

Why Genomic Selection?

Expected genetic gain per unit time
Response to selection

$$G_t = \frac{i r \sigma_a}{T}$$

Intensity

Accuracy

$\sqrt{\text{genetic variance}}$

Time per cycle

Genomic selection

Reference population



Selection candidates



PHENOTYPE AND MARKERS

MARKERS

PREDICTION EQUATION

Genomic Estimate Breeding Value $Y=f(x)=w_1x_1+w_2x_2+....+w_px_p$



Selected breeders

Meuwissen, Hayes, and Goddard (2001)

Bernardo and Yu (2007)

marker effect

$y_i = \mu + \text{Sum}(x_{ij}\beta_j) + \varepsilon_i$

Additive effect of SNPs
-- **linearity** --

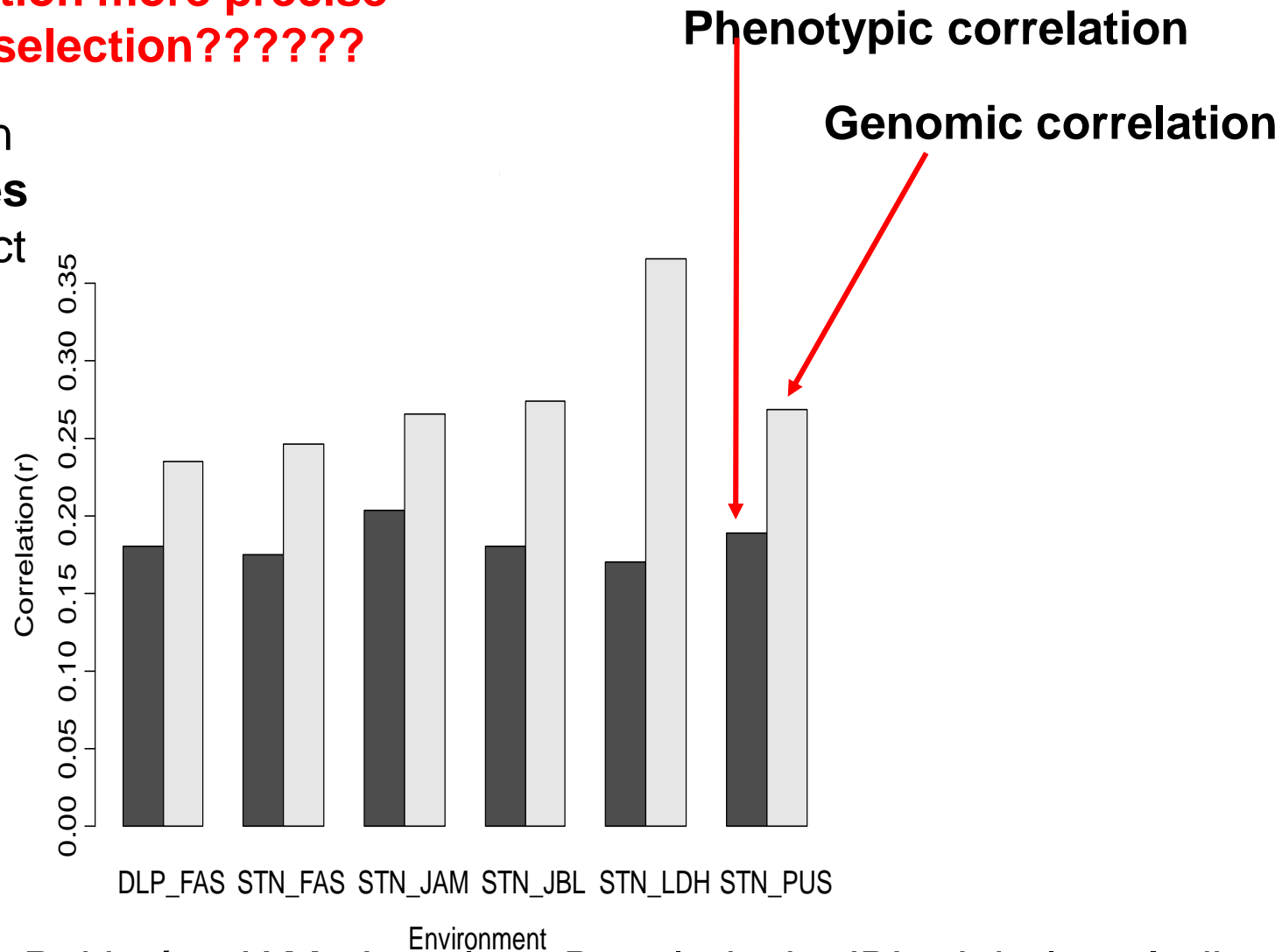
Allele, chromosome, haplotype, etc.

