YIELD IMPROVEMENT OF BRASSICA NAPUS THROUGH INTROGRESSION OF GENES FOR EARLINESS FROM PRIMARY AND SECONDARY GENE POOLS.

N.Thurling and R.Kaveeta

School of Agriculture, University of Western Australia, Nedlands. 6009. Australia.

INTRODUCTION

Although better environments for rapeseed production occur in Western Australia, a major expansion in growing is expected in lower rainfall environments of the main crop production zone (Fig 1). Farmers in this region are better equipped to commence production of a new crop than those primarily engaged in raising sheep and cattle in preferred areas nearer the coast. A sustained expansion of rapeseed growing in this area will depend on the breeding of cultivars better adapted to the lower rainfall environment. The most direct approach to achieving this objective would be selection for early flowering. Experiments were undertaken to determine (1) the extent to which time to flowering in B. napus can be shortened by introgression of genes from primary and secondary (B. campestris) gene pools and (2) the improvement in yield that can be achieved with a reduction in time to flowering.

MATERIALS AND METHODS

The pre-anthesis developmental characteristics of B. napus cv Wesbrook, an advanced B. napus breeding line (RU2) and a B. campestris population (Chinoli C42) were measured in the field at Perth. Times to the main developmental events floral initiation, commencement of stem elongation and first open flower were recorded.

The B. napus cultivar Wesbrook was crossed with RU2 and Chinoli C42 to generate two sets of inbred backcross lines through three successive generations of backcrossing to Wesbrook and three subsequent generations of selfing without selection. Flowering times of B_3S_3 lines from each cross were measured in a controlled environment under a 12h photoperiod at 20°C.

The three earliest lines from each cross were selected for a replicated field trial at a typical wheat belt site for measurements of growth, development and yield.

RESULTS

The primary (RU2) and secondary (Chinoli C42) sources of earliness each developed more rapidly before anthesis than the commercial cultivar Wesbrook (Table 1). Chinoli C42 developed more rapidly than either B. napus line.

Inbred-backcross lines derived from Wesbrook x RU2 varied widely in flowering time (85-137 DAS) in the controlled environment, and some 60% of these lines flowered significantly earlier than Wesbrook (Fig. 2). All B_3S_3 plants derived from the B. napus x B. campestris cross had the normal B. napus chromosomal complement.

These lines also varied widely in flowering time in a controlled environment (81-133 DAS), but over 80% of the lines flowered significantly earlier than Wesbrook (Fig. 3). Three distinct groups of lines were detected: those flowering at the same time as Wesbrook (7 lines), an early group flowering between 100 and 119 DAS (46 lines) and a very early group flowering earlier than 95 DAS (7 lines).

Only one line derived from the Wesbrook x RU2 cross (IB72) had a significantly higher seed yield than Wesbrook in the wheatbelt experiment (Table 2). This line flowered 14 days earlier than Wesbrook, but significantly outyielded three other lines (IB81, IN7, INT88) which also flowered much earlier than Wesbrook. The yield superiority of IB72 was primarily related to a much greater dry matter increment between commencement of flowering and maturity. INT88 was the highest yielding of the three lines derived from crossing B. napus and B. campestris primarily because of a superior pre-anthesis growth rate.

DISCUSSION

Lines flowering much earlier than Wesbrook in the field were derived quite easily through introgression of genes from the primary (RU2) and secondary (Chinoli C42) gene pools. Although RU2 flowered later than Chinoli C42, the earliest flowering lines in populations derived form crosses with Wesbrook had similar flowering times in the controlled environment. The failure to detect Wesbrook x Chinoli C42 lines flowering as early as the B. campestris parent is probably due to the influence of genes on the C genome which was retrieved through backcrossing to Wesbrook. Several Wesbrook x RU2 lines flowered earlier than either parent, this transgressional segregation reflecting recombination within both the A and C genomes.

Higher seed yields in the lower rainfall environment were favoured by earlier flowering, but other characters contributed to an enhancement of yield. The dry weight increment between flowering and maturity was certainly a major yield determinant. A reduction in time to flowering should be accompanied by an increase in post-anthesis dry matter accumulation because more time would be available for growth in the absence of the moisture deficit stresses which increase in severity during post-anthesis development. High yield in lines derived from introgression of genes from B. campestris appears to be more dependent on dry matter accumulation before anthesis, and particularly on a high growth rate before flowering.

CONCLUSION

Significant improvements in the yield of B. napus in lower rainfall areas of the West Australian crop production zone can be achieved through more extensive utilization of the primary gene pool of this species. Higher yielding lines are likely to be extracted from selected breeding populations through selection for early flowering and greater post-anthesis biomass production.

