

GENOMIC IN MAIZE BREEDING (CIMMYT CASE)

- Genomic can be implemented as
 - RAPID CYCLE SELECTION
(Additive effects)
 - PREDICTION IN SPARSE TESTING
(Genetic effects=Additive+Dominance+
Epistasis)

GENOMIC IN MAIZE BREEDING IN CIMMYT

Where to applied GS in maize?

→ **RAPID CYCLING -- Biparental populations at the F2**

maximum LD, low marker density and relatively small population size because this occurs at the cross

F2 x tester. USE ALL MARKERS

THIS WORKS !! (Massman et al., 2012; Beyene et al. 2015)

→ **RAPID CYCLING – Multiparental (synthetics) populations**

Large training population, high marker density

DOES THIS WORK? WE DO NOT KNOW

GENOMIC IN MAIZE BREEDING IN CIMMYT

- MAIZE RAPID CYCLE GENOMIC SELECTION IN DROUGHT ENVIRONEMNTS
 - 8 bi-parental populations 3-4 DROUGHT sites

- MAIZE RAPID CYCLE GENOMIC SELECTION
 - Multi-parental populations (synthetics)

Genetic Gains in Grain Yield Through Genomic Selection in Eight Bi-parental Maize Populations under Drought Stress

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ABSTRACT

Genomic selection incorporates all the available marker information into a model to predict genetic values of breeding progenies for selection. The objective of this study was to estimate genetic gains in grain yield from genomic selection (GS) in eight bi-parental maize populations under managed drought stress environments. In each population, 148 to 300 $F_{2:3}$ (C_0) progenies were derived and crossed to a single-cross tester from a complementary heterotic group. The resulting testcrosses of each population were evaluated under two to four managed drought stress and three to four well-watered conditions in different locations and genotyped with 191 to 286 single nucleotide polymorphism (SNP) markers. The top 10% families were selected from C_0 using a phenotypic selection index and were intermated to form C_1 . Selections both at C_1 and C_2 were based on genomic estimated breeding values (GEBVs). The best lines from C_0 were also advanced using a pedigree selection scheme. For genetic gain studies, a total of 55 entries representing the eight populations were crossed to a single-cross tester, and evaluated in four managed drought stress environments. Each population was represented by bulk seed containing equal amounts of seed of C_0 , C_1 , C_2 , C_3 , parents, F_1 s, and lines developed via pedigree selection. Five commercial checks were included for comparison. The average gain from genomic selection per cycle across eight populations was 0.086 Mg ha^{-1} . The average grain yield of C_3 -derived hybrids was significantly higher than that of hybrids derived from C_0 . Hybrids derived from C_3 produced 7.3% (0.176 Mg ha^{-1}) higher grain yield than those developed through the conventional pedigree breeding method. The study demonstrated that genomic selection is more effective than pedigree-based conventional phenotypic selection for increasing genetic gains in grain yield under drought stress in tropical maize.

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Abbreviations: ASI, anthesis-silking interval; DTMA, Drought Tolerant Maize for Africa project; GEBVs, genomic estimated breeding values; GS, genomic selection; MABC, marker-assisted backcrossing; MARS, marker-assisted recurrent selection; QTL, quantitative trait loci; SSA, sub-Saharan Africa; WEMA, Water Efficient Maize for Africa project.

MAIZE is a staple food in many countries of sub-Saharan Africa (SSA) and is commonly grown by millions of resource-poor smallholder farmers. In SSA, maize covers more than 25 million hectares that produce 38 million metric tons of grain (Shiferaw et al., 2011). The average maize yield in SSA is 1.8 t per hectare (Smale et al., 2011), which is very low compared to that of other maize-growing regions in the developing world. Several factors, including high incidence of abiotic and biotic stresses, high irrigation costs, and inability of farmers to access and purchase good

Published in *Crop Sci.* 55:154–163 (2015).

doi: 10.2135/cropsci2014.07.0460

Freely available online through the author-supported open-access option.

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Brief description of results on genomic selection of CIMMYT maize in Africa (Yoseph Beyene et al.)

Eight populations each with 200 F_2 x tester individuals genotyped with 200 SNPs and evaluated in DROUGHT.

- 200 ($F_2:3$) C_0 were phenotyped and genotyped with 200 SNPs. Top 10% of the C_0 were selected and intermated to form C_1
- Selections both at C_1 and C_2 were based on GEBV.
- Based lines in C_0 were advance using pedigree selection scheme.
- To evaluate genetic gains a total of 55 entries representing the eight populations were crossed to a single tester and evaluated in four DROUGHT environments.
- Each population was represented by bulk seed containing equal amounts of seed of C_0 C_1 C_2 C_3 parents F1 and lines developed via pedigree selection.
- Five commercial checks included.

