



# Genotypic variation in the accumulation of water-soluble carbohydrate in canola and its potential contribution to seed yield in different environments



Heping Zhang\*, Sam Flottmann

CSIRO Agriculture and Food, Private Bag 5, PO Wembley, WA 6913, Australia

## ARTICLE INFO

### Article history:

Received 15 May 2015

Received in revised form 16 June 2016

Accepted 19 June 2016

Available online 30 June 2016

### Keywords:

Canola

Water soluble carbohydrate

Yield

## ABSTRACT

Water-soluble carbohydrates (WSC) stored in the stems and pod wall in canola (*Brassica napus* L.) can be an important source of assimilates contributing to yield. However, genotypic variation in WSC and its contribution to yield have not been investigated. The aims of this work were to quantify genotypic variation of WSC and the extent to which WSC contributes to seed yield. We measured the concentration and content of WSC in a number of hybrid and open pollinated triazine tolerant (TT) and non-TT canola genotypes at flowering, podding and maturity from 2009 to 2011. There were significant repeatable differences in WSC concentration among genotypes (28–108 mg g<sup>-1</sup> at podding) and WSC content (12–113 g m<sup>-2</sup> at podding). The major difference in WSC content occurred between the TT and non-TT canola while the difference between hybrid and open-pollinated canola was small. On average, non-TT canola produced higher amount of WSC (68 g m<sup>-2</sup>) than TT canola (47 g m<sup>-2</sup>). Seed yield increased with the increased amount of remobilized WSC in the limited water-stressed conditions (2009 and 2011). Despite the high amount of WSC in drought (2010) year, no significant relationship was found between yield and the remobilized WSC because the higher WSC was offset by yield penalty from delay in flowering in these varieties. The contribution of WSC to yield was higher in drought (10–22%, 2010) year than in the average (3–9%, 2009) and above-average (7–12%, 2011) rainfall year. Genotype and environment interaction was relatively small compared to genotype effect. The difference in the amount of WSC between the herbicide tolerant groups and among genotypes was repeatable and the rankings of genotypes for WSC remained similar across the years. Both the WSC content and the ratio of remobilized WSC to yield had large broad-sense heritability ( $H = 0.68–0.85$ ). The high heritability, the positive relationships between seed yield and WSC under limited water stress conditions, and the high contribution of WSC to yield under drought conditions suggest that WSC could be used as a breeding trait to augment yield in the limited water-stress condition and maintain yield under drought conditions by reducing the effect of water stress on yield.

© 2016 Elsevier B.V. All rights reserved.

## 1. Introduction

Water-soluble carbohydrates (WSC) accumulated in stems of wheat and barley before grain filling can provide substantial assimilates to maintain yield under terminal drought, and also augment yield under favourable conditions (Bingham et al., 2007; Foulkes et al., 2007; Zhang et al., 2010). Most studies on WSC and its contribution to yield have concentrated on wheat and barley (Bingham et al., 2007; Foulkes et al., 2007; Rebetzke et al., 2007; Zhang et al., 2010; McIntyre et al., 2012). These studies have led to high WSC

being used as a drought tolerance trait in wheat breeding programs (Rebetzke et al., 2008; McIntyre et al., 2012) and as a trait to increase yield potential (Foulkes et al., 2007).

Little is known about the accumulation of WSC and its contribution to yield in canola (*Brassica napus* L.). Studies have been conducted on few genotypes, and only in Europe (Habekotte, 1993), where the contribution of WSC to yield was reported to be from a negligible amount to 12% of yield (Habekotte, 1993; Mendham, 1995). This is considerably lower than the 30–40% for wheat and barley reported in both well-water and water-stressed environments (Foulkes et al., 2002; Shearman et al., 2005; Zhang et al., 2010). No study has previously addressed the extent and nature of genotypic variation in WSC in canola or its contribution to seed

\* Corresponding author.

