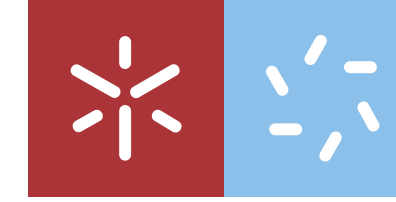




**Grapevine response to cold -
study of starch metabolism in woody tissues**

UMinho | 2019

Tiago Daniel Machado da Silva

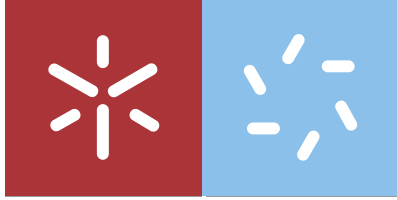


Universidade do Minho
Escola de Ciências

Tiago Daniel Machado da Silva

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metabolism in woody tissues**

Outubro de 2019



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Grapevine response to cold - study of starch metabolism in woody tissues

Tese de Mestrado

Biologia Molecular, Biotecnologia
e Bioempreendedorismo em Plantas

Trabalho efetuado sob a orientação do

Doutor Henrique Noronha

e do

Professor Doutor Hernâni Varanda Gerós

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“Every living thing is a masterpiece, written by nature and edited by evolution.”

Neil deGrasse Tyson, 2014

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STATEMENT OF INTEGRITY

I hereby declare having conducted this academic work with integrity. I confirm that I have not used plagiarism or any form of undue use of information or falsification of results along the process leading to its elaboration.

I further declare that I have fully acknowledged the Code of Ethical Conduct of the University of Minho.

Abstract

Grapevine (*Vitis vinifera* L.) is one of the most important agronomical species in the world, but in the context of the ongoing climate changes, extreme temperatures, high light intensities and water deficit are becoming important threats in many important viticultural areas worldwide. Among these, stress caused by cold has been shown to influence its productivity, metabolism and gene expression, which prompted us to study some molecular mechanisms involved in grapevine response to low temperature. In this regard, cv. Vinhão canes were harvested and incubated at 4 °C for 7, 14 and 30 days to unravel physiological changes, identify and characterize key genes involved in response to cold. Results showed that starch levels steadily decreased during the incubation period at 4 °C, and that the expression of the amylolytic gene *VvAMY2* increased along time, while the expression of *VvBAM5* decreased. Furthermore, HPLC analysis showed an increase in sucrose, fructose and glucose during the incubation at 4 °C. Additional expression studies of key-genes involved in sugar metabolism showed that the steady-state transcript levels of *VvpGT2* and *VvSWEET2b* transporters as well as *VvSusy* and *VvSPS* enzymes increased along time, while the expression of the transporters *VvTMT1* and *VvSUC27* was downregulated. The *VvpGT2* gene was selected for further studies regarding organ specific expression and function. *VvpGT2* steady-state transcript levels were high in mature berries and flowers. Following heterologous expression in a mutant yeast (EBY.VW4000) lacking monosaccharide transporters, no *VvpGT2* transport activity of fructose, glucose and sucrose could be detected. Raffinose and stachyose levels in the grapevine canes were quantified by HPLC because the metabolism of raffinose has been linked to cold response. Results showed a steadily increase of raffinose levels along incubation at 4 °C and transcriptional studies also revealed a noticeable increase of the steady-state levels of the galactinol synthase genes *VvGolS1* and *VvGOLS3* raffinose synthase *VvRafS5*.

Key-words: Abiotic stress, qPCR, Starch metabolism, Sugar transport, *Vitis vinifera*.

Resumo

A videira (*Vitis vinifera* L.) é uma das espécies agrícolas mais importantes ao nível global, contudo temperaturas extremas, altas intensidades de luminosidade e a secura constituem ameaças importantes em muitas regiões vitivinícolas ao nível mundial, no contexto das alterações climáticas em curso. Em particular, o stresse causado pelo frio afeta a sua produtividade, metabolismo e expressão genética, o que nos motivou a estudar alguns mecanismos moleculares de resposta da planta a temperaturas reduzidas. Varas atempadas de videira da variedade Vinhão foram colhidas e incubadas a 4 °C durante 7, 14 e 30 dias para se estudar as modificações fisiológicas e identificar e caracterizar genes-chave envolvidos na resposta ao frio. Os níveis de amido quantificados nas varas de videira diminuíram durante o tempo de incubação e, em paralelo, observou-se um aumento da expressão do gene *VvAMY2* que codifica uma enzima amilolítica. Contudo, os níveis de transcritos do gene *VvBAM5* diminuíram. Estudos de HPLC mostraram que ocorreu um aumento de sacarose, frutose e glucose em resposta ao frio. Estudo da expressão de genes-chave envolvidos no metabolismo dos açúcares mostraram um aumento dos níveis de transcritos dos transportadores *VvpGT2* e *VvSWEET2b* e das enzimas *VvSusy* e *VvSPS*, no entanto os níveis de transcritos dos transportadores *VvTMT1* e *VvSUC27* diminuíram. Quando se estudou o perfil de expressão do gene *VvpGT2* em diversos órgãos observou-se que os níveis de transcritos são mais elevados em bagos maduros e flores. Estudos de expressão heteróloga do gene *VvpGT2* numa levedura mutante. Estudos de expressão heteróloga do gene *VvpGT2* numa levedura mutante (EBY.VW4000) incapaz de transportar açúcares, mostraram que a proteína *VvpGT2* é incapaz de transportar glucose, frutose e sacarose.

No presente trabalho foram ainda avaliados por HPLC os níveis de rafinose e de estaquiase nas varas de videira uma vez que tem sido observado que o metabolismo dos oligossacarídeos da família da rafinose está envolvido na resposta das plantas ao frio. Com efeito, durante a incubação a 4 °C observou-se um aumento de rafinose durante o período de incubação a 4 °C bem como dos níveis de transcritos das enzimas galactinol sintetase, *VvGoIS1* e *VvGoIS3*, e da rafinose sintetase, *VvRafS5*.

Palavras-chave: qPCR, Metabolismo do amido, Stress abiótico, Transporte de açúcares, *Vitis vinifera*.

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List of abbreviations and acronyms

ADP	Adenosine diphosphate
ADP-Gluc	Adenosine diphosphate glucose
AGPase	Adenosine diphosphate glucoypyrophosphorylase
AMY	α -amylase
ATP	Adenosine triphosphate
BAM	β -amylase
Ca ²⁺	Calcium
CaCl ₂	Calcium chloride
cDNA	Complementary DNA
CO ₂	Carbon Dioxide
CTAB	Cetyltrimethyl ammonium bromide
cv.	Cultivar
DNS	3,5-dinitrosalicylic acid
DTT	Dithiothreitol
DW	Dry weight
EDTA	Ethylenediaminetetraacetic acid
FW	Fresh weight
G1-Pi	Glucose-1-phosphate isomerase
G6-Pi	Glucose-6-phosphate isomerase
Gal	Galactose
GBSS	Granular-bound starch synthases
GPT	Glucose-6-phosphate/ phosphate translocator
H ⁺ /ATPase	Proton-pumping Adenosine triphosphatase
H ₂ O	Water
HCl	Hydrochloric acid
HPLC-RI	High performance liquid chromatography with refractive index
LDA	Limit dextrinase
MES	2-(N-Morpholino)ethanesulfonic acid
MEX	Plastidic maltose transporter

mRNA	Messenger RNA
Na	Sodium
NaCl	Sodium chloride
NADPH	Nicotinamide adenine dinucleotide phosphate
NaOAc	Sodium Acetate Anhydrous
NTT	Plastidic nucleotide transporter
PCR	Polymerase Chain Reaction
PEG	Polyethylene glycol
PGM	Plastidic phosphoglucomutase
pGT	Plastidic glucose transporter
PMSF	Phenylmethylsulfonyl Fluoride
PPi	Pyrophosphate
PVPP	Polyvinylpyrrolidone
RafS	Raffinose synthase
RFO	Raffinose family oligosaccharides
SD	Standard deviation
SE-CC	Sieve element-companion cell
SS	Starch synthases
Suc	Sucrose
SUT/SUC	Sucrose transporter genes
SWEET	Sugars will eventually be exported transporters
TMT1	Tonoplast monosaccharide transporter 1
TPT	Triose-phosphate/phosphate translocator
UDP-Gal	Uridine diphosphate galactose

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1. Introduction

1. Introduction

Grapevine (*Vitis vinifera* L.), a woody perennial domesticated about 6000-8000 years ago, is recognised as one of the most valuable agricultural crops worldwide (McGovern et al., 2017). It has long been cultivated in temperate climate regions with sufficient rain, warm and dry summers and relatively mild winters (Jones et al., 2005; Ali et al., 2010). Due to its socioeconomic importance, grape growing has resulted in various uses of its fruit, from wine making to distillation of liquors, dried raisins and table grapes (Lecourieux et al., 2013). In 2017, it was estimated that 7.5 million hectares throughout the world were occupied by vineyards, corresponding to a total grape production of 73.3 million tons (OIV, 2018).

1.1. Biotic and abiotic stress factors affecting grapevine yield

Viticulture is famously sensitive to climate (White et al., 2006) and, along with other crops, it faces increased biotic and abiotic pressures linked to climate change. As a consequence of this phenomenon, the suitability of different crops like wheat, maize, soybean, rice, olive and grapevine has been affected in many areas, resulting in alterations in the production levels (Van Dingenen et al., 2009; Lobell et al., 2012; Ray et al., 2015; Moriondo et al., 2013a,b).