RESULTS RAPID CYCLE

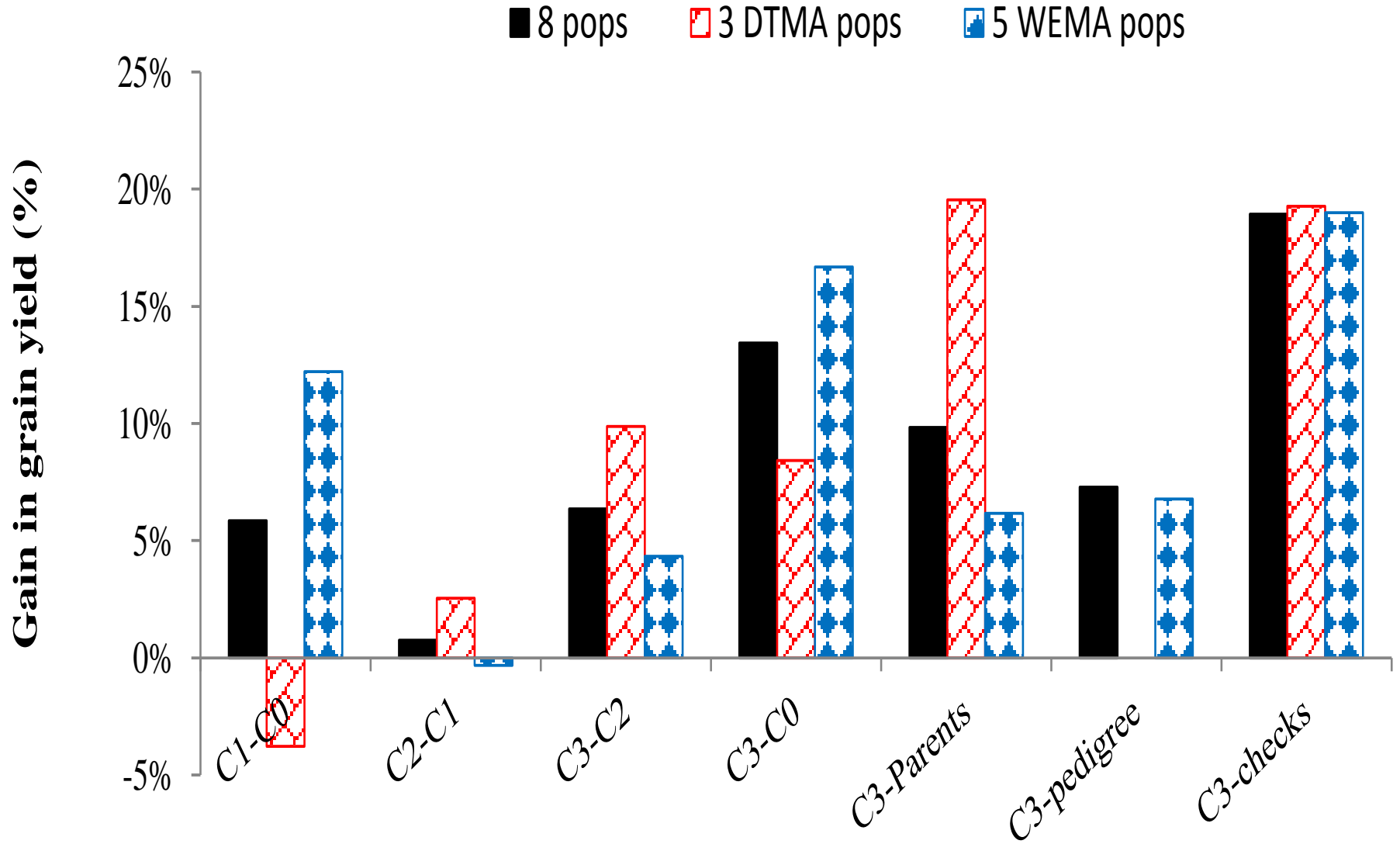
- Average gain from genomic selection per cycle across the eight populations was of **0.089 ton/ha.**
- The average grain yield of C_3 -derived hybrids was significantly higher than that of hybrids derived from C_0
- Hybrids derived from C_3 produced 7.3% (0.176 ton/ha) higher grain yield than those developed through the conventional pedigree breeding method

Table 1. Mean grain yield performance (Mg ha^{-1}) at cycle 0 (C_0), cycle 1 (C_1), cycle 2 (C_2), cycle 3 (C_3), F_1 , pedigree-selected lines and commercial checks for the **eight** bi-parental populations evaluated in four managed **drought stress environments**, and average grain yield gains per selection cycle including and excluding C_0 .

Entries	Across eight populations			Three DTMA populations			Five WEMA populations		
	GY (Mg ha^{-1})	AD (days)	PH (cm)	GY (Mg ha^{-1})	AD (days)	PH (cm)	GY (Mg ha^{-1})	AD (days)	PH (cm)
C_0	2.286	63.910	179.900	2.410	63.670	189.160	2.212	64.060	174.300
C_1	2.420	64.080	181.900	2.319	63.940	188.320	2.482	64.160	178.100
C_2	2.438	64.410	184.600	2.378	64.830	193.340	2.474	64.160	179.400
C_3	2.593	64.100	182.200	2.613	64.720	193.220	2.581	63.730	175.600
Pedigree	2.417	64.400	181.700	-	-	-	2.417	64.400	181.700
F_1	2.394	63.930	175.600	-	-	-	2.394	63.930	175.600
Parents	2.361	64.000	178.400	2.186	64.130	183.030	2.431	63.950	176.600
Checks	2.180	64.310	180.100	2.191	63.930	181.030	2.169	64.700	179.300
$\text{LSD}_{0.05}$	0.219	0.700	5.260	0.342	1.130	6.900	0.257	0.850	6.320
Average gain per cycle (C_0, C_1, C_2, C_3)	0.094	0.090	0.960	0.069	0.404	1.720	0.110	-0.105	0.520
Average gain per cycle (C_1, C_2, C_3)	0.086	0.010	0.150	0.151	0.390	2.450	0.050	-0.215	-1.250

Table 1. Mean performance for grain yield (Mg ha⁻¹), anthesis date (days), and plant height (cm) at cycle 0 (C₀), cycle 1 (C₁), cycle 2 (C₂), cycle 3 (C₃), hybrid (F₁), and pedigree-selected lines for all eight bi-parental populations evaluated in four managed drought stress environments, and average grain yield, anthesis days and plant height per selection cycle including and excluding C₀.