E-mail address: [heping.zhang@csiro.au](mailto:heping.zhang@csiro.au) (H. Zhang).

**Table 1**

The total number of genotypes and the number of genotypes classified by flowering time, pollination and a combination pollination and herbicide tolerance (HT) groups in each year. OP: open-pollinated; TT: triazine tolerant.

Year	Number of genotypes	Flowering time			TT		Non-TT	
		Early	Mid	Late	Hybrid	OP	Hybrid	OP
2009	17	4	9	4	2	6	6	3
2010	20	4	12	4	3	8	7	2
2011	6	0	4	2	2	2	2	0

yield under either the limited water-stressed or water stressed growing conditions.

Canola is becoming an increasingly important crop in Australia as a cash crop in the high rainfall area and as a breakcrop in the wheat-based farming system in the low and medium rainfall areas, hence it is grown across a wide range of rainfall zones (Zhang et al., 2016). This begs the question of whether there is genetic variation in WSC among canola genotypes, and to what extent it contributes to yield under low and high rainfall conditions. Answering these two questions would be of value to maintain yield under drought condition frequently encountered in the low rainfall area and augment yield in the limited water-stressed conditions.

To answer these questions it is important to evaluate genotypes with different yield potential. To this end we chose elite subsets of Triazine tolerant (TT) and non-TT, and hybrid and open-pollinated (OP) canola because TT types have a yield penalty associated with lower rates of photosynthesis, while the heterosis contrast provides differences in early vigour, both of which could be expected to influence WSC accumulation and its contribution to yield. We hypothesize that the greater photosynthesis rate in non-TT than TT canola and higher vigour in hybrid than OP canola enable non-TT canola to produce more WSC than TT canola and hybrid canola to produce more WSC than OP canola. The aims of this study were to i) quantify the genotypic difference in WSC using a wide range of genotypes and the contribution of WSC to seed yield; and ii) evaluate the potential of stored stem WSC as a useful trait for breeding drought tolerance canola in the low rainfall environment and for improving yield potential in high yielding environment.

## 2. Materials and methods

A number of spring canola genotypes (Tables 1 and 3) were sown on 20 May 2009 (17), 21 May 2010 (20), and 20 May 2011 (6) to evaluate their yield performance at Kojonup, Western Australia where canola is widely grown. The genotypes were classified into herbicide tolerance (HT) groups: TT and non-TT groups within which genotypes were sub-grouped into hybrids and OP based on heterosis (Table 1). The non-TT canola included the imidazoline-tolerant and conventional canola because these two types of canola do not have yield penalty associated with the TT gene. The genotypes were also classified as early, mid, and late flowering based on the time of flowering. The early flowering canola flowered about 20 days earlier than the late flowering ones. The experiment was arranged using a randomized design with four replicates in all years. The plot size was 20 m by 1.54 m. The crop was sown to achieve 50 plants m<sup>-2</sup> by adjusting seeding rates according to seed size. In all 3 years, the crop was supplied with 120 kg N ha<sup>-1</sup> split as follows: 20 kg N ha<sup>-1</sup> at sowing, 50 kg N ha<sup>-1</sup> at 6 leave stage, and 50 kg N ha<sup>-1</sup> at 50% flowering. The initial soil available N in 0–120 cm soil profile at sowing was 80–120 kg N/ha, varying from year to year. All crops were supplied with 12 kg P/ha and 18 kg S/ha at sowing and 50 kg K/ha at 6 leave stage. Soil sulfur was at 20 mg/kg soil at the 0–40 cm soil profile and increased to 50–100 mg/kg below the 40 cm, being greater than the critical value of canola showing yield response to sulfur (Anderson et al., 2013). No

**Table 2**

Summary of analysis of variance for the content of water soluble carbohydrate (WSC-A) in stem/pod wall at flowering, podding and maturity, the remobilized WSC (WSC-R) and its contribution to yield (WSC-R/yield) at Kojonup, Western Australia, from 2009 to 2011. HT: Herbicide tolerance groups (TT vs non-TT); Gen: genotype.