Table 1.Times from sowing to indicated developmental events in a June sowing of parental lines at Perth.

Population	Developmental Events		
	Floral initiation (DAS)	Stem elongation (DAS)	First open flower (DAS)
B. napus cv Wesbrook	36	48	85
B. napus RU2	28	44	78
B. campestris Chinoli C42	25	31	52
LSD ($p<0.05$)	-	1	2

Table 2. Line means for developmental, growth and yield parameters in the field at East Beverly, W.A.

Line	Flowering time (DAS)	LAI[a] (at flowering)	TDW[b] (at flowering) ($g.m^{-2}$)	TDW (at maturity) ($g.m^{-2}$)	TDW increment after flowering ($g.m^{-2}$)	Seed yield ($g.m^{-2}$)	Harvest index
Wesbrook	94	3.3	252	656	404	151	0.23
RU2	84	3.0	212	858	646	225	0.26
Chinoli C42	75	2.3	209	560	368	157	0.29
Wesbrook x RU2							
IB42	83	2.4	236	634	398	147	0.24
IB72	80	2.4	245	965	720	252	0.26
IB81	81	3.1	178	727	549	185	0.26
Wesbrook x Chinoli C42							
INT7	81	1.7	128	460	332	133	0.29
INT19	92	2.5	176	415	239	113	0.28
INT88	78	2.7	255	650	395	173	0.27
LSD ($p<0.05$)	4	0.8	70	184	197	41	0.04

(a) Leaf area index
(b) Total dry weight of above ground parts

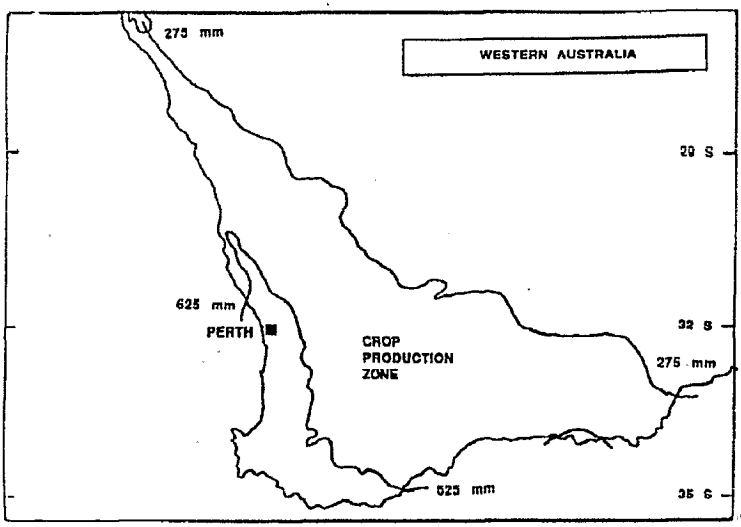

Fig. 1. Map of southern Western Australia showing region with potential for rapeseed production

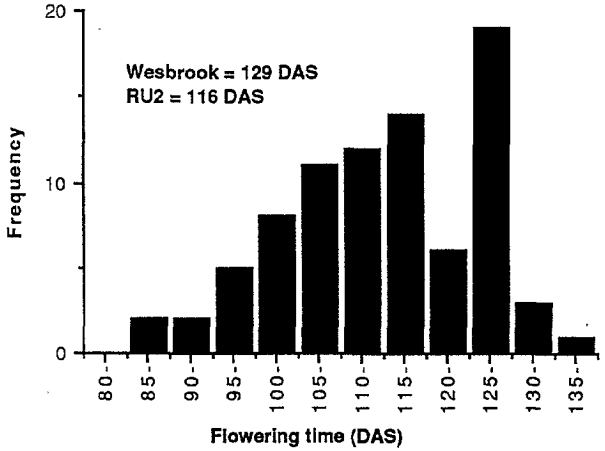

Fig.2. Distribution of Wesbrook x RU2 line means for flowering time

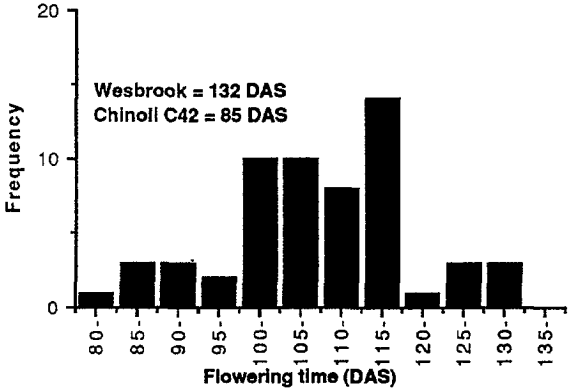

Fig.3. Distribution of Wesbrook x Chinoli C42 line means for flowering time