	CML440/ CML504	CML441 /CML444	CML444/ Malawi	6x1008	6x1016	6x1017	6x1020	6x1028
-----Grain yield (Mg/ha)-----								
Cycle0	2.171	2.517	2.540	2.283	2.261	2.532	2.141	1.844
Cycle1	2.592	2.237	2.129	2.697	2.583	2.384	2.317	2.429
Cycle2	2.185	2.333	2.562	2.471	2.573	2.965	2.263	2.098
Cycle3	2.622	2.387	2.883	2.754	2.918	2.375	2.734	2.127
F ₁	-	-	-	2.28	2.957	2.120	2.436	2.177
Parents	2.133	2.248	2.181	2.635	2.464	2.446	2.4	2.214
Pedigree	-	-	-	2.47	2.423	2.456	2.327	2.413
LSD _{0.05}	0.832	0.831	0.536	0.631	0.516	0.392	0.498	0.430
Average gain per cycle (C ₀ , C ₁ , C ₂ , C ₃)	0.095	-0.040	0.146	0.119	0.192	0.011	0.173	0.052
Average gain per cycle (C ₁ , C ₂ , C ₃)	0.015	0.048	0.377	0.029	0.168	-0.005	0.208	-0.150



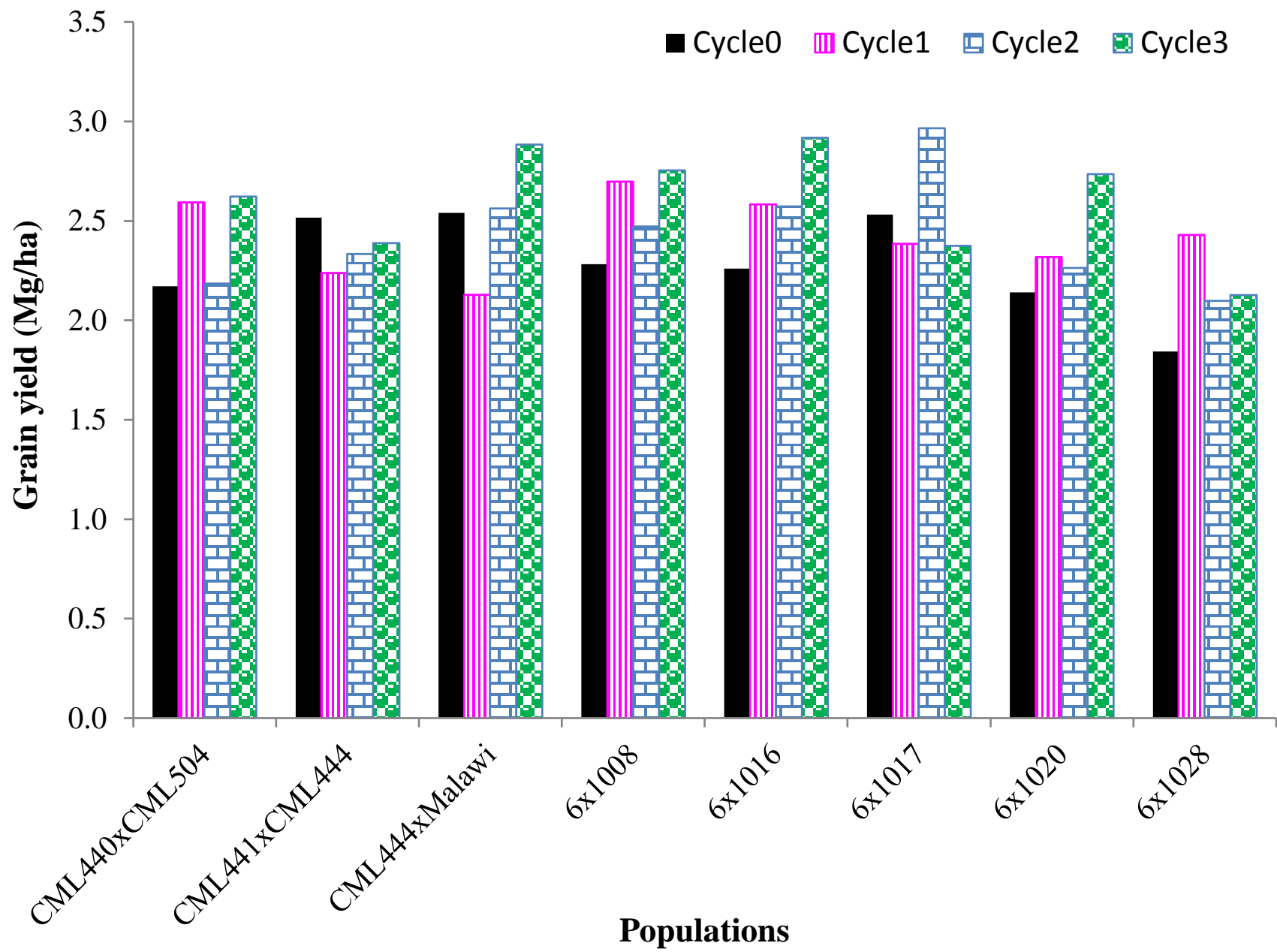
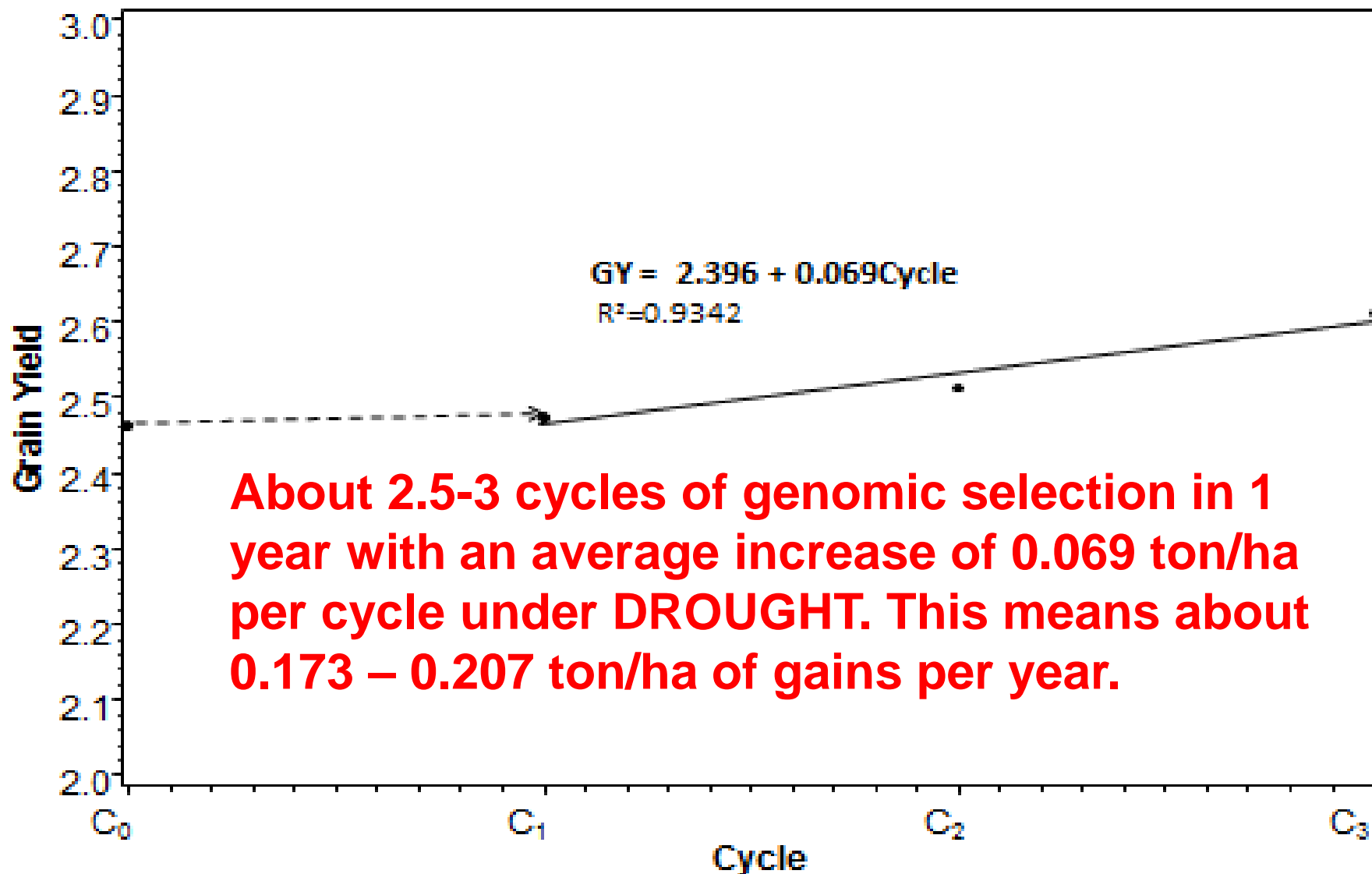