Grapevine is particularly affected by cold stress (Sawicki et al., 2015), heat stress (Kriedemann and Smart 1971), water shortage (Hardie and Considine, 1976; Lovisolo and Schubert, 1998), water excess (Striegler et al., 1993), and from rises of CO₂ concentration in the atmosphere (Martínez-Lüscher et al., 2015). Gene expression and plant metabolism alterations caused by cold stress will lately affect many biological functions (Chinnusamy et al., 2007; Sawicki et al., 2015). For instance, feedback inhibition of photosynthesis process is a consequence of the cessation of growth, the reduced energy and electron utilization by the Calvin Cycle and photosynthetic chain (Ruelland and Zachowski, 2010; Theocharis et al., 2012). The study of the mechanisms of grapevine response to abiotic and biotic stress has a direct impact in agricultural industry and may assist biotechnology protocols aiming the selection of highly productive and stress-resistant grapevine varieties (Ollat et al., 2017; Nenko et al., 2018).

1.2. Carbon assimilation and sucrose synthesis in autotrophic tissues

The carbohydrate status is responsible for the modulation and coordination of internal regulators and environmental cues that control growth and development (Ruelland et al., 2010; Theocharis et al., 2012). Sucrose, produced through photosynthesis in the mesophyll of mature leaves, is the main

carbohydrate used for long distance transport in grapevine (Swanson and El Shishiny 1958; Keller, 2015). During the day, the Calvin-Benson cycle assimilates carbon from atmospheric CO₂ through the use of products of the light reactions (ATP and NADPH). The intermediates produced in the previous step, trioses-phosphate (Trioses-P), are used not only to synthesize transient starch in the chloroplast but are also translocated to the cytosol by the triose-phosphate/phosphate translocator (TPT, Fischer et al., 1994), serving as precursors of sucrose formation (Figure 1A). During the night, the coordinated action of α - and β -amylases, and the debranching enzymes (isoamylase and limit dextrinase), degrade transient starch to maltose and glucose that are then exported to the cytosol by the plastidic maltose transporter (MEX; Niittylä et al., 2004) and plastidic glucose transporter (pGT; Weber et al., 2000), respectively, allowing a constant sucrose synthesis to provide carbon to sink tissues (Figure 1B).

1.3. Long distant sugar transport

Sugars, synthesized in the mesophyll cells, but also, water, minerals and amino acids, are translocated by plants through the vascular system (Keller, 2015). Sugars transport and allocation between the photosynthetic “source tissues” and the heterotrophic “sink tissues” is known as assimilate partitioning, which has evolved in land plants as a major determinant of plant growth and productivity (Kingston-Smith 2001).

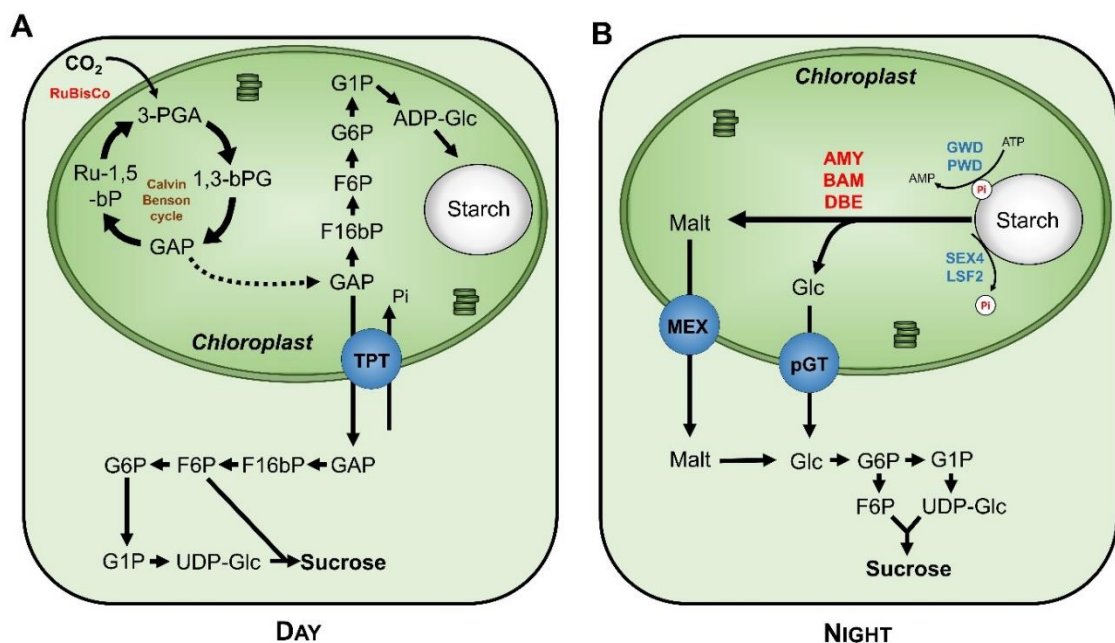


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1.3.1 Phloem loading and unloading

In higher plants, sucrose is loaded from sites of biosynthesis into the phloem by membrane carriers and transported to the sites of use and storage (Lalonde et al., 2004). For the delivery of sucrose into the SE/CC complex two pathways have been proposed: apoplastic and symplastic. In symplastic loading, sucrose moves from mesophyll cells to the SE-CC complex through small pores between adjacent cells, the plasmodesmata, that allow sucrose to move from the bundle sheath into the companion cell.

Conversely, the apoplastic loading mechanism requires the export of sucrose from the mesophyll cells to the apoplast and its uptake in the SE-CC complex by a H^+ /ATPase symporter located in the same cells. Recently it was proposed that sucrose release in the apoplast, more precisely in the vicinity of the SE-CC complex, is mediated by *SWEET* (*sugars will eventually be exported transporters*) facilitators (Chen et al., 2011).

In agreement with Munch's mass flow hypothesis, sucrose moves across the phloem from high concentration sites (autotrophic tissues) to low concentration organs (heterotrophic tissues) (Münch, 1930; Conde et al., 2007). In heterotrophic or sink tissues, unloading takes place either by transmembrane export or through plasmodesmata, although the first steps are often symplastic (Fisher and Oparka, 1996). Also, it has been postulated that sucrose efflux transporters may work as facilitators or as proton antiporters (Walker et al., 1995). Sucrose in the apoplast can be taken up directly to the sink cell through sucrose/ H^+ symporters or by hexose transporters after its hydrolysis into glucose and fructose by invertases.

1.4. Carbon storage in grapevine sink tissues

Carbohydrates are stored in perennial structures mainly as starch (Yang and Hori, 1979; Mullins et al., 1992). In all grapevine varieties studied, starch represents the most important part of sugar reserves and is mobilized or accumulated according to the plant needs (Winkler and Williams, 1938; Bouard,

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1966; Mullins et al., 1992; Zapata et al., 2001). Starch metabolism and photosynthesis are the two key processes determining sugar availability and during the annual grapevine cycle, a complex carbohydrate flux is set up between annual and perennial organs.

Sugars accumulated in heterotrophic plastids (amyloplasts, found in roots, woody tissues, fruits, seeds, tubers, and pollen grains) obtained from long-distance sugar transport through the phloem (Lalonde et al., 2004; Lemoine et al., 2013) are the first source of sugars used by emerging shoots in the spring (Scholefield et al., 1978). Tubers, fruit and seeds are also considered to be major sinks during the reproductive stages (Wardlaw, 1990), relying on the use of available carbohydrate resources produced by photosynthesis to support their growth and development.

1.4.1. Starch in grapevine storage organs

Grapevine has an annual growth that can be divided into several distinct developmental stages: dormancy, bud break (budburst), bloom (anthesis or flowering), fruit set (berry set or setting), *veraison* (color change or onset of ripening), harvest (ripeness or maturity), and leaf senescence and subsequent fall (Lebon et al., 2008). During winter dormancy, starch is mainly located in the ray parenchyma of the roots (Zapata et al., 2004), trunks and canes. Plant metabolism is reactivated in early spring, (Huglin, 1986) and starch becomes the only source of carbohydrates in grapevine (Scholefield et al., 1978; Huglin and Schneider, 1998; Zapata et al., 2004), and is progressively mobilized by the growth of annual vegetative and reproductive organs (Bates et al., 2002; Zapata et al., 2004) inducing bud break. Depending on the variety, reserve mobilization in the grapevine occurs approximately until anthesis, (Yang et al. 1980; Candolfi-Vasconcelos et al., 1994; Caspari et al., 1998). After that, starch accumulates again in annual (Bates et al., 2002) and perennial (Mullins et al., 1992; Bates et al., 2002; Zapata et al., 2004) tissues from fertilization until the beginning of berry ripening (*veraison*) (Candolfi-Vasconcelos et al., 1994; Caspari et al., 1998).

1.4.2. Starch structure

Starch is the predominant carbohydrate reserve in many plants found in both photosynthetic and nonphotosynthetic tissues (Slatery et al., 2000). It contributes with 50-70% of the energy in the human diet (Coopeland et al., 2009) and is additionally utilized as commercial feedstock and in numerous industrial applications (Kavakli et al., 2000).

Starch is composed by amylose and amylopectin (Figure 2A), which comprise 98–99% of native granules dry weight, but small amounts of lipids, minerals, and phosphorus in the form of phosphate

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esterified to glucose hydroxyls can also be found in starches structure (Copeland et al., 2009). Starch granules range in size (from 1 to 100 μ m diameter) and shape (polygonal, spherical, lenticular), and can vary greatly with regard to content, structure and organization of the amylose and amylopectin molecules, the branching architecture of amylopectin, and the degree of crystallinity (Lindeboom et al., 2004) (Figure 2B). These polymers share the same basic structure but differ in their length and degree of branching (Slattery et al., 2000).

