

# Tackling Acrylamide in Canadian Wheat Bakery Products

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## Introduction



- Monitored by WHO & European Commission
- Benchmark levels set

- Mainly Caused by wheat asparagine (ASN)

### Gene editing to reduce asparagine

1. Identifying genes related to ASN
2. Knocking down suspect genes
3. Develop low asparagine cultivars

## Objective

To understand which genes are involved in accumulation of ASN in Canadian commercial wheat cultivars

## Materials & Methods

Four commercial wheat cultivars (AAC Brandon, BW5011, Glenn, Prosper) were grown at two MB locations (2020) under 90 lb of Nitrogen per acre.

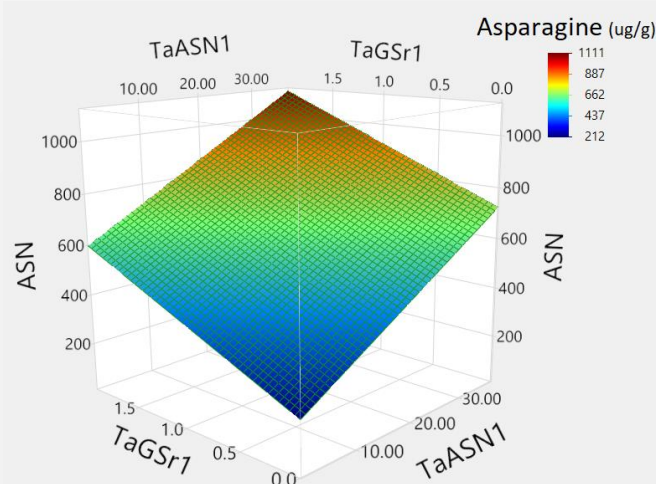
Whole wheat flour of mature seeds was analyzed for ASN level using an enzymatic kit and UV-Vis Spectrometry.

Seeds at 14 & 21 days post anthesis (dpa) were used for gene expression studies. Expression patterns of 10 genes from *ASN synthetase*, *glutamine synthetase* & *asparaginase* gene families were studied using RT-qPCR.

## Results

**Table 1.** Expression levels of genes in studied cultivars at 14 and 21 dpa

Cultivar	dpa	Relative Expression		
		TaASN1	TaASP2	TaGSR1
Brandon	14	7.02	0.59	1.16
	21	26.1	0.06	0.27
BW5011	14	4.79	1.20	1.90
	21	19.8	0.11	0.58
Glenn	14	4.83	0.91	0.59
	21	19.4	0.12	0.48
Prosper	14	1.25	0.86	0.58
	21	6.89	0.29	0.42



**Figure 1.** Relationship between TaASN1, TaGSR1 and wheat ASN concentration

- Significant differences in the expression levels among cultivars (Table 1)
- No effect of location on expression levels of almost all genes
- Significant change in expression levels of genes from 14 dpa to 21 dpa (Table 1)
- Strong correlations between ASN and expression levels of asparagine synthetase and glutamine synthetase genes (Figure 1)

## Highlights

- Significant differences in expression levels among Canadian varieties for asparagine and glutamine synthetase genes
- Genes targeted for development of low ASN cultivars through gene-editing identified

## Reference

Curtis et al. (2020). Contrasting gene expression patterns in grain of high and low asparagine wheat genotypes in response to sulphur supply. *Ann Appl Biol.* 2020;1–17.

## Acknowledgement



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