Fig. 2

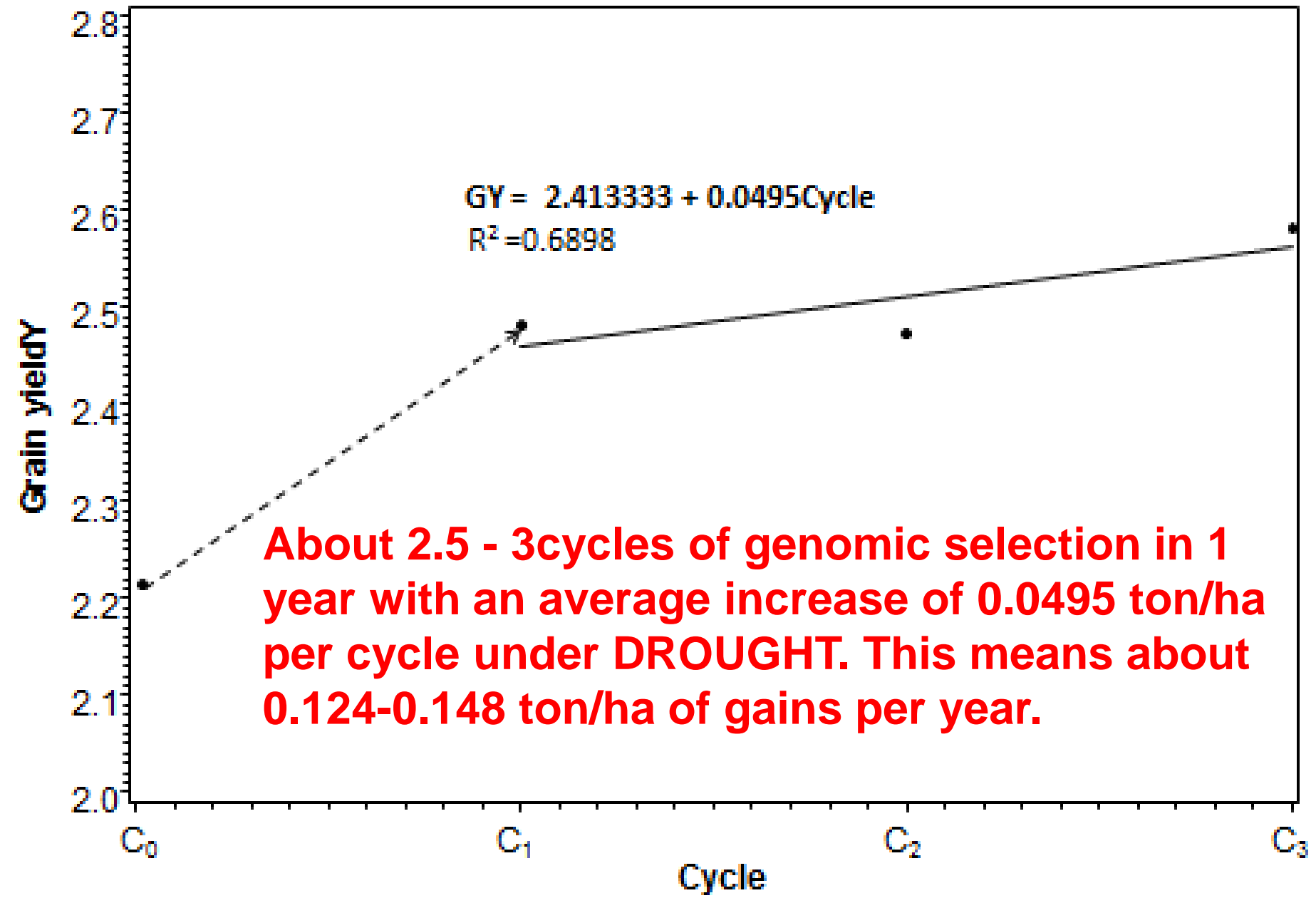
Drought DTMA Across Populations



About 2.5-3 cycles of genomic selection in 1 year with an average increase of 0.069 ton/ha per cycle under DROUGHT. This means about 0.173 – 0.207 ton/ha of gains per year.

Fig. 3

Drought WEMA across populations



DISCUSSION -- RESULTS RAPID CYCLE

- In SSA, preliminary estimates of yield gains from conventional selection revealed 0.039 to 0.080 ton/ha/year under optimal conditions, but only 0.018 ton/ha/year under DROUGHT stress.
- A recent study using 67 hybrids developed at CIMMYT and released between 2000 and 2011 showed genetic gains of 0.032 and 0.109 ton/ha/year for grain yield under managed drought and well-watered conditions, respectively

DISCUSSION RESULTS RAPID CYCLE

- Therefore, the average gain observed under DROUGHT in our study using GS was two- to - four folds higher than what has been reported from conventional phenotypic selection under drought stress in SSA
- In the the United States, yield gains during the past 70 years have been positive and linear, varying from 0.065 to 0.075 ton/ha/year which is comparable to the overall genetic gain in our studies

