Creating Rapid Cycling Winter Wheat Genotypes

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Introduction

- Usually, breeding winter wheat only has two generations per year, however, a goal for plant breeding is to develop new cultivars as efficiently and speedily as possible (Lewis and Kernodle, 2009). To accelerate the breeding scheme for backcross breeding, 'Apogee', a very early flowering spring wheat which was developed for bioregenerative life support systems in space was crossed with Nebraska winter wheats to introgress early flowering genes into 'winter' wheat background.
- A previous research found that there are 4 dominant or partially dominant genes from vernalization pathway and photoperiod pathway that are *vrn-A1*, *VRN-B1*, *vrn-D3* and *PPD-D1* involved in early flowering in Apogee.
- The F_1 of Nebraska winter wheat crossed with spring wheat will be crossed back to Nebraska winter wheat parent for 4 or 5 generations to create rapid cycling genotypes with primarily Nebraska background genes and these rapid cycling genotypes will be used in backcross breeding for introgressing traits more rapidly than in traditional backcross scheme.
- For recovering the winter growth habit, the final backcross will be to the winter recurrent parent (e.g. Overland, Goodstreak, or NW07505), the BC_nF_1 selfed, and the BC_nF_2 will be planted in Nebraska in the fall, where only the winter growth habit segregants will survive and be harvested.

Objective

- To add early flowering genes that remove the vernalization requirement and photoperiod sensitivity of Nebraska winter wheat.
- to create a rapid cycling, spring growth habit 'winter' background for accelerated backcrossing cycles.

Figure 1. Rapid cycling winter wheat scheme.

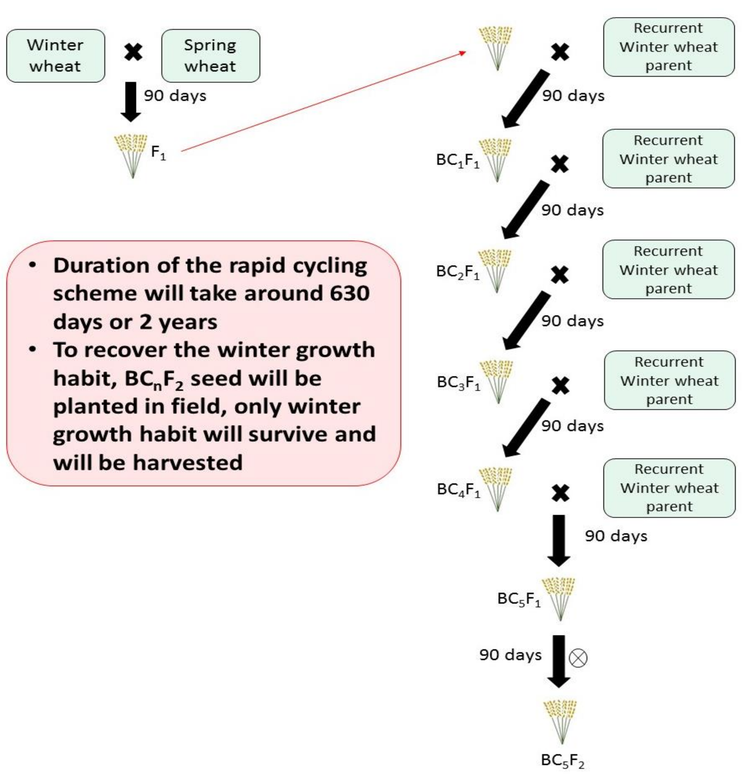

Table 1. KASP markers WMAS000033 for *Vrn-A1* and WMAS0000024 for *Ppd-D1* gene were used to detect variation between winter wheat and spring wheat parent.

Genotype	*Vrn-A1*	*Ppd-D1*
Apogee	A	A
Goodstreak	B	B
Overland	B	B
NW07505	B	B

Materials and Methods

- Nebraska wheat parents are 'Overland': a semi-dwarf and moderately late in maturity hard red winter wheat , 'Goodstreak': a medium in maturity and tall hard red winter wheat, and 'NW07505': a medium early and semi-dwarf white wheat for organic wheat purposes.
- Spring wheat parent is 'Apogee': a very early flowering and rapid development, full-dwarf hard red spring wheat was used as a donor parent carrying genes for early flowering, was crossed to Overland, Goodstreak, and NW07505.
- The F_1 plants from 'Goodstreak x Apogee', 'Overland x Apogee', and 'NW07505 X Apogee' populations will be selected and crossed back to recurrent parent (Goodstreak, or Overland, or NW07505). Alternatively, we may use the earliest F_2's for backcrossing.
- Experiment will be performed in greenhouse, (16 hrs. photoperiod, average night-time temperature is 18 °C and average daytime temperature is 24 °C with fluctuation).
- The number of days from planting to flowering and plants height will be measured.
- KASP markers WMAS000033 and WMAS0000024 were used to detect variation of *Vrn-A1* gene and *Ppd-D1* gene in winter wheat and spring wheat parents.

Table 2. Days from planting to flowering of ten earliest flowering F_3 of Goodstreak x Apogee lines and their BC_1F_1 from crossed back to Goodstreak , Goodstreak (GS) and Apogee(AG) . Data are mean ± standard deviation.

Generations	10 earliest flowering lines of Goodstreak x Apogee										Parents	
	8	44	84	101	146	170	184	205	210	227	AG	GS
	Days from planting to flowering											
F_3	49 ± 2	50 ± 2	50 ± 2	50 ± 1	46 ± 1	47 ± 3	49 ± 3	47 ± 2	50 ± 3	51 ± 4	46 ± 2	117 ± 1
BC_1F_1	70 ± 2	60 ± 7	55 ± 2	58 ± 2	72 ± 15	61 ± 2	60 ± 3	56 ± 2	56 ± 2	73 ± 12	43 ± 1	117 ± 1

Figure 2. Routine winter killing of spring types at Mead, NE. Only winter types in BC_nF_2 will survive.

Future direction

- Days to flowering and plant height of each backcrossing generation will be collected and analyzed
- Molecular markers for early flowering genes will be tracked during backcrossing

Reference

- Lewis, R.S. and S.P. Kernodle. 2009. A method for accelerated trait conversion in plant breeding. Theor. Appl. Genet. 118:1499-1508. doi: 10.1007/s00122-009-0998-1

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