

# Improvement of *Brassica napus* L. Restorers Using a Recurrent Selection Strategy

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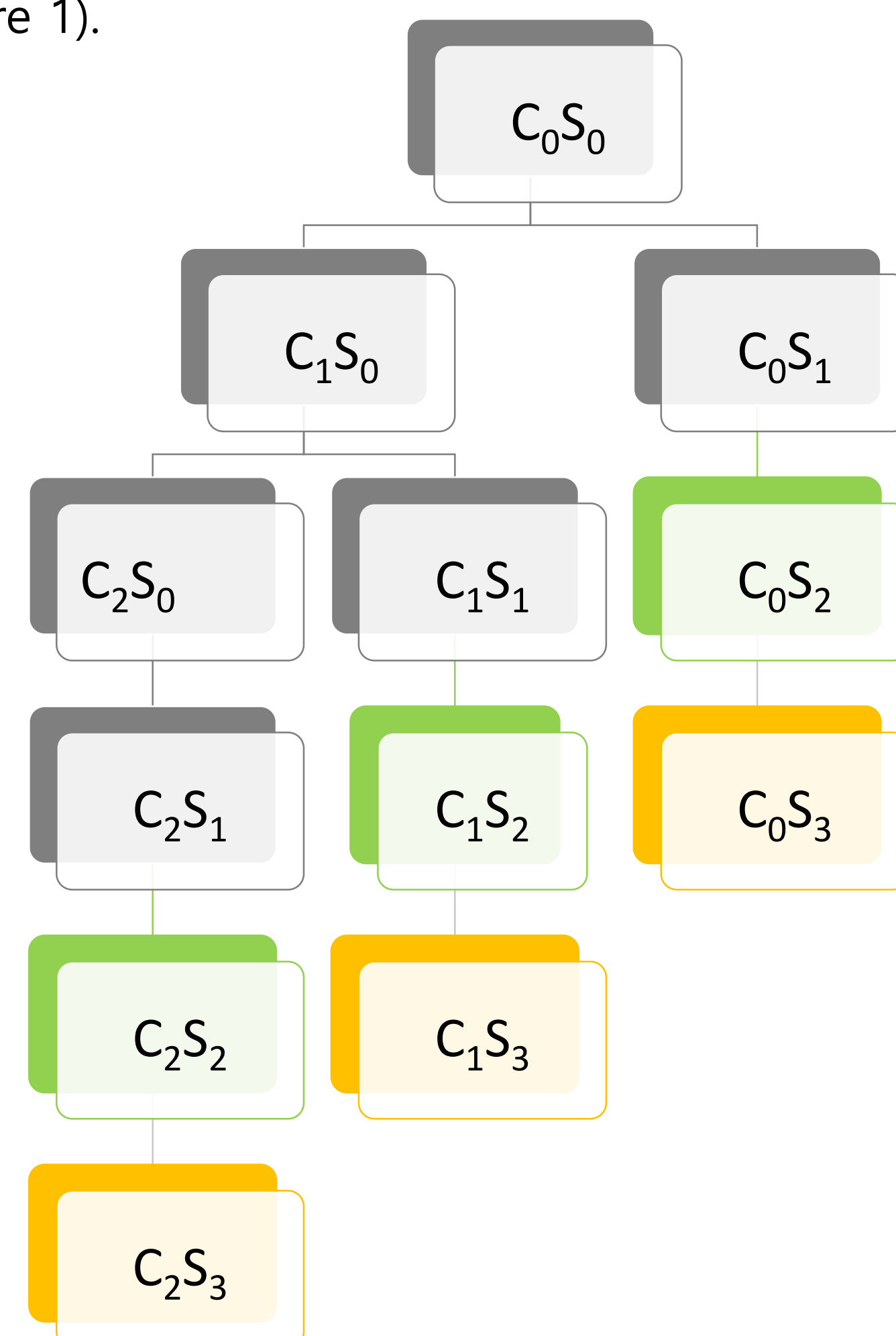
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## Introduction

- Ogu-INRA Cytoplasmic Male Sterility (CMS) is a pollination control system used for hybrid development in rapeseed (*Brassica napus* L.).
- The CMS system requires 3 lines: A-lines (male-sterile), B-lines (fertile maintainer lines) and R-lines which contain the *Rfo* gene and restore fertility.
- The *Rfo* gene was introgressed into *B. napus* from radish (*Raphanus sativus*) (Delourme et al., 1998).
- A large piece of the radish chromosome was introgressed along with the *Rfo* gene and derived in characteristics such as poor agronomic performance and high levels of glucosinolates (Hu et al., 2008).
- The objective was to test the effectiveness of recurrent selection and to determine the number of intermating cycles necessary to achieve improved restorer lines.