Amylopectin, a large branched polymer that typically makes up 75% or more of this polysaccharide, is considered the basic unit of the starch granule (Myers et al., 2000; Denyer et al., 2001; Zeeman et al., 2010). Amylose is an essentially linear polymer of glucosyl residues linked via α -1,4 glucosidic linkages, whereas amylopectin exists as a branched α -1,4: α -1,6 D-glucan polymer (Slattery et al. 2000). Amylose is smaller than amylopectin, 10^6 - 10^8 Da, with longer chains and a limited number of branch linkages (Buléon et al., 1998). Glycogen, a storage polysaccharide of animals, is a glucose polymer composed of α -1,4-linked, α -1,6-branched chains, but a higher degree of branching in comparison with amylopectin (Copeland et al., 2009). The multiplicity in branching is a common feature of both amylopectin and glycogen (Buléon et al., 1998). Plants ability to synthesize amylopectin has evolved from an ancestral capacity to make glycogen (Copeland et al., 2009; Zeeman et al., 2010). The conserved architecture of starch granules, the dense packaging of glucose units in organized clusters, is determined by the packing of amylopectin molecules.

1.4.3. Starch synthesis in heterotrophic tissues

In spite of the fact that most biochemical steps of starch synthesis operating in leaves are conserved in heterotrophic tissues, some are particular to sink organs. For instance, in heterotrophic tissues, starch is synthesized in amyloplasts following the incorporation of glucose-6-phosphate (G6-Pi) from the cytosol by a glucose-6-phosphate/ phosphate translocator (GPT; Kammerer et al., 1998). Initial evidence for the import of G6-Pi into starch synthesizing plastids came from experiments with different plant species (Neuhaus et al., 1993; Kang and Rawsthorne 1994; Wischmann et al., 1999). In *Arabidopsis thaliana* and *Vitis vinifera*, two GPTs have been identified, *AtGPT1,2* and *VvGPT1-2* respectively, operating as glucose-6-phosphate transporters *in planta* (Niewiadomski et al., 2005; Noronha et al., 2015).

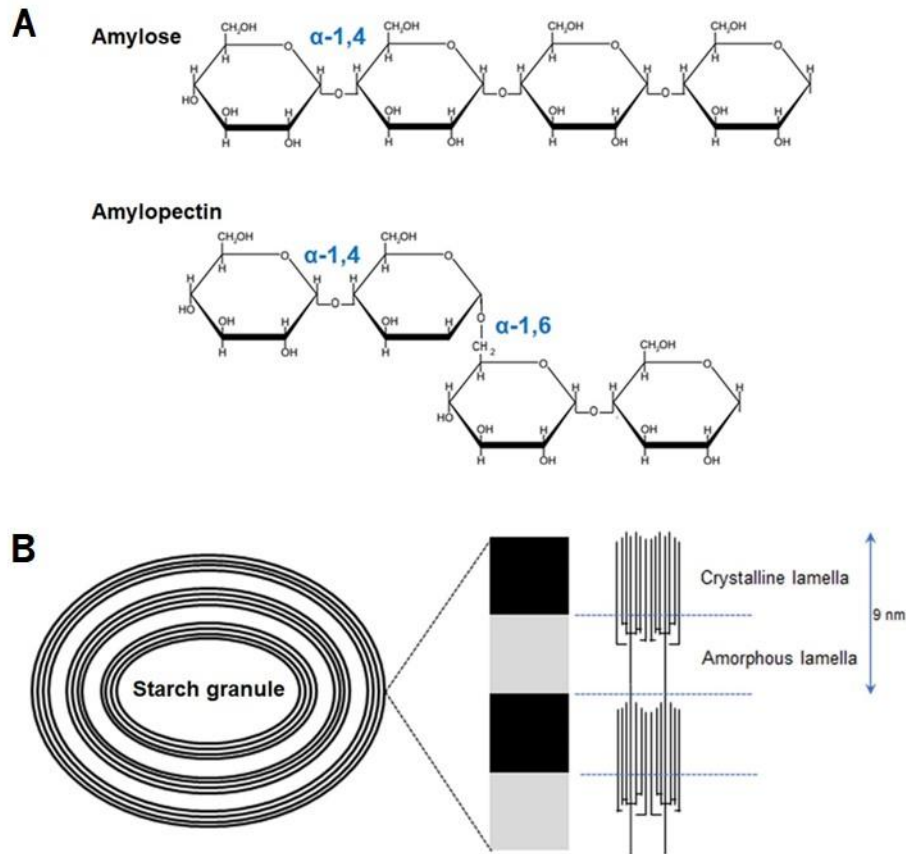


Figure 2. Composition and structure of the starch granule. Starch granules are composed by an array of semicrystalline lamellae, amylopectin and amylose (A), divided by amorphous growth rings. Double helical structures are formed within a cluster as a result of the branch points present in amylopectin. This structure packs together in a consistent manner that allows the formation of a crystalline lamellae, which intersperses with the amorphous lamellae, where the branch points are placed, leading to the formation of a semicrystalline matrix. Within the granule, stacks of semicrystalline lamellae are separated by amorphous growth rings (B). Adapted from Tester et al., 2004 and Huijbrechts 2008.

Additionally, the interconversion of glucose-1-phosphate (G1-Pi) and G6-Pi for starch biosynthesis is likely the result of a plastidic phosphoglucomutase (PGM). There are two PGM isoforms in plants, one localized in the plastids and the other in the cytosol (Muhlbach and Schnarrenberger, 1978). Deficiency in the plastidic PGM activity lead to a “*starchless*” phenotype in *Arabidopsis* and *Nicotiana sylvestris*.

In the case of G6-Pi, ATP required for the synthesis of ADP glucose is imported by heterotrophic plastids from the cytosol. During starch biosynthesis in potato tubers, G1-Pi is converted to ADP-Gluc by AGPase. Plastidic nucleotide transporter (NTT), an ATP/ADP translocator, supplies ATP-dependent reactions in non-photosynthetic plastids, such as starch and fatty acid biosynthesis with cytosolic ATP (Schünemann et al., 1993; Kang and Rawsthorne, 1994).

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Higher plants, that produce ADP-Gluc and pyrophosphate (PPi) from G1-Pi and ATP, possess the ADP-Glucopyrophosphorylase (AGPase) catalyzing the first key regulatory step in the starch biosynthetic pathways. Its activity is localized exclusively inside the plastid in all tissues except in the cereal endosperm where most of its activity is cytosolic (Denyer et al., 1996; Burton et al., 2002).

Starch synthases, found within the plastids, consists of two distinct classes designated granular-bound starch synthases (GBSSs) and others that can be found in the soluble phase or granular bound are known as starch synthases (SS). GBSSs are responsible for amylose synthesis (Kuipers et al., 1994) and SS are involved in amylopectin synthesis (Smith et al., 1997). It was reported that *waxy* mutants of cereals, and equivalent mutations also affect the starch of pea embryos, potato tubers, the perisperm of Amaranthus seeds, and Chlamydomonas cells. All of these mutants lack activity of GBSSI and consequently only have amylopectin, supporting the role of GBSS in the amylose synthesis (Slattery et al., 2000).

1.5. Starch metabolism during winter

Chilling markedly reduces grapevines growth, photosynthesis and delays flowering (Hendrickson et al., 2004; Bertamini et al., 2006; Ait Barka et al., 2006; Bertamini et al., 2006). In order to overcome such conditions, woody perennial trees, such as grapevine, not only need to synthesize proline and phenolic compounds, but also need to accumulate starch and soluble sugars (Ait Barka et al., 2006; Fernandez et al., 2012). This will allow a greater degree of freezing tolerance in response to low, non-freezing temperatures and vegetative growth in the following spring (Figure 3).

Carbohydrate metabolism has been reported to have greater instantaneous low temperature sensitivity than other components of photosynthesis (Fernandez et al., 2012). Seasonal dynamics of starch and soluble carbohydrates have been described in the canes of some varieties (Eifert et al., 1960; Bouard, 1966). More precisely, the raffinose family oligosaccharides (RFOs) are responsible for protecting plant cells against damage during abiotic stresses for numerous species, such as poplar (Sauter and van Cleve 1991, 1994), *Pinus strobus* L. (Hinesley et al., 1992), birch (Kasuga et al., 2007) and willow (Ögren 1999).

Carbohydrate accumulation at low temperatures may be explained through the activation of specific enzymes (Bohnert and Sheveleva, 1998; Couee et al., 2006). Galactinol is responsible for donating activated galactose (Gal) moieties to sucrose (Suc). Uridine diphosphate (UDP-Gal) and galactinol synthase assure galactinol and myo-inositol synthesis accordingly (Peterbauer and Richter 2001). Raffinose, that is synthesized by raffinose synthase (RafS), will later receive a Gal residue leading to the

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formation of stachyose. The action of specific galactosyltransferases regulates the formation of other oligosaccharides of this pathway (manninotriose and melibiose), using galactinol as a galactosyl moiety donor (Figure 3).

Spinach and Arabidopsis leaves exposed to cold treatment (Schneider and Keller 2009) demonstrated that most of the enzymes involved in raffinose synthesis are localized in the cytosol (Schneider and Keller 2009). In another study, chestnut *CsDSP4*, a homolog of the Arabidopsis *SEX4* phosphatase associated with starch degradation in leaves (Zeeman and Rees 1999; Niittylä et al., 2006), was found to be induced in woody tissues during autumn starch catabolism to increase the accumulation of sugars (Berrocal-Lobo et al., 2011). In Arabidopsis, plants acclimated to low temperature (+5 °C), up-regulation of *SUTs*, *SUC1* and *SUC2* expression suggests an alternative mechanism for maintaining sucrose transport to sinks, mainly young leaves (Lundmark et al., 2006). The activity of sucrose phosphate synthase, a cytosolic enzyme that synthesizes sucrose-6-phosphate from UDP-glucose and fructose-6-phosphate (Ito et al., 2011), has been reported to increase in various plant species as a response to cold treatments (Guy et al., 1992; Holaday et al., 1992; Hurry et al., 1995).