Source	WSC-A			WSC-R	WSC-R/ yield
	Flowering	Podding	Maturity		
HT	***	***	***	***	***
Year	***	***	***	***	***
HT × Heterosis	***	ns	**	ns	ns
HT × Year	**	ns	***	ns	ns
HT × Heterosis × Gen	***	***	**	***	***
HT × Heterosis × Year	ns	ns	ns	ns	ns
HT × Heterosis × Gen × Year	***	*	ns	*	**

\* \*\* \*\*\*: significant at  $P < 0.05$ ,  $P < 0.01$ ,  $P < 0.001$ , respectively.

ns: Not significant at the 0.05 probability level.

additional sulfur was applied. All canola were managed as conventional for weed management because of the different herbicide tolerance among the genotypes. The growing season rainfall in the three years was 455 mm in 2009 (average year), 250 mm in 2010 (drought year) and 540 mm in 2011 (above-average year) (Zhang et al., 2004; Zhang and Flottmann, 2016).

Crop growth stages were scored according to a decimal scale code developed by Sylvester-Bradley and Makepeace (1984). Crop samples were collected using a quadrat of 0.54 m<sup>2</sup> at flowering (4.5) and the beginning of pod filling (5.8) (referred as podding thereafter), and a quadrat of 1.08 m<sup>2</sup> at physiological maturity (6.8) for each genotype. The plant samples were taken on different dates as individual varieties reached the specified growth stage. At each sampling stage, three to five plants were randomly sub-sampled and partitioned into leaves, stems, and pods. Pods were threshed to separate seed from pod wall. All samples were dried to constant weight in a fan-forced dehydrator with temperature set at 60 °C and weighed. Grain yield was reported at a 5% moisture content basis. Harvest index (HI) was calculated as the ratio of seed yield to dry matter from 1.08 m<sup>2</sup> samples at physiological maturity. The stem and pod wall samples were ground and passed through a 1 mm sieve and used to determine the concentration and amount of WSC in the stems at the three stages. WSC were extracted from 0.1 g of ground stem material by extracting once with 8 ml of 80% ethanol at 80 °C followed by 2 extractions with 8 ml distilled water at 60 °C. The extraction was centrifuged at room temperature for 600 s at 3400 rpm and the extracts were combined. Total carbohydrates in the samples were analyzed by the anthrone method (Yemm and Willis, 1954). WSC concentration (WSC-C) was expressed in mg g<sup>-1</sup> and WSC content (WSC-A) was calculated by multiplying stem/pod wall biomass by its WSC-C and expressed in g m<sup>-2</sup>.

The apparent remobilization of WSC (WSC-R) was taken as the maximum difference in WSC between podding (or flowering) and maturity. The remobilized WSC was converted into glucose-equivalent energy requirements for biosynthesis of the constituents of canola seed yield based on Penning de Vries et al. (1974) who estimated that 1.0 g glucose is required for the biosynthesis of 0.82 g carbohydrate, or 0.40 g protein, or 0.33 g lipid. For canola yield at a 40% of oil content, 1.6 g WSC is required to produce 1 g of seed yield (Hocking et al., 1997). The contribution of WSC to yield was calculated as the percentage of yield based on glucose-equivalent requirements.

We used linear mixed models with the ASReml package in R (Butler et al., 2009) to assess the differences in the WSC traits by nesting HT/heterosis/genotype × Year. Wald statistics with conditional sum squares was used to test the significance of difference in WSC-C, WSC-A, WSC-R, and the ratio of WSC-R to yield between the HT groups (non-TT and TT), between hybrid and OP canola

Download English Version:

<https://daneshyari.com/en/article/6374515>

Download Persian Version:

<https://daneshyari.com/article/6374515>

[Daneshyari.com](https://daneshyari.com)