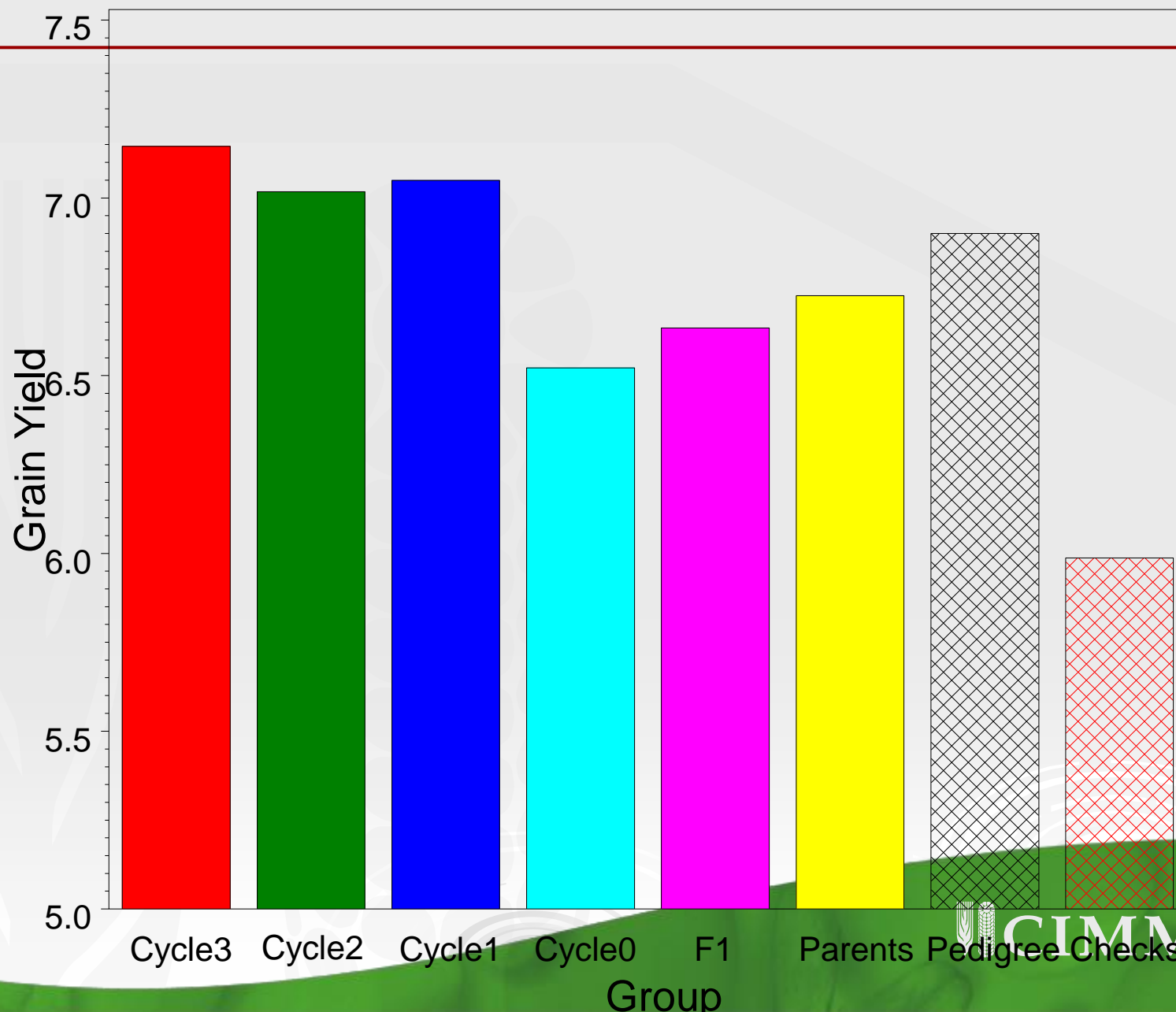
MARKER ASSISTED SELECTION IN 10 BI-PARENTAL POPULATIONS

- Marker-assisted recurrent selection (MARS) uses a subset of molecular markers that are significantly associated with target traits of interest to predict the breeding value of individual plants, followed by rapid cycle recombination and selfing.
- 148-184 $F_{2:3}$ (defined as C_0) progenies were derived, crossed with a single cross tester, and evaluated under water-stressed (WS) and well-watered (WW) environments. The C_0 populations were genotyped with 190-225 single nucleotide polymorphism (SNPs) markers

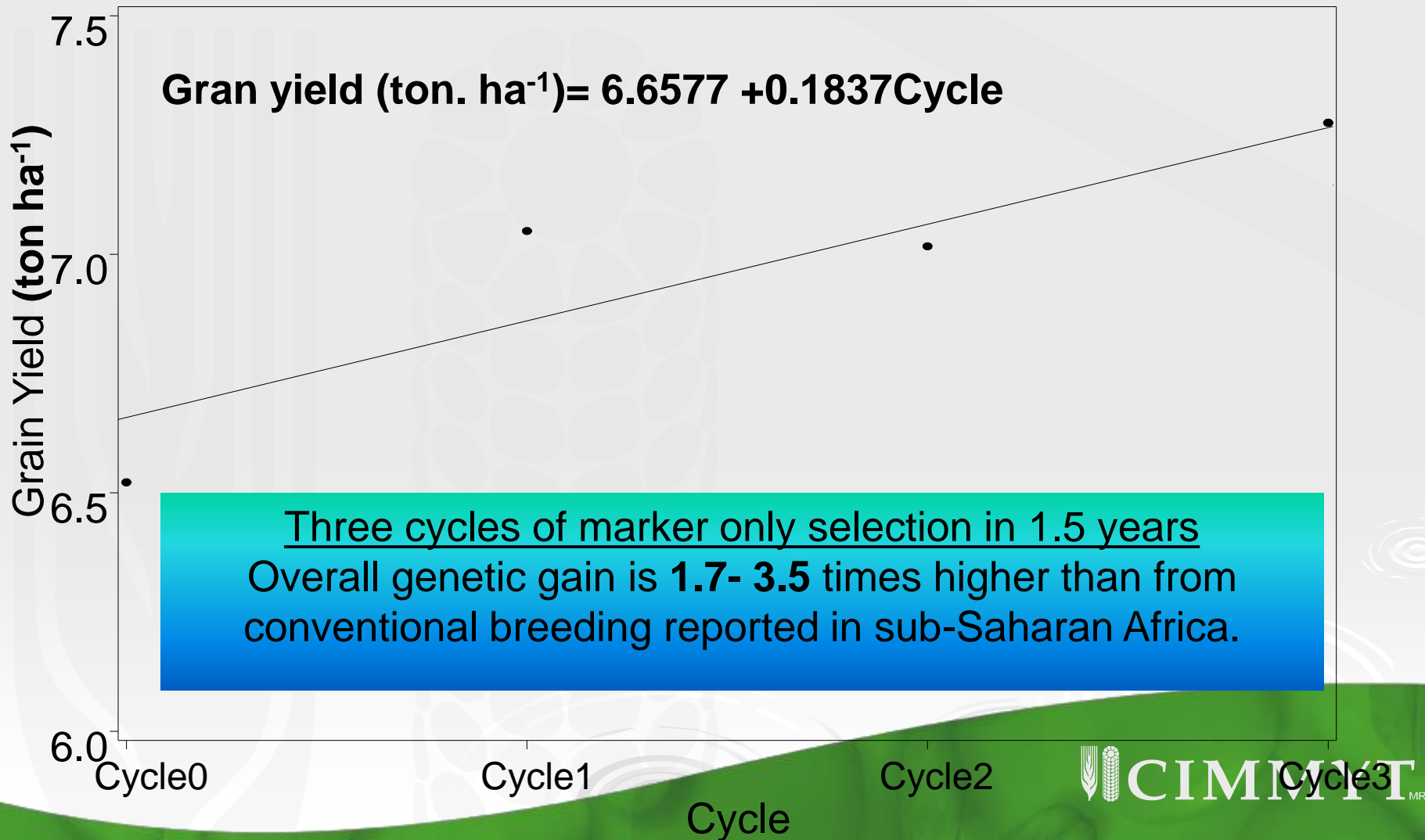
Table. Means of eight groups of entries (C_0 , C_1 , C_1S_1 , C_1S_2 , F_1 , founder parents, pedigree and commercial checks) across 10 MARS populations evaluated under four water-stressed (WS) and four well-watered (WW) environments in sub Saharan Africa for grain yield (GY, Mg ha⁻¹), anthesis date (AD, days), anthesis silking interval (ASI) and plant height (PH, cm). For each trait, the highest values for each environment are underscored. Least Significant Differences at the 0.05 probability level ($LSD_{0.05}$).