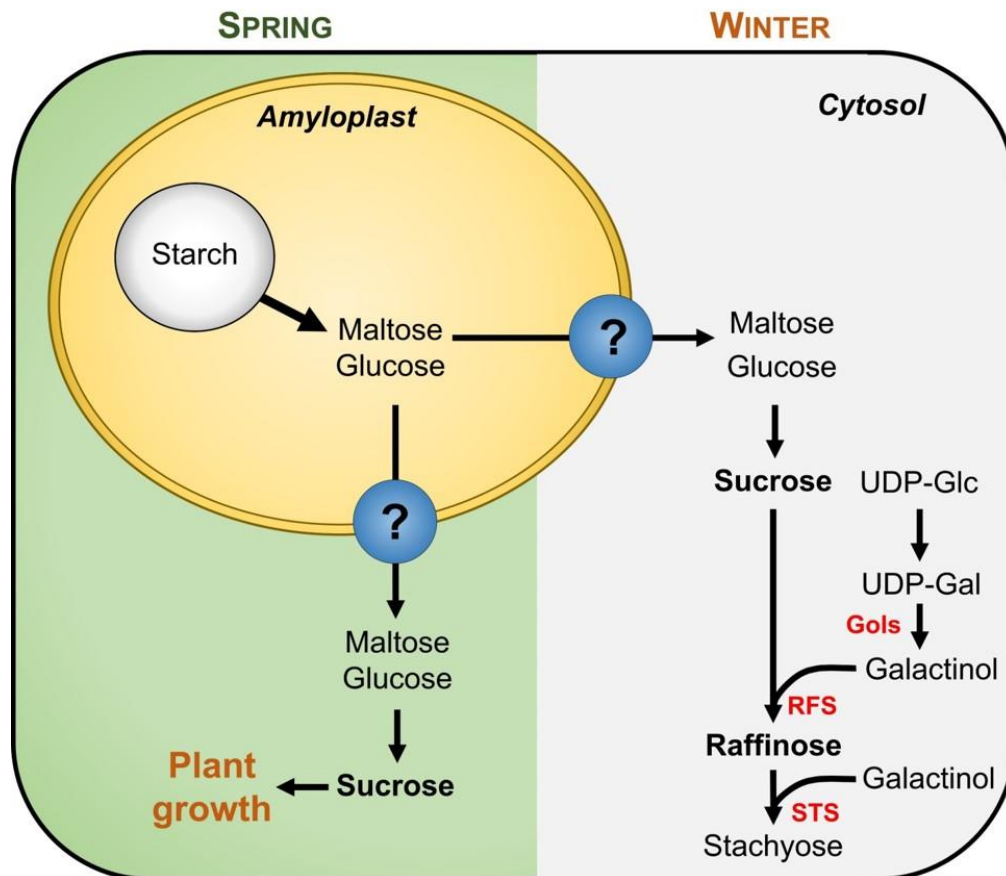


Figure 3. Carbon reserves mobilization during spring and in winter induced by cold in woody tissues. During spring, starch may be converted to maltose and glucose inside the amyloplast followed by the formation of sucrose, to sustain plant growth and metabolism. During winter, maltose and glucose are mobilized to the cytosol allowing the formation of sucrose and its conversion to raffinose and stachyose, in this order. Gols, Galactinol synthase; RFS, raffinose synthase; STS, stachyose synthase; UDP-Gal, uridine diphosphate-galactose; UDP-Glc, uridine diphosphate-glucose. Adapted from Noronha et al., 2018.

1.6. Objectives

The effects of climate change on natural ecosystems and on human activities, including agriculture, have been extensively described (IPCC 2018). In the long term, the sustainability of wine production in several viticultural regions may be threatened (Schultz and Jones, 2010; Hannah et al., 2013). During the past decades, a change in grapevine phenology has been reported for several grape-growing areas (Duchêne and Schneider, 2005, Petrie and Sadras, 2008, Ramos et al., 2008). Among various environmental stresses, low temperature is one of the most critical factors limiting the productivity and distribution of plants (Theocharis et al., 2012). Many physiological and biochemical cell functions have been associated with visible symptoms after cold-stress, such as, cessation of growth, reduced energy

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and electron utilization by the Calvin cycle and photosynthetic chain, starch mobilization to fuel the synthesis of compatible solutes (Zheng et al., 2009; Ruelland et al., 2010).

In the present study we wanted to address the hypothesis that the response of grapevine to cold involves modifications of starch metabolism together with the reprogramming of the expression of key genes involved in sugar metabolism. To address this hypothesis, *Vitis vinifera* canes from an important regional variety - Vinhão - were incubated for 7, 14 and 30 days at 4 °C. Starch and soluble sugars content were quantified in tissue extracts and Real Time PCR analysis evaluated expression of key sugar transporters and enzymes involved in starch and RFO metabolism.

2. Materials and Methods

2. Material and Methods

2.1. Plant Material

Cuttings from field-grown grapevines (*Vitis vinifera* L.) of cv. Vinhão were used in the present work. Canes were collected, after fruit harvest, from a commercial vineyard in Ponte de Lima and incubated for 7, 14 and 30 days at 4 °C. At each incubation period, 4 similar sized canes were selected from each sample (Figure 4) and the bud region and outer layers of the periderm were removed with scissors and scalpel. Then, they were cut in small segments, frozen with liquid nitrogen, and grounded using a mill (IKA) and stored at -80 °C. In addition, an aliquot of this material was lyophilized in a Christ-Alpha 2-4 LD lyophilizer for subsequent quantification studies (Conde et al., 2015).

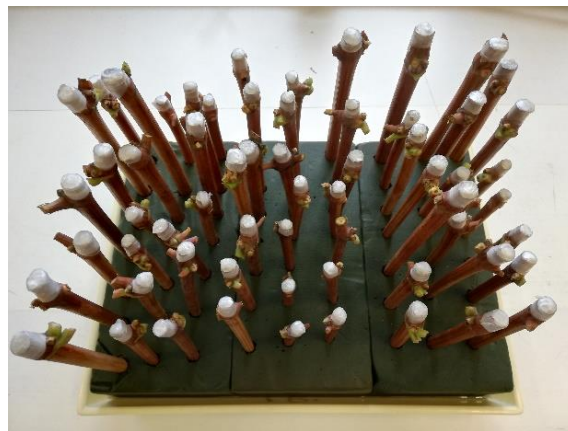


Figure 4. Incubated canes from *Vitis vinifera* cv. Vinhão for 7, 15 and 30 days at 4 °C.

2.2. Starch quantification

Starch was quantified in canes according to the protocol by Smith and Zeeman (2006). In order to remove soluble sugars, lyophilized cane (0.05 g DW) tissues were extracted three times with 5 mL 80% ethanol, and starch grains were gelatinized by autoclaving. Starch was enzymatically degraded due to the inclusion of α -amylase (AMY; 1U, Sigma–Aldrich) and β -glucosidase (10U, Sigma–Aldrich) in a medium containing 200 mM sodium acetate (pH 5.5) and glucose was measured through the DNS method.

2.3. RNA isolation and cDNA synthesis

To isolate total RNA from cane tissues the protocol by Reid et al. (2006) was adapted. For each condition, 500 mg of frozen tissue were used, which were mixed with 1 mL of extraction buffer containing 300 mM Tris HCl (pH 8.0), 25 mM EDTA, 2.0 M NaCl, 2% CTAB, 2% PVPP and 1.0 M DTT. Samples were then incubated at 60 °C for 15 min and shaken every 5 min. Then, mixtures were extracted twice with 850 μ l of chloroform:isoamyl alcohol (24:1) followed by a centrifugation at 13500

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rpm for 15 min at 4 °C for 15 minutes. To the aqueous phase were added 0.1 vol of 3 M NaOAc (pH 5.2), 0.6 vol of isopropanol followed by incubation at -80 °C for 1 h. The pellet was centrifuged at 13500 rpm at 4 °C during 30 min and later resuspended in 100 µl of ultrapure H₂O. In order to purify the samples, the GRS Total RNA Kit – Plant (GriSP, Lda.) was used following the manufacturer's instructions from step 5. RNA concentration and purity were quantified by spectrophotometry in the Nanodrop ND-1000 (Thermo Fisher Scientific Inc.) and integrity checked in a 1% agarose gel. The synthesis of the first cDNA strand was performed using Xpert cDNA Synthesis Mastermix protocol (GriSP, Lda.), according to the manufacturer's instructions.

2.4. Real-time PCR studies

Quantitative real-time PCRs were performed with Xpert Fast SYBR Blue (GriSP, Lda.) along with the conditions previously optimized in a CBX96 Real-Time Detection System (Bio-Rad). The amplification protocol included an initial denaturation step at 95 °C for 3 min, followed by additional 40 cycles which were composed of a denaturation step for 3 seconds at 95 °C, annealing for 20 seconds at 55 °C and a final extension step for 20 seconds at 72 °C. Experiments were done in biological replicates and then interpreted with the software Bio-Rad CFX Manager (Bio-Rad), while *VvGAPDH* (glyceraldehyde-3-phosphate dehydrogenase) was used as internal control. The primers presented below (Table 1) were used to study gene expression.