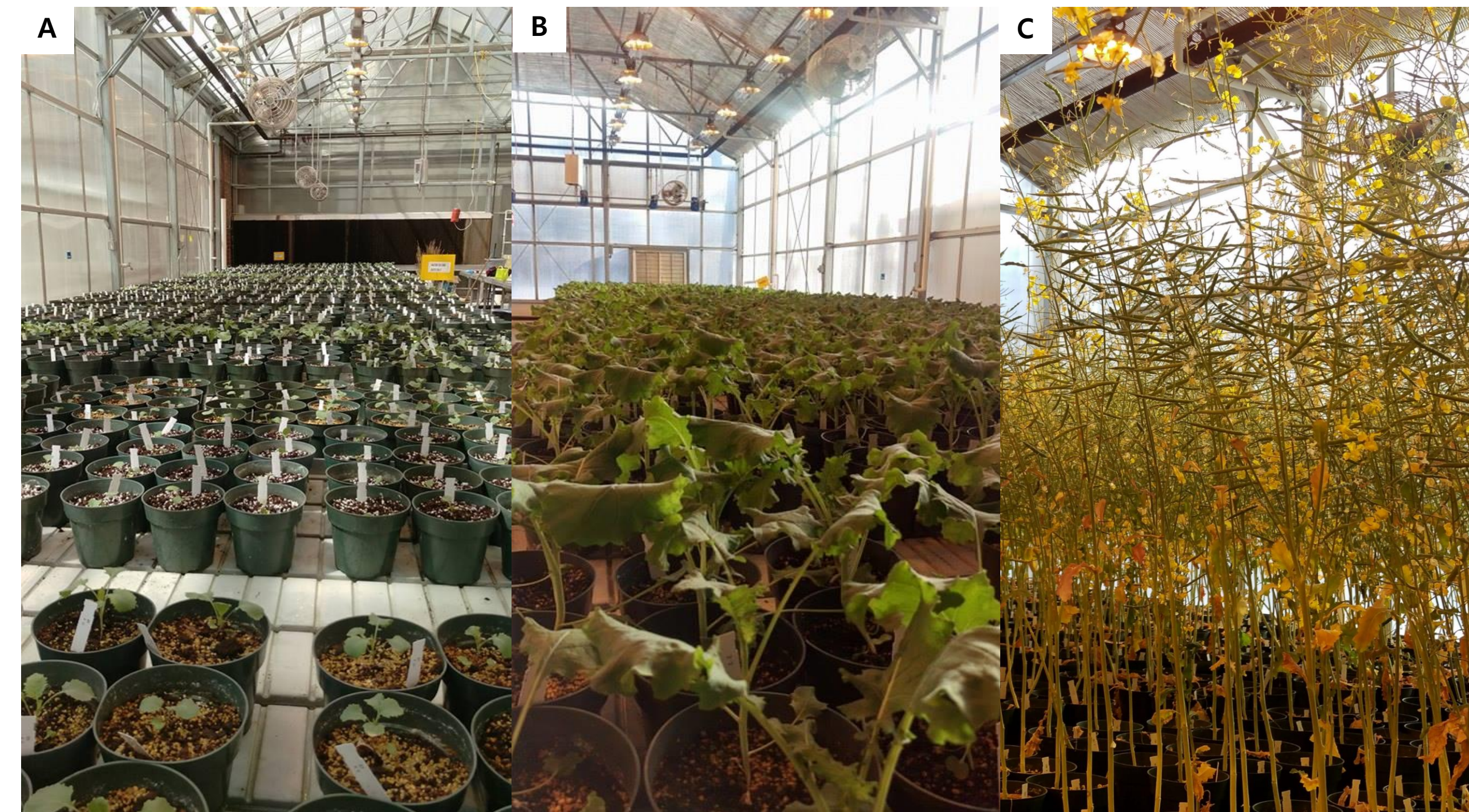
## Materials and Methods

- A base population  $C_0S_0$  was developed by designing five R-line by R-line crosses.
- Twenty plants from each initial cross were grown and chain-crossed at random, without any selection other than the presence of the *Rfo* SCAR marker.
- Twelve flowers from each plant were crossed and the remainder of the plant was selfed (Figure 1).



**Figure 1.** Development of three subpopulations in each cycle of recurrent selection. Populations from the second selfing cycle (green) will be compared in replicated experiment 1 and the third selfing cycle (orange) will be compared in replicated experiment 2.

- Three intermating/crossing cycles ( $C_0$ ,  $C_1$  and  $C_2$ ) were completed and each was selfed in order to compare all populations at the  $C_0S_2$ ,  $C_1S_2$  and  $C_2S_2$  (experiment 1).
- The  $S_2$  generation was then selfed again in order to compare the crossing cycles at  $C_0S_3$ ,  $C_1S_3$  and  $C_2S_3$  (experiment 2).



**Figure 2.** Experiment 1 at different growth stages. **A** The 2268 plants from the experiment transplanted at the rosette stage with second true leaves (stage 12). **B** Plants at vegetative stage 23. **C** At ripening, stage 85.

- The two experiments consisted of 60 genotypes from each cycle from which four plants were planted per replicate with three replicates, including the original parents as controls (Figure 2).
- The following traits were evaluated for each experiment: pod number, thousand seed weight, yield per plant and an overall pod rating. Data was analyzed using AGROBASE®.
- Plants were rated using a 1-9 scale where pod length and shape (Figure 3) were evaluated as well as pod distribution and overall plant structure.