Group	Water-stressed				Well-watered			
	GY	AD	PH	ASI	GY	AD	PH	ASI
C1S2	<u>2.68</u>	63.25	<u>186.60</u>	1.03	<u>7.15</u>	67.27	240.78	1.13
C1S1	2.52	64.02	184.75	0.81	7.02	67.70	242.62	0.83
C ₁	2.58	63.93	184.54	0.93	7.05	67.11	<u>245.23</u>	0.88
C ₀	2.51	62.73	179.23	1.30	6.52	66.72	235.00	1.39
F ₁	2.54	62.83	177.66	1.25	6.63	66.43	233.58	1.43
Parents	2.47	62.98	175.38	1.30	6.73	66.32	234.14	0.95
Pedigree	2.53	63.60	181.32	0.97	6.90	<u>67.55</u>	238.40	1.18
Checks	1.94	<u>64.23</u>	179.30	<u>1.93</u>	5.99	67.28	244.62	<u>2.13</u>
$LSD_{0.05}$	0.17	0.83	5.03	0.45	0.33	0.83	4.89	0.43

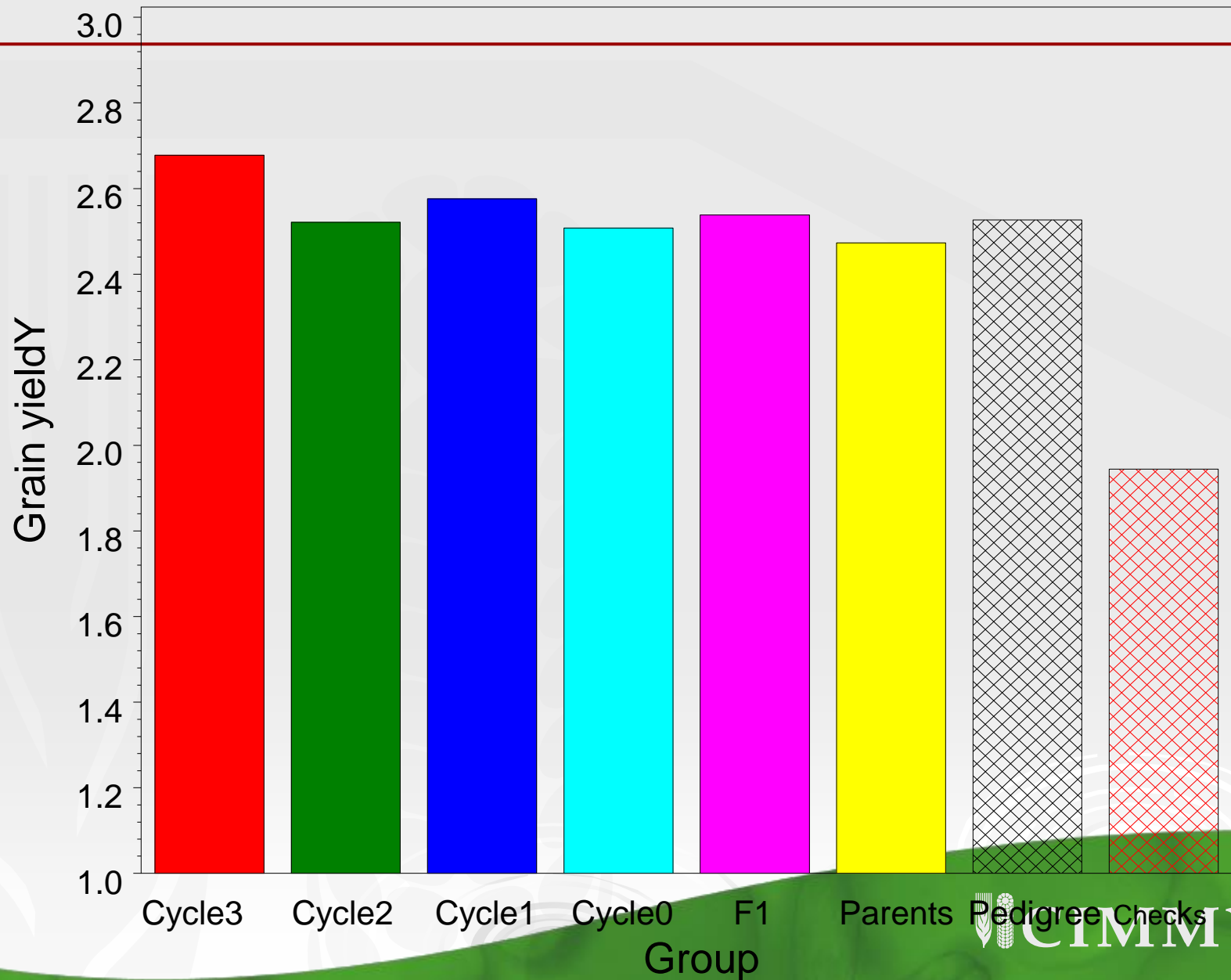
Across 10 biparental populations – OPTIMUM ENVIRONMENTS