Table 1: Primers forward and reverse used for gene expression analysis by qPCR. Sequences accession numbers were taken from Grape Genome Browser 12x.

Gene	Primer Forward (5'-3')	Primer Reverse (5'-3')	Sequence accession number
<i>VvAMY2</i>	TCAGTCTGCTGCATCTGAAGGG	TGGGTACCATAGTGGGATGCATTG	GSVIVT01031740001
<i>VvAMY5</i>	TGGCCTTCAAGGGCTGTCACATTC	AAGGCCAATGAGCCTGTGTTGAG	GSVIVT01008714001
<i>VvBAM2</i>	CCAGTTTACGTAATGCTCCCTCTG	GCTGTTTCTCAAGCCCGTCTTTG	GSVIVT01030642001
<i>VvBAM3</i>	GTTCAAGGGTGCCAGTGTTC	GCTTTAGTCCATGCCTTTGC	GSVIVT01013272001
<i>VvBAM4</i>	TGCAACCCTTGCCATTTGAGGAAAC	CACCAATAGACTGCTGGAACCTTG	GSVIVT01036911001
<i>VvBAM5</i>	CGCCAACCTATCTTTGCAGTCC	TCTTCGACACGGTCCATATCTGC	GSVIVT01014681001
<i>VvMEX</i>	GTCTTGTGGCCGTTGTTATGGC	TGGCATCCACATGAAGAGAAGTG	GSVIVT01024263001
<i>VvGT2</i>	TCAATGCTCTTGGAGCTGCCATC	CTTCTCACTGCTTTGCCTGA	GSVIVT01015361001
<i>VvGT1</i>	ATTGGGAGTTACCTGGGAATGGC	AGTTGTTTCACTGCGGAAATG	GSVIVT01030495001
<i>VvGT4</i>	TAACAAGCTTTGCTGGGATGGC	GGGCACTCCAAGTGAAAGAGAAGG	GSVIVT01031006001
<i>VvSPS1</i>	GGTTTGCTATTGTTGCCACCAG	CAAGAAGGCCATTGTCAAGTACCC	GSVIVT01012825001
<i>VvSuSy</i> (Hren et al., 2009)	TGTTAAGGCTCCTGGATTCAATTA	AGCCAAATCTTGCAAGCA	GSVIVT01015018001

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<i>VvSUC27</i> (Pastene et al., 2014)	TGCTTGGCACTGACGGTACT	GCTGTAGGTGATCGCAAGAGG	GSVIVT01034886001
<i>VvTMT1</i>	TTCTTTGCTGTTGGTGCAAG	CAGAGAGCCCCTGAAAGTTG	GSVIVG01009024001
<i>VvGoS1</i> (Pillet et al., 2012)	TGATTACAGCAGCGTTTTGCC	CGAGAGTACTGGCCTCTTCTA G	GSVIVG01028174001
<i>VvGoS3</i>	TGCCGAGCAGGACTATTTGA	CAAGTTGTAGGTGGGTGGA	GSVIVT01031274001
<i>VvRafS1</i>	TCCTGCCAGAGATGGAATAAGCC	GGCAATTGAACACACCCACGAC	GSVIVT01014778001
<i>VvRafS5</i>	CCATCTTGAGGTGCCAGTACTACG	ATGGTGTGCCGTCGTGAAGAG	GSVIVT01032425001
<i>VvGAPDH</i> (Gairza-Cortés et al., 2012)	TTCCGTGTTCTACTGTTG	CCTCTGACTCCTCCTTGAT	GSVIVT00009717001

2.5. Sugar extraction and quantification by high performance liquid chromatography (HPLC) analysis

The extraction of sugars was performed as reported by Conde et al. (2015) which was previously adapted from Eyéghé-Bickong et al. (2012). In short, 150 mg of lyophilized cane tissue was mixed with 1 mL of ultrapure H₂O, exhaustively vortexed, and then a proportional volume of chloroform was added to the mixture. The biphasic solvent was promptly vortexed for 5 min to mix and incubated at 50 °C for 30 min with a continuous shaking (1400 rpm). After this, the samples were centrifuged at 13400 rpm for 10 min at room temperature and the supernatant collected. The extracted sugars were filtered with a 0.45 µm nitrocellulose filter and quantified by HPLC-RI using a Rezex RCM–Monosaccharide Ca²⁺ (8%) column (Phenomenex) column at a flow rate of 0.6 ml min⁻¹ at 40 °C using water as the mobile phase. An injection volume of 20 µl was used. 20 g/L sucrose and 10 g/L of raffinose, glucose, fructose and stachyose were used as pattern curves. Sugars concentration of each sample were identified through the comparison of the peak area and retention time with the standard sample curves.

2.6. Cloning and functional characterization of *VvpGT2*

The *pAG416GPD-VvpGT2* construct was prepared following the Gateway technique (Invitrogen). Recombination sequences were introduced by PCR in the *VvpGT2* cDNA and the fragment recombined into the entry vector pDONR221 with the BP clonase enzyme. *VvpGT2* cDNA was then recombined into the *pAG416GPD* vector by the LR clonase enzyme. The *pAG416GPD-VvpGT2* plasmid was introduced in the hexose transporter-deficient yeast strain EBY.VW4000 using the LiAc/SS-DNA/PEG method (Gietz and Woods 2002) and selected on solid synthetic medium [0.7% YNB (Alfa Aesar), 1.3% dropout (US Biological; without uracil), 0.5% ammonium sulphate, 2% glucose and 2% agar].

Yeast drop-test assays were performed as described previously (Noronha et al., 2016). Briefly, yeast cells harboring *pAG416GPD-VvpGT2* construct and the *pAG416GPD* empty (control) vector were grown in liquid media until the OD_{640 nm} reached 1.0. After this, cells were washed with sterile H₂O,

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serial dilutions were made and 5 μ L drops were added to YNB media supplemented with 2% sucrose, fructose, glucose or maltose.

2.7. Statistical Analysis

The results were statistically analyzed by Analysis of Variances tests (one-way and two-way ANOVA) using Prism vs. 7 (GraphPad Software, Inc.). Statistical differences between mean values are marked with letters for the different conditions

3. Results

3. Results

3.1. Starch quantification in grapevine woody canes exposed to cold

To study how low winter temperatures can affect starch metabolism in grapevine, *Vitis vinifera* cv. Vinhão canes were incubated for 7, 14 and 30 days at 4 °C, as described in Material and Methods. As can be seen in Figure 5, a steadily decrease in the total amount of starch in woody canes was observed during the incubation period.

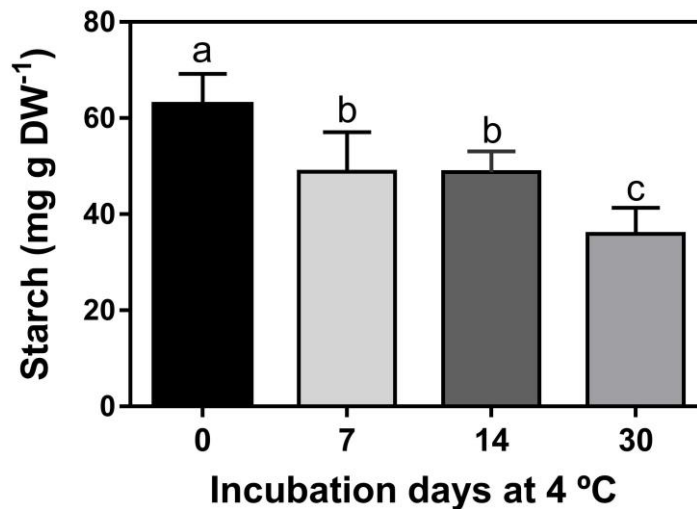


Figure 5. Reserve starch in woody canes of *Vitis vinifera* cv. Vinhão incubated at 4 °C up to 30 days. Results indicate the mean \pm SD of four independent experiments. Different letters stand for significant differences ($P \leq 0.05$).

3.2. Transcriptional analysis of grapevine α - and β -amylase genes

The expression of 2 α -amylase and 4 β -amylase genes was studied by qPCR, and results showed that the expression of *VvAMY2* decreased over time, while the expression of *VvAMY5* was only detected after the onset of the cold treatment (Figure 6A). Regarding β -amylases the steady-state transcript levels of *VvBAM2*, *VvBAM3* and *VvBAM4* decreased while the expression of *VvBAM5* was clearly upregulated after 30 days of incubation (Figure 6B).

