

Earliness improvement through molecular backcross breeding approach in corn

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Abstract

Corn (*Zea mays* L. ssp. *Mays*) is one of the most economically important monocot food crops worldwide. Development of high yielding varieties with desirable traits and allele combinations in a short time span is an important breeding objective in many programs. Trait introgression through backcross breeding has been a common method to incorporate one or a few genes from a donor into adapted varieties that are used in plant breeding for nearly a century, but it is time consuming. However, use of Marker Assisted Selection (MAS) expedites the recovery of more than 99 % recurrent parent percent (RPP) in just three backcross generations, indicating that use of molecular markers increases the efficiency of introgressing the trait of interest. To meet the increased demands of the growing market, corn acres have expanded into the northern Great Plains of the United States. These regions were previously planted with cool season cereal crops such as wheat and barley. Corn grown in these “non-traditional” areas faces a much cooler and shorter growing season than corn grown across the traditional US Corn Belt. Therefore, the need arises to develop early maturing corn hybrids and parent lines that will mature and yield in these cooler and shorter growing regions. Our goal is to introgress donor segments from early lines into high yielding elite lines through marker assisted backcross breeding. At Dow AgroSciences, we have made significant progress in converting a few late maturing lines by optimizing population size, collecting appropriate phenotypic parameters and making selections by comparing SNP marker and phenotypic data. This approach aids in recovering high percentage of the recurrent parental genome which is associated with yield components while retaining donor segments associated with earliness.

Introduction

- Corn is one of the core crops of Dow AgroSciences and economically the most important crop worldwide
- To expand our business in non-traditional corn growing areas and also to increase the number of hybrids in corn belt we develop hybrids that are adaptable to cooler climatic conditions
- Our approach to improve earliness is through marker assisted backcross breeding by introgressing segments of early maturing donors into late maturing and high yielding elite lines.

Simulation analyses to determine population size and earliness improvement

Three simulation studies differing in selection methods were conducted based on current information about the lengths of the ten chromosomes.

- Five major donor and 20 elite alleles were randomly placed in the genome with equal additive effects.
- Each study consisted of 3 backcross generations with 15 individual plants advanced at each generation.
- Results were collected and evaluated for 100 simulated experiments
- **Utilizing 48 or 96 plants for marker assisted selection in BC1 and 2 captures the most donor QTL (Table 1)**

	Phenotype only			Phenotype and Genotype*		
	Donor QTL	Elite QTL	Ave P(RPP>80%)	Donor QTL	Elite QTL	Ave P(RPP>80%)
BC1	4.2	7.27	7%	4.13	8.5	20%
BC2	3.53	11.7	73%	3.27	13.2	100%
BC3	3.07	14.2	100%	2.67	15.97	100%

* - Average of 15 selected progenies advanced to next generation; **Donor QTL**: The number of donor QTL captured in each generation out of 5; **Elite QTL**: The number of elite QTL captured in each generation out of 20

Table 1: Comparison between selections made phenotype only and phenotype and genotype simulations

Case Study

Inbred A is an elite DAS inbred line with good GCA maturity zone 6 (Recurrent Parent) (Table 2) as crossed with an early maturing Inbred Z (Donor). Table 2a & b indicates the % yield performance of inbred A with different cross combinations in 2008 and 2009.

Goal

- To develop Inbred A selections that will flower significantly earlier than the original inbred A
- Hybrids made from these selections must flower earlier, have lower harvest moisture, retain most of the yield, and be able to be grown one to two maturity zones further north in the Corn Belt than inbred A

A

Pedigree	H2O	Yld% Ck
Inbred B/Inbred A	22.1	102
Inbred C/Inbred A	23.3	105
Inbred D/Inbred A	20.6	103
Inbred E/Inbred A	18.6	107

B

Pedigree	H2O	Yld% Ck
Inbred F/ Inbred A	24	104
Inbred G/ Inbred A	24	103

H2O: Moisture content;
Yld% Ck: Yield % compared with check

Table 2a & b. Yield Data of inbred A in 2008 and 2009 with different crosses (Hybrid Testing) respectively in maturity zones 6 & 7

Project scheme and timeline

Summer	Crossing of parents	Advance best hybrid	Summer
Fall (WN)	F1 x RP (making BC1)	BC2S2; BC2S3 and Test cross	Fall
Winter	BC1 x RP (making BC2)	BC2 self (making BC2S1)	Summer
	Markers Phenotype	Markers Phenotype	

Figure 1. Project scheme and timeline of marker assisted backcross breeding

Results

- We ran molecular markers in backcross 1 and backcross 2 generations
- Table 3 indicates the experimental details and the results
- Our selections after marker analysis at BC2 flowers 5-8 days earlier than recurrent parent

Marker assisted backcross breeding

Generation	Pop. Size	Selections	RP (DF)	Donor (DF)	Trait range (DF)	# of markers	RPP	% GC
BC1	94	17	54	-	48-50	33	70-80	72.63
BC2	149	37	75	67	67-70	53	81-95	77.15

DF- Days to flowering; RPP- Recurrent Parent Percentage; GC- Genome coverage, BC- Backcross

Table 3. Screening of backcross populations using molecular markers

Pedigree	H2O	Yld% Ck
Hybrid Check 1	18.9	97
Hybrid Check 2	21	113
Core Genetic Check 1	19.8	105
Core Genetic Check 2	17.3	84
Core Genetic Check 3	17.3	84
Core Genetic Check 4	20.1	100
Core Genetic Check 5	19.2	101
Inbred A/Inbred Z=B=145-132/Tester 1	20.7	108
Inbred A/Inbred Z=B=145-140/Tester 1	20.6	107
Inbred A/Inbred Z=B=143-114/Tester 1	20.4	106
Inbred A/Inbred Z=B=143-119/Tester 2	19.6	104
Inbred A/Inbred Z=B=143-110/Tester 2	19.6	102
Inbred A/Inbred Z=B=059-15/Tester 2	19.9	102

H2O: Moisture content;
Yld% Ck: Yield % compared with check

Table 4. Yield data of converted Inbred A selections that are early with two testers in maturity zone 5

Conclusions

- Marker Assisted Introgression is an effective tool in earliness improvement
- We successfully developed Inbred A derivative that are adapted to earlier zone while maintaining its eliteness (Table 4)
- We optimized the appropriate population size that are cost-effective using simulation
- Correct phenotyping in the field is critical
- If markers are only going to be used twice with multigenic traits, their most efficient use is in the BC1 and BC2
- Selections are a balance between RPP and phenotype and try to keep multiple families alive