**Figure 3.** Rating scale for pods; 1 represents a straight full pod, and 9 represents an aborted pod with no seed.

## Results and Discussion

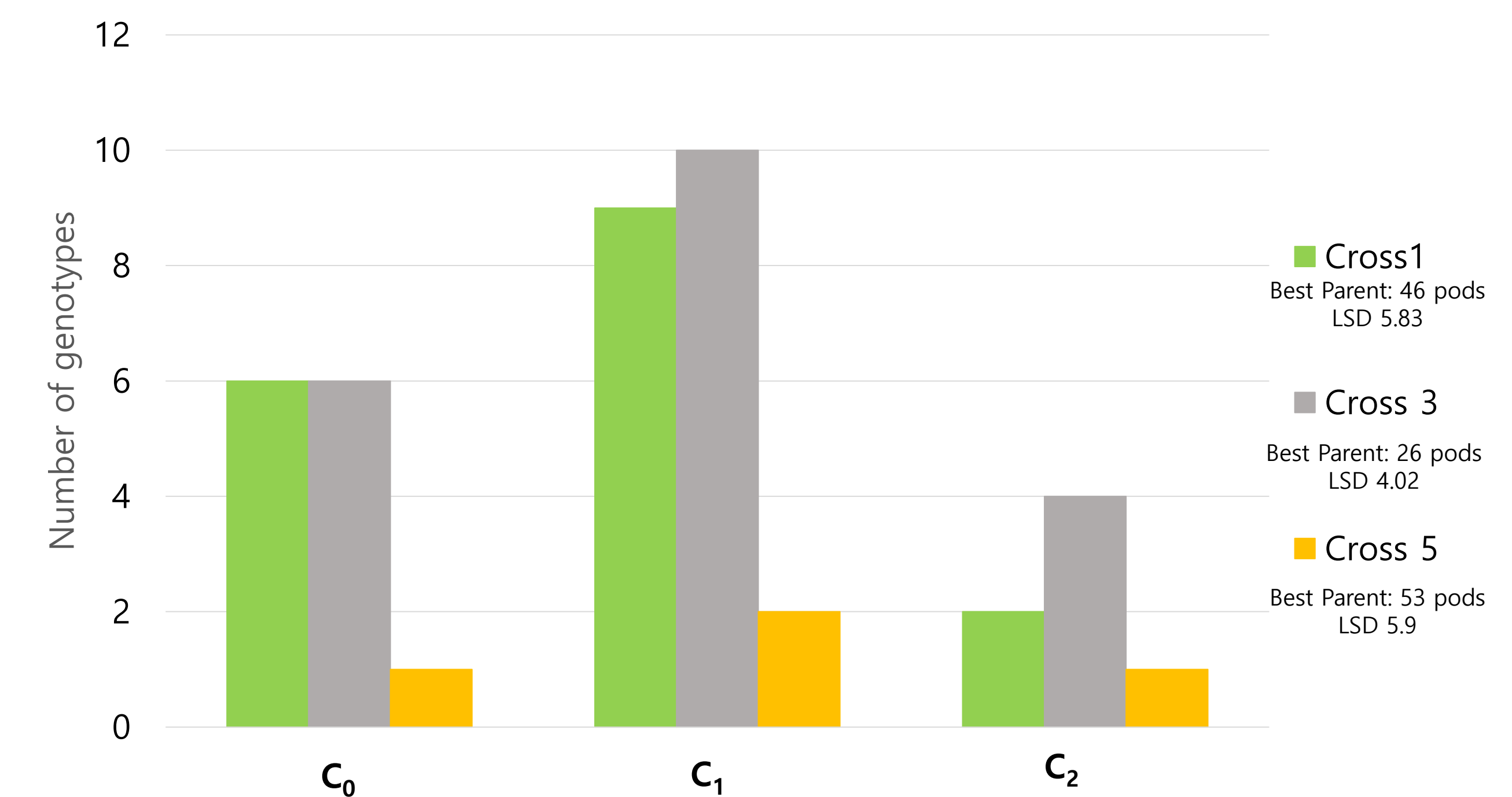
- The largest significant improvement in pod number was observed in the second experiment ( $S_3$ ) at  $C_1$  (Table 1).

**Table 1.** Pod number and rating for Cross 3 at  $S_2$  and  $S_3$ .

	Pod Number						Rating					
	Parents	$C_0$	$C_1$	$C_2$	LSD		Parents	$C_0$	$C_1$	$C_2$	LSD	
$S_2$	86.0	92.5	79.1	81.2	88.4	6.95	7.9	7.0	8.0	7.9	8.2	0.14
$S_3$	18.9	26.1	30.7	38.9	22.0	4.02	7.6	7.0	7.6	7.4	7.0	0.13