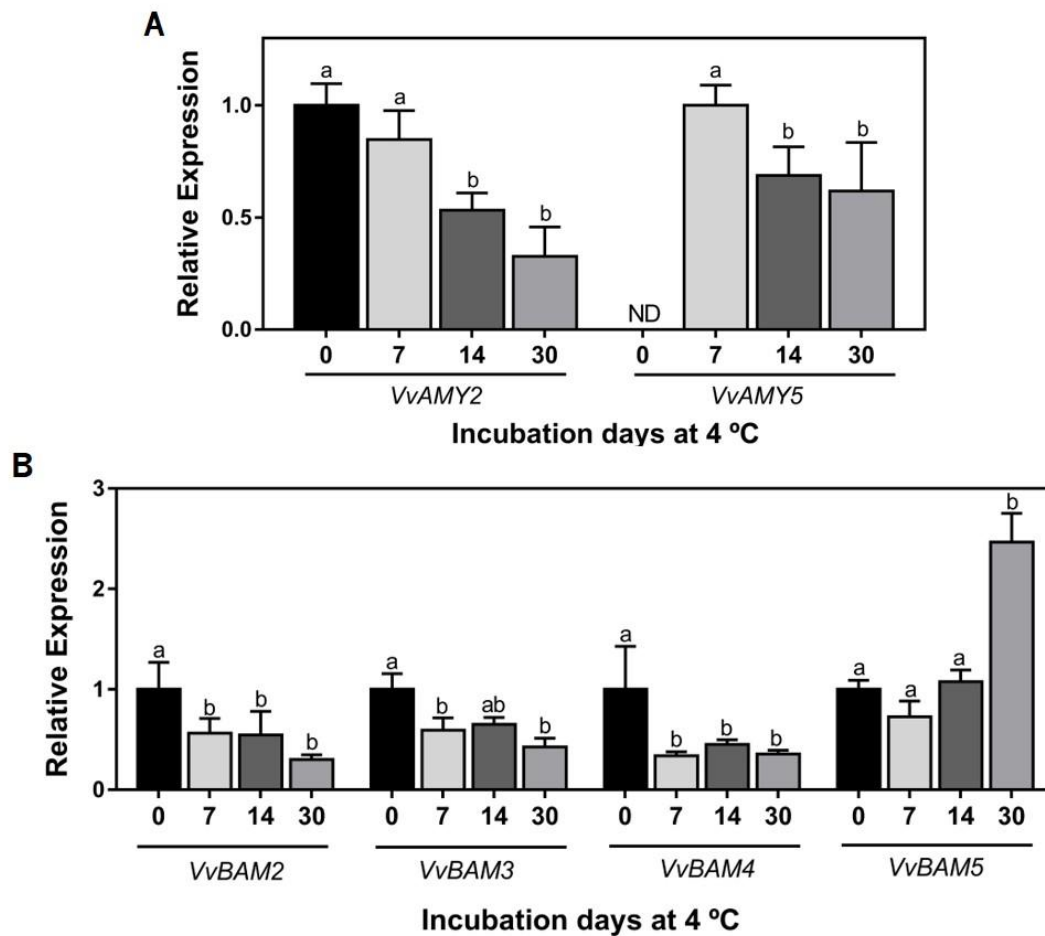


Figure 6. Expression of α -amylases (*VvAMY2* and *VvAMY5*) (A) and β -amylases (*VvBAM2*, *VvBAM3*, *VvBAM4*, *VvBAM5*) (B), from woody canes of *Vitis vinifera* cv. Vinhão incubated at 4 °C up to 30 days. Results indicate the mean \pm SD of four independent experiments. Different letters stand for significant differences ($P \leq 0.05$). ND, not detected.

3.3. Low temperatures promote a transcriptional modification of key-genes involved in glucose and maltose metabolism

Following the observed decrease in starch content in grapevine canes incubated at 4 °C we speculated that the expression of genes involved in the transport of sugars from the plastid to the cytosol could be changed. Results showed that the expression of the plastidic maltose transporter *VvMEX* was downregulated following incubation at 4 °C, while the expression pattern of three plastidic glucose transporters did not follow a similar trend (Figure 7). In particular, a steadily increase in the expression of *VvPGT2* was observed.

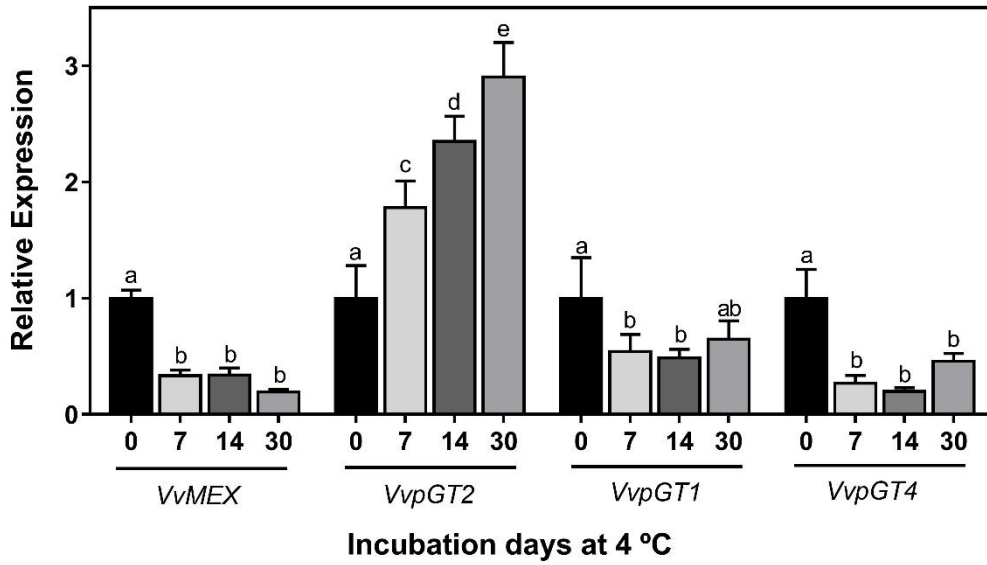


Figure 7. Expression of genes involved in maltose (*VvMEX*) and glucose (*VvpGT1*, *VvpGT2* and *VvpGT4*) plastidial transport from woody canes of *Vitis vinifera* cv. Vinhão incubated at 4 °C up to 30 days. Results indicate the mean \pm SD of four independent experiments. Different letters stand for significant differences ($P \leq 0.05$).

3.4. Soluble sugar concentration increases in response to cold

Soluble sugars from woody canes were also analyzed by HPLC (see Materials and Methods). Results showed that sucrose, glucose and fructose levels increased throughout the experiment (Figure 8), mainly glucose that changed from 8.31 ± 0.54 mg g FW⁻¹ at the time $t=0$ to 16.12 ± 0.44 mg g FW⁻¹ after 30 days of incubation at low temperature.

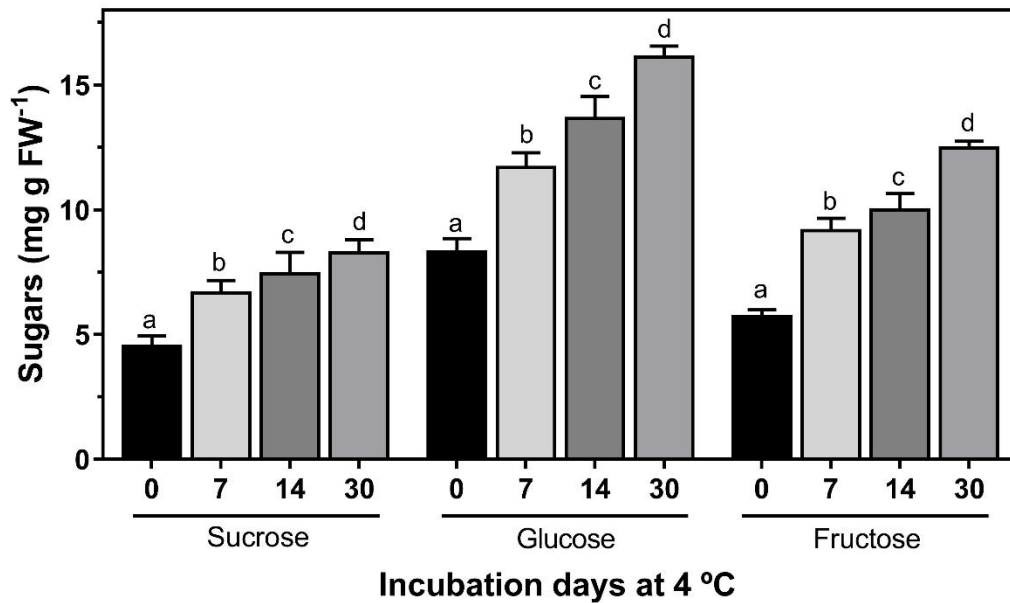


Figure 8. Concentration of major sugars (sucrose, glucose and fructose) from woody canes of *Vitis vinifera* cv. Vinhão incubated at 4 °C up to 30 days. Results indicate the mean \pm SD of four independent experiments. Different letters stand for significant differences ($P \leq 0.05$).

3.5. Cold leads to a transcriptional adjustment of key genes involved in the transport and metabolism of soluble sugars

The steady-state transcript levels of *VvSPS* (sucrose synthesis) increased after 7 days of cold treatment and then slightly decreased up to day 30. The expression of *VvSusy* (sucrose degradation) was also upregulated by cold, but 30 days after incubation the steady-state transcript levels decreased abruptly (Figure 9A).

The cold treatment downregulated the expression of the sucrose/H⁺ symporter *VvSuc27* and the transcript levels of the plastidic monosaccharide transporter *VvTMT1* also decreased, while a strong upregulation of the expression of *VvSWEET2b* was observed up to day 14. However, thirty days after the experiment the expression of *VvSWEET2b* was reduced to the basal levels observed at the time t=0 (Figure 9B).

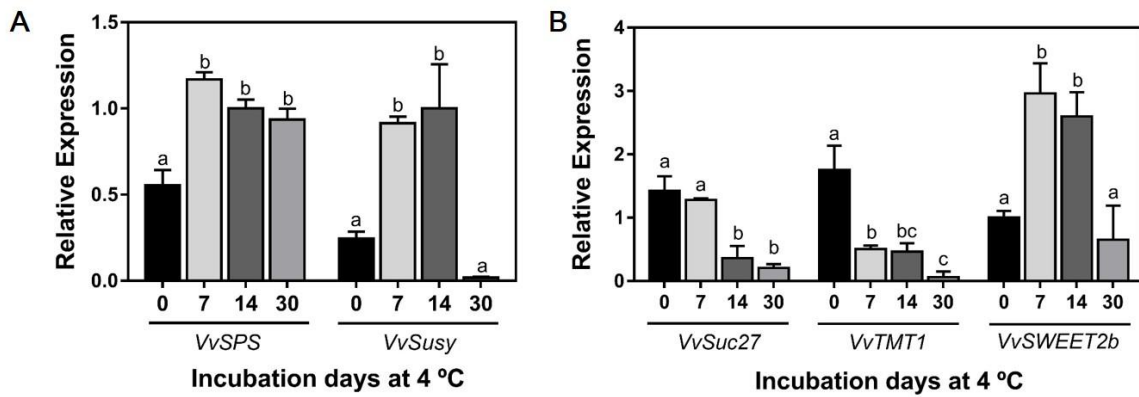


Figure 9. Expression of genes involved in sucrose synthesis and degradation, *VvSPS* and *VvSusy* accordingly (A) and transport, *VvSuc27*, *VvTMT1* and *VvSWEET2b* (B) from woody canes of *Vitis vinifera* cv. Vinhão incubated at 4 °C up to 30 days. Results indicate the mean \pm SD of four independent experiments. Different letters stand for significant differences ($P \leq 0.05$).

