

## SWITCH GENES AS A KEY TO UNDERSTAND THE GRAPEVINE RIPENING DISORDER BERRY SHRIVEL?

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### Abstract:

**Context and purpose of the study** - The ripening of grapevine berries encompasses complex morphological and physiological processes, especially at veraison. Berry shrivel (BS) is a ripening physiological disorder affecting grape berries with visible symptoms appearing short after veraison. The main symptoms of BS are a strong reduction in sugar accumulation, inhibited anthocyanin biosynthesis and high pH values. The most popular red grape cultivar in Austria "Blauer Zweigelt" (*Vitis vinifera* L.) is specifically prone to develop the BS ripening disorder and up to date a no specific cause or causes could be identified. Recently omics approaches have identified and characterized key processes during grapevine ripening. Among them a small subset of genes, called SWITCH, have been described as markers for the onset of the ripening process in fruits. The peculiarity of a switch gene is to be expressed in a low level during the immature/green phase of development, to switch on at the onset of ripening and being significantly induced and highly expressed during the mature/ripening phase.

**Material and methods** - In this study, for the first time a transcriptomic analysis was undertaken to understand the metabolic modifications induced by the disorder. Different stages of berry development were considered including pre- and symptomatic berries. Samples selected for analyses were collected at 30, 44, 51, 58, 65, and 72 DAA. 50% veraison occurred approximately at 55 DAA.

**Results** - Different stages of berry development were considered including pre- and symptomatic berries. The total number of differentially expressed genes (DEG) between the two conditions was 3122. The number of DEG in the three pre-veraison samples was 0, 1, and 0; while the number of DEG modulated by BS in post-veraison was 297 (75 up-regulated, 222 down-regulated) at 58 DAA, 1489 (955 up-regulated, 534 down-regulated) at 65 DAA and 2452 (1415 up-regulated, 1036 down-regulated) at 72 DAA. During this key transition (58 DAA at veraison) we could identify 297 DEG. Most of them (75%) were down-regulated in BS. Among the 190 grapevine switch genes, at 58 DAA we identified 67 switch genes differentially expressed; all of them were down-regulated in BS samples. Our results showed no metabolic alterations in pre-symptomatic and pre-veraison samples. Interestingly, at veraison, with still not visible symptoms appearing on the berry, a subset of switch genes previously suggested as master regulators of the ripening onset in grape berries, were strongly lower expressed in BS. Later during the ripening phase and with visible symptoms of the disorder, more than 3000 genes were differentially expressed. Most of them with significant lower expression during ripening belonged to the flavonoid pathway, and others were involved in the sugar metabolism. In conclusion, these results highlight a pivotal role of the switch genes in grapevine ripening, as well as their possible contribution to induce the ripening disorder berry shrivel, although it remains unclear whether this is part of the cause or consequences of the BS disorder.

**Keywords:** grapevine ripening, Berry Shrivel, SWITCH genes, physiological disorders

### 1. Introduction.

# To Switch or not: is that the question for berry shriveling ripening disorder?



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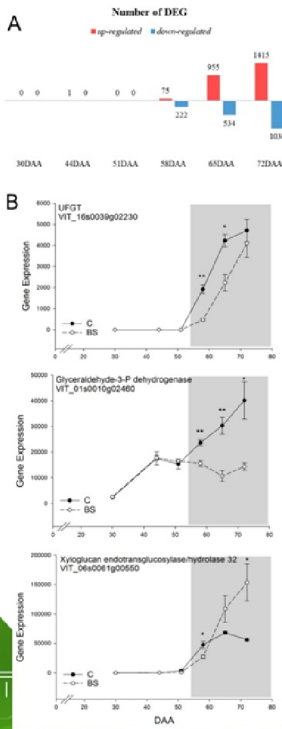
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## Introduction

The ripening of grapevine berries encompasses complex morphological and physiological processes, especially at veraison. Berry shrivel (BS) is a ripening physiological disorder affecting grape berries with visible symptoms appearing short after veraison. Main symptoms are: strong reduction in sugar accumulation, inhibited anthocyanin biosynthesis and high pH values. The red grape cultivar "Blauer Zweigelt" (*Vitis vinifera* L.) is specifically prone to develop the BS ripening disorder and up to date no specific cause or causes could be identified. Recently omics approaches have identified and characterized key processes during grapevine ripening. Among them a small subset of genes, called SWITCH, have been described as markers for the onset of the ripening process in fruits.

## Objectives

- Identify key processes affected in BS berries by a transcriptomic approach
- Identify the time window of BS induction



## Key results

- ❖ No metabolic alterations in the berry transcriptome and in the metabolite content was observed in pre-symptomatic and pre-veraison samples (Fig. 1A)
- ❖ Total number of DEG was 3122, 2455 higher expressed, 1792 lower expressed in BS berries
- ❖ SWITCH genes suggested as master regulators of the onset of ripening are strongly lower expressed as veraison 58 DAA (Fig. 2); in total 67 sign. reduced of 190
- ❖ Metabolic processes affected e.g.: secondary metabolism as UDP glucose:flavonoid 3-O-glucosyltransferase (VviUFGT); carbohydrate metabolism as Glyceraldehyde 3-P-dehydrogenase or cell wall metabolism as endotransglucosylase/hydrolase (VviXTH32)
- ❖ Glycolysis, TCA cycle and polyphenol pathway are strongly impaired in BS berries

## Conclusions

- ❖ No changes before veraison
- ❖ SWITCH genes as possible key of BS induction

Fig.1: (A) number of DEG in our RNASeq analyses; (B) time course of three selected genes as logFC

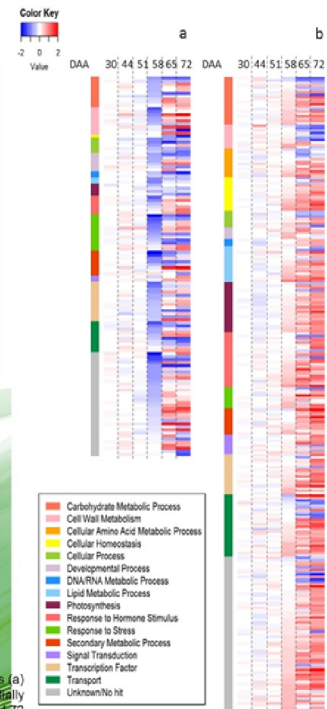


Fig.2: Complete list of Switch Genes (a) and Neighbor Gene (b) differentially expressed at 30, 44, 51, 58, 65 and 72 DAA

## Materials and Methods

a transcriptomic analysis was undertaken by applying RNASeq. Different stages of berry development were considered including pre- and symptomatic berries. Samples selected for analyses were collected at 30, 44, 51, 58, 65, and 72 DAA. 50% veraison occurred approximately at 55 DAA. 3 biological repeats were used for each sampling timepoint and tissue.

## Reference

Savoi S, Herrera JC, Forneck A, Griesser M (2019) Transcriptomics of the grape berry shrivel ripening disorder. *Plant Molecular Biology*

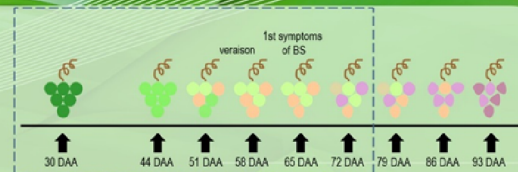


Fig.3: Scheme of the sampling timepoints 2013, pre-veraison till ripening and pre-symptomatic till shrinking berries; the first 6 sampling dates were used for RNASeq.