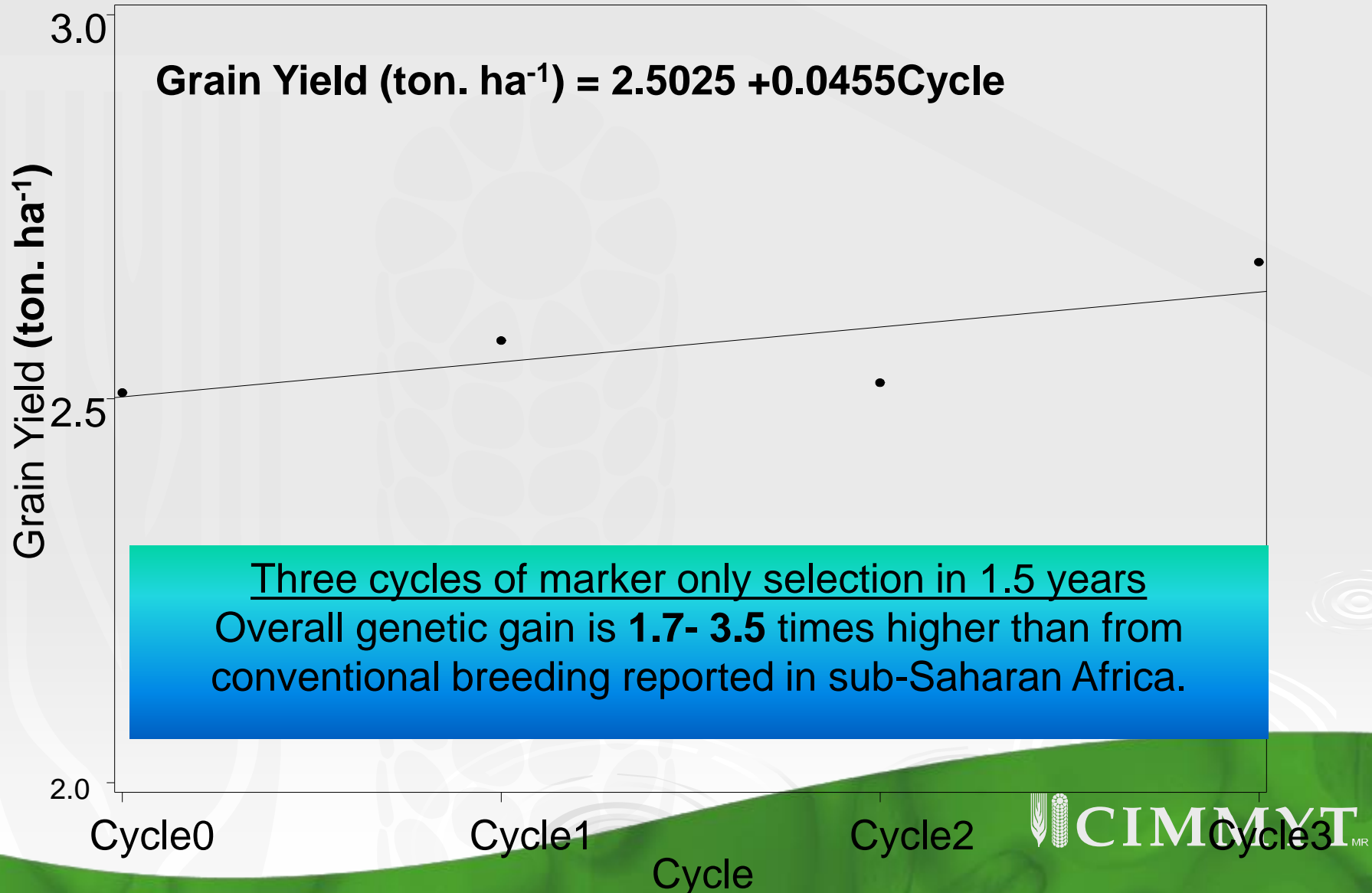
Across 10 biparental populations – OPTIMUM ENVIRONMENTS



Across 10 biparental populations – DROUGHT ENVIRONMENTS



Across 10 biparental populations – OPTIMUM ENVIRONMENTS



<http://genomics.cimmyt.org>

Thanks!!

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