3.6. Raffinose family oligosaccharides concentration increase with cold treatment

Raffinose and stachyose levels in the grapevine canes were quantified by HPLC because the metabolism of raffinose has been linked to cold response. Results showed that both raffinose and stachyose levels increased during the experiment.

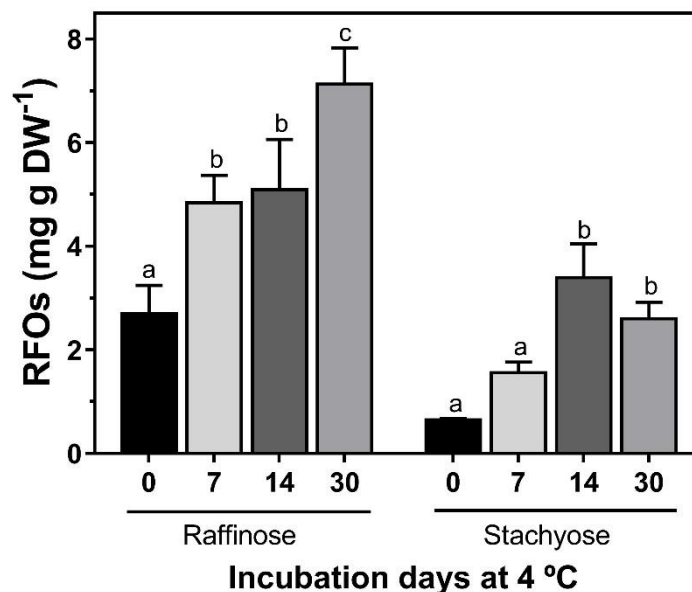


Figure 10. Concentration of oligosaccharides (raffinose and stachyose) from woody canes of *Vitis vinifera* cv. Vinhão incubated at 4 °C up to 30 days. Results indicate the mean \pm SD of four independent experiments. Different letters stand for significant differences ($P \leq 0.05$).

3.7. Cold promotes a transcriptional modification of key genes involved in galactinol and raffinose metabolism

Real Time PCR analysis was performed to determine the expression of genes coding for enzymes responsible for the synthesis of RFOs. Results showed that cold treatment strongly upregulated the expression of *VvGolS1* and *VvGolS3* (galactinol synthesis) together with *VvRafS5* (raffinose synthesis) (Figure 11).

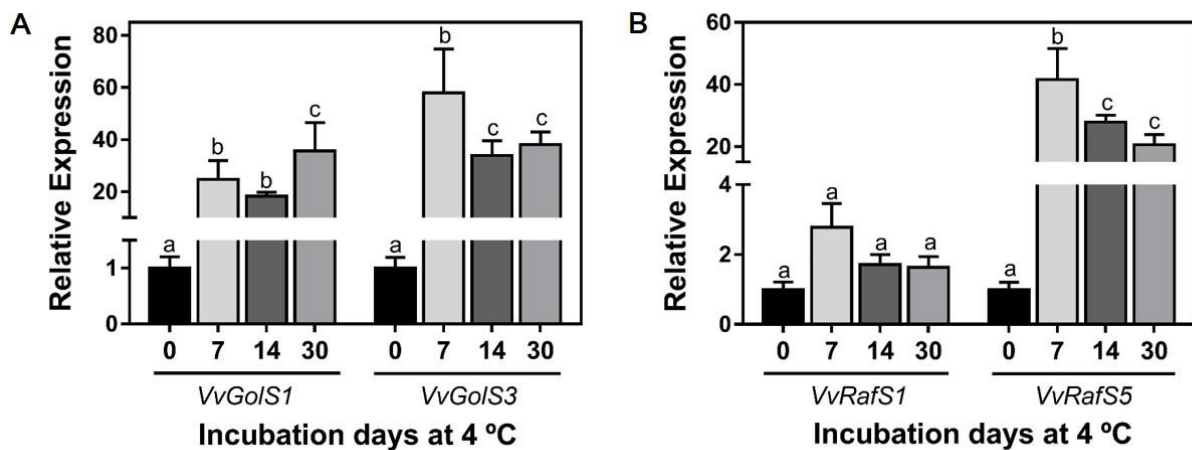


Figure 11. Expression of genes responsible for galactinol synthesis (*VvGolS1*, *VvGolS3*) (A) and raffinose synthesis (*VvRafS1*, *VvRafS5*) (B) from woody canes of *Vitis vinifera* cv. Vinhão incubated at 4 °C up to 30 days. Results indicate the mean ± SD of four independent experiments. Different letters stand for significant differences ($P \leq 0.05$).

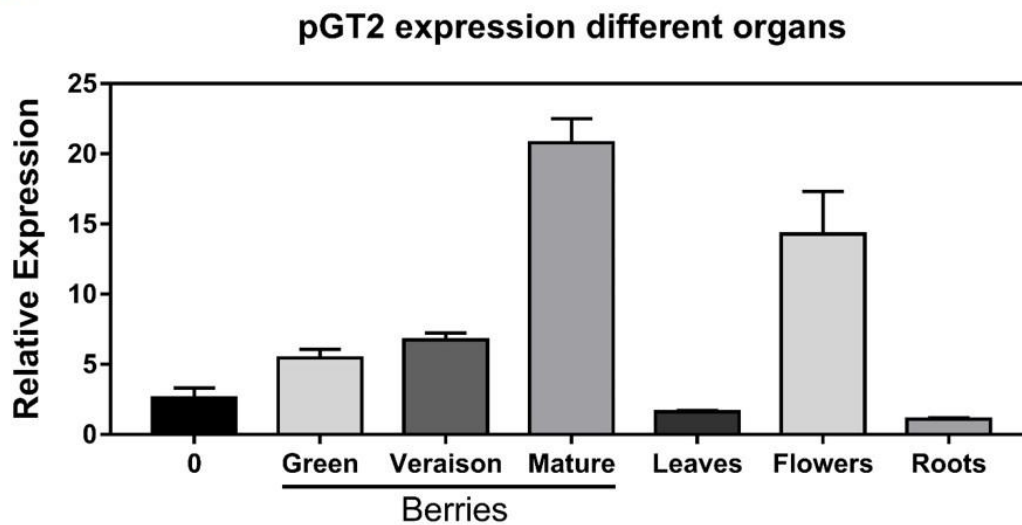
3.8. Tissue specific expression and functional characterization of the plastidic translocator *VvpGT2*

Following the above observation that *VvpGT2* was strongly upregulated during cold treatment we proceeded with the characterization of this gene in more detail. mRNA was extracted from different grapevine organs (canes, flowers and roots) and from berries at different development stages (green, *veraison* and mature), and results showed that showed that *VvpGT2* is mainly expressed in mature berries and in flowers (Figure 12A).

Results

To address the hypothesis that *VvpGT2* codes for a functional sugar transporter, the gene was heterologously expressed in the monosaccharide-defective mutant strain *EBY.VW4000*. Results of the drop-test experiments are shown in figure 12B. As can be seen, the transformed yeast was unable to grow in solid media supplemented with glucose, fructose and sucrose, suggesting that *VvpGT2* is not able to transport none of these sugars. Currently we are checking if the protein is being correctly target to the plasma membrane using GFP fusion proteins. Further transport experiments will be performed with radioactive substrate to improve the accuracy of the analysis.

A



B

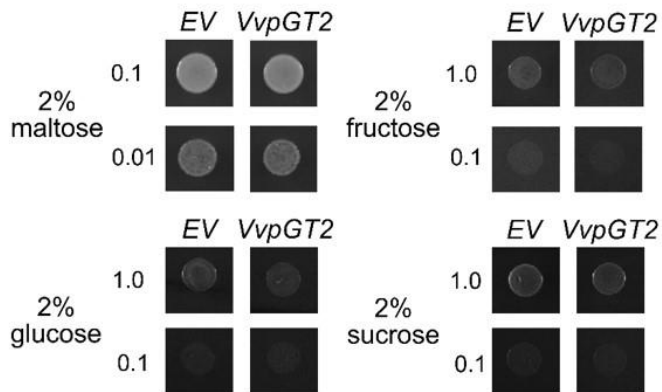


Figure 12. Expression analysis of *VvpGT2* and growth assays. Relative expression of *VvpGT2* in different *Vitis vinifera* cv. Vinhão organs (A) and growth assays in different sugars with the *Saccharomyces cerevisiae* EBY.VW4000 strain overexpressing *VvpGT2* (B). Results indicate the mean \pm SD of seven independent experiments.

