotype	(g-1)	SSg	M7	(SSg/SSTrt)*100	....
Environment	(e-1)	SSe	M6	(SSe/SSTrt)*100	....
GxE interaction	(g-1)(e-1)	SSge	M5	(SSge/SSTrt)*100	....
IPCA1	(g+e-1-(2x1))	*SSIPCA1	M4	....	(SSIPCA1/SSge)*100
IPCA2	(g+e-1-(2x2))	*SSIPCA2	M3	....	(SSIPCA2/SSge)*100
Residual	(Dfge - (DfIPCA1+DfIPCA2))	SSresid.	M2	....	(SSresid./SSge)*100
Pooled error	(r-1)(ge-1)	SSError	M1		
Total	(ger-1)	SSTotal			

\*  $SS_{IPCA} = \lambda =$  the eigenvalue value of the IPCA axis