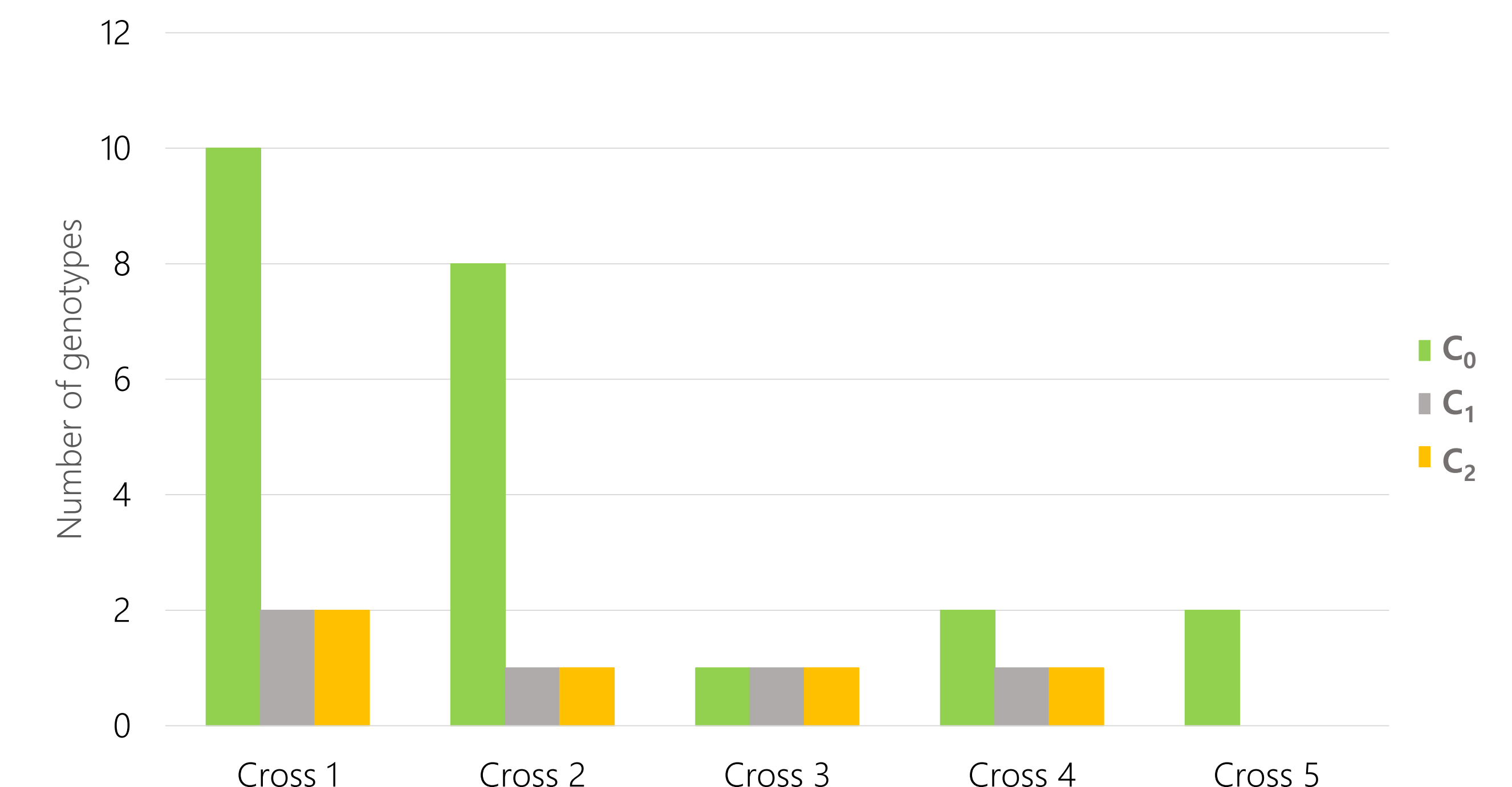
Least significance difference (LSD, P, 0.05) is included for comparison between means of different experiments

- The two experiments were conducted at different times of the year which had a visible impact on the growth and development of the plants. This effect is shown in table 1, where the number of pods decreased across all genotypes as well as in the parents in  $S_3$ .



**Figure 4.** Number of genotypes with significantly improved pod number when compared to the best parent. Twelve genotypes from each cycle were grown for each of the crosses with 3 replicates (4 plants per replicate). Crosses where cycles showed significant ( $P < 0.05$ ) differences are presented.

- In the three crosses presented in Figure 4, one cycle of intermating ( $C_1$ ) showed the highest number of significantly improved genotypes for pod number, whereas the second cycle of intermating ( $C_2$ ) had fewer improved genotypes.
- A different trend was observed for the overall pod rating where the best rated cycle was  $C_0$ . (Figure 5).



**Figure 5.** Number of genotypes with significantly ( $P < 0.05$ ) improved rating scores when compared to the parents. Twelve genotypes from each cycle were grown for each of the crosses with 3 replicates (4 plants per replicate).

## Conclusions and Future Work

- No single cycle produced the greatest improvement for all traits in all crosses.
- Combined statistical analysis of the 5 crosses demonstrated that  $C_2$  had the lowest scores for all traits.
- More than one cycle of intermating can have detrimental effects on *B. napus* restorer lines.
- Future work will evaluate the best restorers developed in this experiment in the field to obtain agronomic and seed quality data.

## Acknowledgements

The technical assistance of Judith Nugent-Rigby and everyone in the Brassica breeding program is greatly appreciated. Special thanks to all of our sponsors listed below.