4. Discussion

4. Discussion

4.1 Cold reduces storage starch in grapevine woody canes

Starch is the most widespread and abundant storage carbohydrate in plants. We depend upon starch for our nutrition, exploit its unique properties in industry, and use it as a feedstock for bioethanol production (reviewed by Zeeman et al., 2010), so it is not surprising that many studies have been performed in starch crops like in cereals. Therefore, while the mechanisms of starch mobilization during germination in the dead endosperm of cereal seeds are well described, the molecular and biochemical mechanisms involved in starch storage in the heterotrophic tissues of woody plants and its utilization in spring and winter are still puzzling. The knowledge on starch storage and mobilization in woody tissues is pivotal to understand (and to optimize) some common practices in the field that modify source–sink relationships, such as pruning and defoliation, as well to understand the mechanisms of acclimation to cold (Reviewed by Noronha et al., 2018), which is the research topic we address in the present study.

In grapevine, the majority of studies examining cold-temperature effects have been performed in leaves and berry tissues (Tattersall, 2007; Yang et al., 2012; Xin et al., 2013; Xu et al., 2014; Sun et al., 2016), thus in the present work we aimed to test the hypothesis that the response of grapevine to cold also involves modifications of the sugars stored in the woody tissues. Results clearly showed that that woody canes exposed cold for up to 30 days resulted in a clear decrease in starch content, thus supporting our hypothesis. Concordantly, this decrease was associated with the induction of α -amylase gene *VvAMY5* whose expression was only detected after the onset of the cold treatment. In spite of this, other amylases may account for the degradation of starch in response to cold because the expression of the amylase genes like *VvAMY2* and *VvBAM2* was also observed, although their expression decreased during the treatment. A previous report in *Populus* also showed a decrease in starch quantity in xylem ray cells in response to cold (Sauter and Kloth, 1987). Other studies in Poplar wood have reported an increase in the biochemical activity of starch-degrading enzymes in the period of starch-sugar conversion (Elle and Sauter, 2000).

4.2. Cold promotes the accumulation of soluble sugars in woody canes and alters sucrose metabolism

Carbohydrates work as regulators of source–sink interactions in the whole plant both under normal environmental conditions and under stress conditions (Roitsch, 1999) In the present study we observed an increase in sucrose, fructose and glucose in grapevine wood in response to cold. These changes were concomitant with a transcriptional reprogramming of genes involved in sugar metabolism and transport. Thus, the steady-state transcript levels of *VvpGT2* and *VvSWEET2b* transporters, as well as

VvSusy and *VvSPS* enzymes increased along time, while the expression of the transporters *VvTMT1* and *VvSUC27* was downregulated. Our results go in agreement with previous studies showing that carbohydrates, mainly sucrose, are involved in the response to cold (Parker, 1962; Sakai, 1966; Kandler et al., 1979; Santarius et al., 1979; Höll, 1985; Sauter and Van Cleve, 1991; Nägele et al., 2012). Glucose, fructose, sorbitol, stachyose and raffinose, can also accumulate during this process (Korn et al., 2010; Findling et al., 2014), much like we observed in the present study in grapevine wood.

Previous reports have already highlighted the pivotal role of enzymes involved in sucrose synthesis, like *Susy*, during starch metabolism in heterotrophic tissues. Thus, lower accumulation of starch in potato tubers was observed in *Susy* defective mutants (Zrenner et al., 1995), and an increased starch accumulation was observed in seed endosperm of maize overexpressing *Susy* (Li et al., 2013). In the present study we confirmed the role of *Susy* during starch degradation in grape vine wood in response to cold when its expression levels increased up to day 14.

Our results showed that the cold treatment downregulated the expression of the sucrose/H⁺ symporter *VvSuc27* and the transcript levels of the plastidic monosaccharide transporter *VvTMT1*, while the expression of the vacuolar *VvSWEET2b* increased up to day 14. In agreement, increasing number of sugar transporters like SUTs have been reported to take part in the response to abiotic stress (Gong et al., 2015; Jia et al., 2015; Cai et al., 2017; Xu et al., 2018) but further experiments are still necessary to elucidate the role of sugar transporters and sucrose metabolizing enzymes during the response of grapevine wood to cold.

4.3 *VvRafS5* is likely involved in the accumulation of raffinose and stachyose in grapevine wood in response to cold

In this study, it was found that the levels of raffinose and stachyose, detected by HPLC, increased during cold and that the transcript levels of genes putatively involved in the synthesis of raffinose and stachyose, particularly *VvRafS5*, increased several fold. In agreement, in poplar wood during late autumn and winter, the extent of starch consumption has also been reported to be closely related to increased levels of sucrose, raffinose and stachyose (Sauter and Kloth, 1987; Sauter and van Cleve, 1991). RFOs have been proposed to play multiple functions, from supply and storage of carbon to protection against abiotic stresses (Peterbuer and Richter, 2001). Multiple biophysical roles have been suggested for raffinose, including in reducing osmotic potential and cells water freezing point (Burke et al., 1976), and a structure-preserving effect at the time of protein binding (Steponkus, 1980).

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Furthermore, accumulation of galactinol and raffinose has been postulated to function as a radical scavenger thereby helping the plant to detoxify ROS that accumulate under high salinity and low temperatures (Nishizawa et al., 2008). Besides this, raffinose and stachyose, accumulate during seed development (Ooms et al., 1993; Nishizawa-Yokoi et al., 2008).

Interestingly, in *Arabidopsis thaliana* seeds, stachyose and raffinose accumulation is regulated by *AtRS4* and *AtRS5* (Gangl et al., 2015) and another study concluded that *AtRS5* is the only RafS in *Arabidopsis* responsible for stress induced raffinose formation (Gangl and Tenhaken, 2016). These results suggest that *VvRafS5* could be fundamental in the observed accumulation of raffinose in response to cold in grapevine woody tissues.

Our results also suggested that *VvGoS1* and *VvGoS3* could play a role in grapevine woody tissues response to cold by providing galactinol to fuel the RFO metabolism. The observed increase of the transcript levels of *VvSusy* (following 7 and 14 days of cold storage) that catalyzes the conversion of sucrose to fructose and UDP-glucose, with the latter being a precursor of galactinol synthesis is consistent with the proposed hypothesis. GoS genes are involved in various developmental and environmental responses. Besides being described as a signal molecule, galactinol, together with sucrose, are the substrates for raffinose synthesis. Also, the addition of galactose moieties to raffinose allows the synthesis of stachyose. The mRNA expression level of *GoS* in *Arabidopsis* was found to be induced by cold (Liu et al., 1998). Up-regulation of *AtGoS1* and *AtGoS2* in response to water and salinity stress was also reported, while *AtGoS3* is solely induced during low-temperature exposure (Taji et al., 2002). *AtGoS1* is also involved in plants response against *Botrytis cinerea* infection (Song et al., 2010). In tomato (*Lycopersicon esculentum*), dehydration caused an accumulation of LeGOLS-1 mRNA but, when under cold conditions, no alteration was observed in germinating seeds. However, both stresses induced the accumulation of LeGOLS-1 mRNA in seedling leaves (Downie et al., 2003).

As whole, our results, together with the reported studies, strongly suggested that the response of grapevine wood to cold involves the metabolism of starch towards the accumulation of compatible solutes.

4.4 What is the role of *VvPGT2* whose expression steadily increases in grapevine wood in response to cold?

The final products of starch degradation in the chloroplast during the night are mainly maltose and some glucose (Weise et al., 2004), which are exported to the cytosol by MEX (Niitylä et al., 2004) and plastidic glucose translocator pGT (Weber et al., 2000), respectively. Glucose transport across the

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chloroplast envelope was first shown by Schäfer et al. (1977), from which it was lately identified the pGT (Weber et al., 2000).

In the present study we wanted to test the hypothesis that pGT2 involved in sugar export from the chloroplast could also be involved in sugar export from the amyloplast for the synthesis of soluble in response to cold. The observed steadily increase of the transcript levels of *pGT2* in grapevine wood in response to cold strongly supported our idea. To gain further knowledge into the physiological role of *VvpGT2*, the gene was cloned and expressed in a HXT-Null *Saccharomyces cerevisiae* unable to transport glucose, but no sugar transport activity was observed when growth plate assays with glucose, sucrose and fructose were performed. Currently we are checking if the protein is being correctly target to the plasma membrane using GFP fusion proteins. Further transport experiments will be performed with radioactive substrates to improve the accuracy of the analysis and also using an *Escherichia coli* mutant without sugar transporters as an expression system.

4.5 Conclusions

Carbohydrates accumulation during autumn and winter and its mobilization during the summer is essential to support a rapid seasonal growth in the coming spring of perennial woody plants. In the present study, we found that, during cold storage, there is a decrease in reserve starch concomitant with an accumulation of sugars (sucrose, glucose and fructose) and RFOs (raffinose and stachyose), which could be related to the expression of several key-genes, like *VvpGT2*, *VvGoS1*, *VvGoS3* and *VvRafS5*. These observations supported our main hypothesis that the response of grapevine to cold involves modifications of starch metabolism together with the reprogramming of the expression of key genes involved in sugar metabolism towards the the accumulation of compatible solutes.

Additional studies are already in progress to consolidate some conclusions of this thesis. For instance, as reported above, although we were unable to demonstrate sugar transport mediated by *VvpGT2* we will confirm if the protein is, indeed, correctly targeted to the plasma membrane of the yeast mutant using GFP-tagged proteins. We will also use more accurate strategies to measure sugar uptake using radioactive sugars. In the case these strategies fail we will test a different expression system, such as bacteria. Another study with interest is the cloning and functional characterization of *VvRafS5* because few raffinose synthase genes have been studied in detail. Our experimental approach can also be adjusted to study the effect of other environmental constrains that affect grapevine in the context of ongoing climate changes, like heat waves, which may alter winter carbohydrate reserves and, thus, the bud-burst in the following spring.

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