$Y = G + e$

GENOMIC-ENABLED PREDICTION

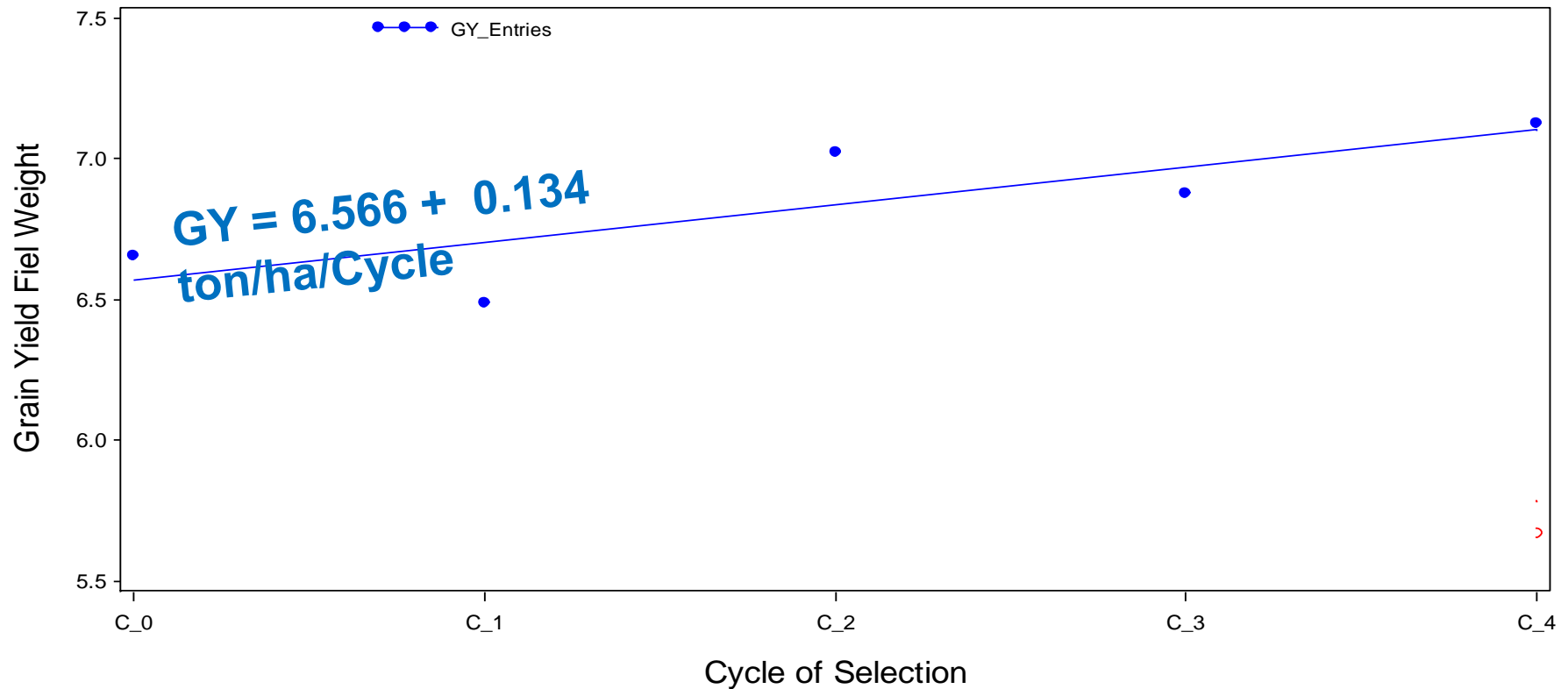
Is Genomic selection more precise than phenotypic selection?????

Use information on 60,000 **wheat lines** in Mexico to predict GY of 500 lines in South Asia



FAS=Faisalabad, Pakistan; JAM=Jamalpur, Bangladesh; JBL=Jabalpur, India; LDH=Ludhiana, India, OBR=Obregon, Mexico; PUS=Pusa, India.
Standard management conditions (STN), and delayed planting conditions (DLP)

Rapid cycling gains in MAIZE grain yield using GS in multi-parental populations (Zhang et al, 2017)



One year = 2.5 cycles

Rapid cycling gains in grain yield using GS in multi-parental populations

Estimate genetic gains (t/ha) across three locations in Mexico

Cycle	Entry	GROUPING
C4	8.326	A
C3	8.107	B
C0	7.759	C
C1	7.559	D
C2	7.184	E

Genomic selection for more than just grain yield

Pay for genotyping once- use the data for prediction or to improve BLUP estimation for many other traits



Session 5: Genomic selection for wheat quality improvement

- Genomic selection models for predicting end-use quality traits in CIMMYT spring bread wheat. *Diego Jarquin*, UNL, USA
- Genome-wide association and prediction of grain and semolina quality traits in durum wheat breeding populations. *Xuehui Li*, NDSU, USA.
- Improving genomic-enabled prediction accuracy by modeling the genotype-by-environment interaction for quality traits in Kansas wheat. *Reka Howard*, UNL, USA.
- Accelerating wheat breeding for end-use quality with multi-trait genomic predictions incorporating near infrared and nuclear magnetic resonance-derived phenotypes. *Ben Hayes*, AUSTRALIA