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Protein chemistry of dry bean

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Canada

Genetically related lines with storage protein deficiency

SANILAC × G12882

↓

SARC1 (Arl)

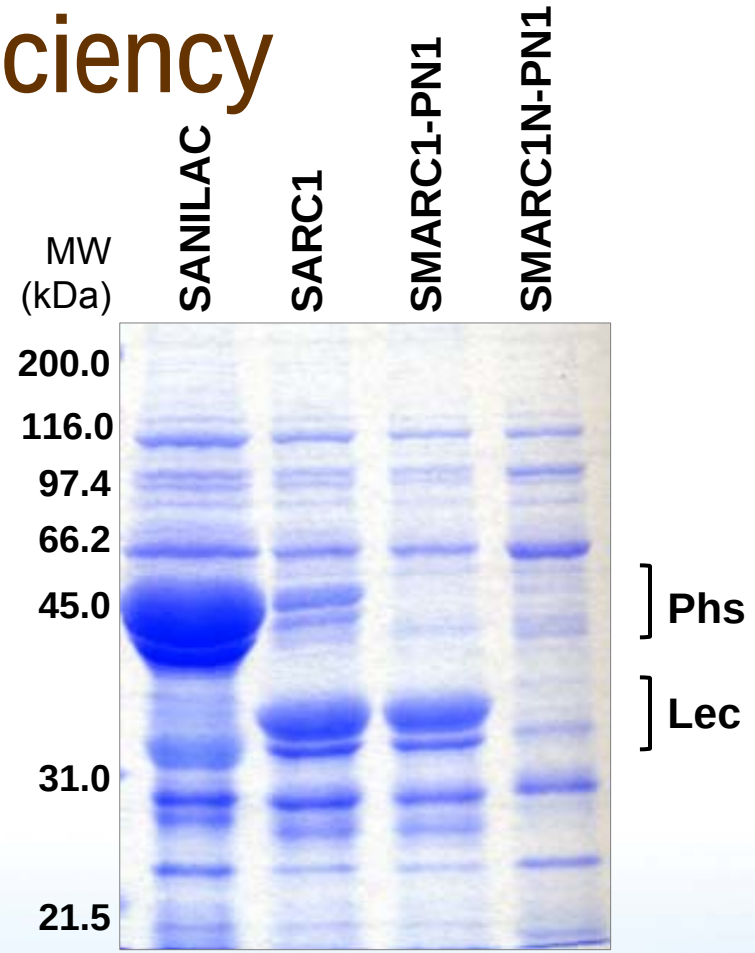
↓ × ***P. coccineus***

SMARC1-PN1 (phas$^-$)

↓ × **Great Northern 1140**

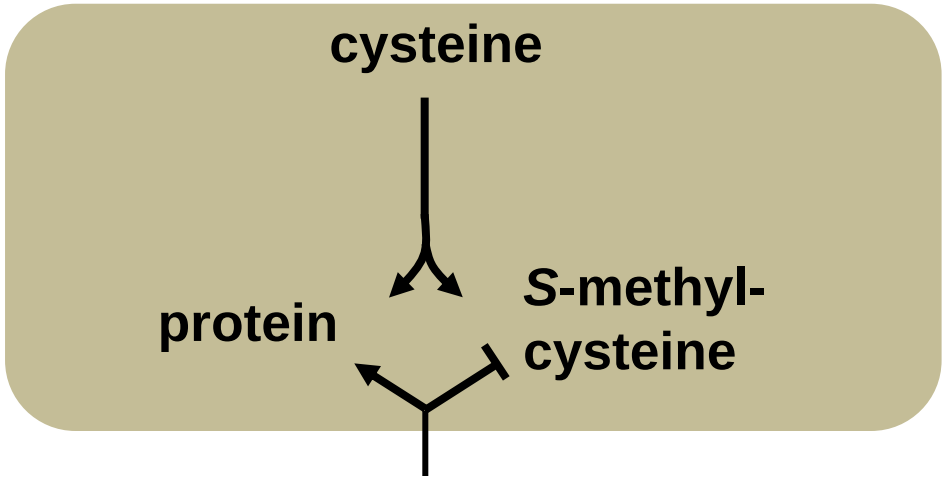
SMARC1N-PN1 (phas$^-$, lec$^-$, arl$^-$)

(Osborn et al. 2003 Crop Sci 43, 1570)



(Taylor et al. 2008 J Agric Food Chem 56, 5647)

Genetically related lines with storage protein deficiency



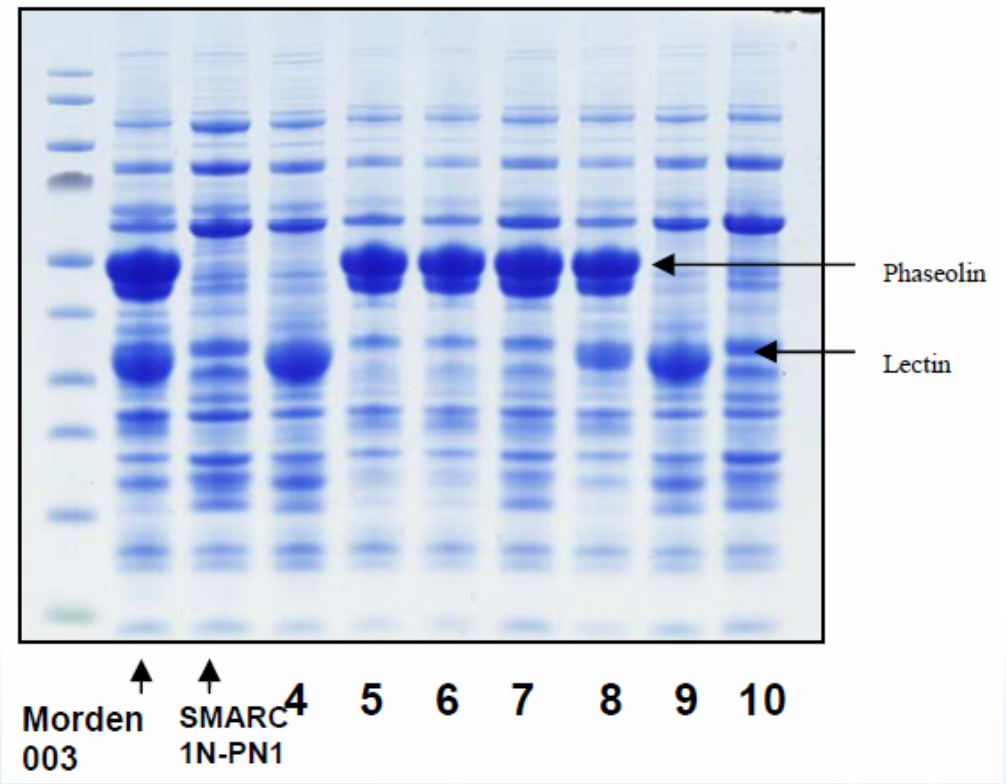
Lack of phaseolin, phytohemagglutinin and arcelin

- FAO requirement scoring pattern (2007): Met + Cys = 22-28 mg g^{-1} protein:
  - From 18.9 mg g^{-1} (SARC1) to 26.7 mg g^{-1} (SMARC1N-PN1) (+ 42%)

Genetics and breeding

- Newly approved project “Genetic improvement of protein quality in edible beans with adaptation to Manitoba”. Manitoba Pulse Growers’ Association, PI Anfu Hou, co-PI Robert Conner, Morden Research Station, 2012-2015
- Recombinant inbred population derived from Morden003 × SMARC1N-PN1

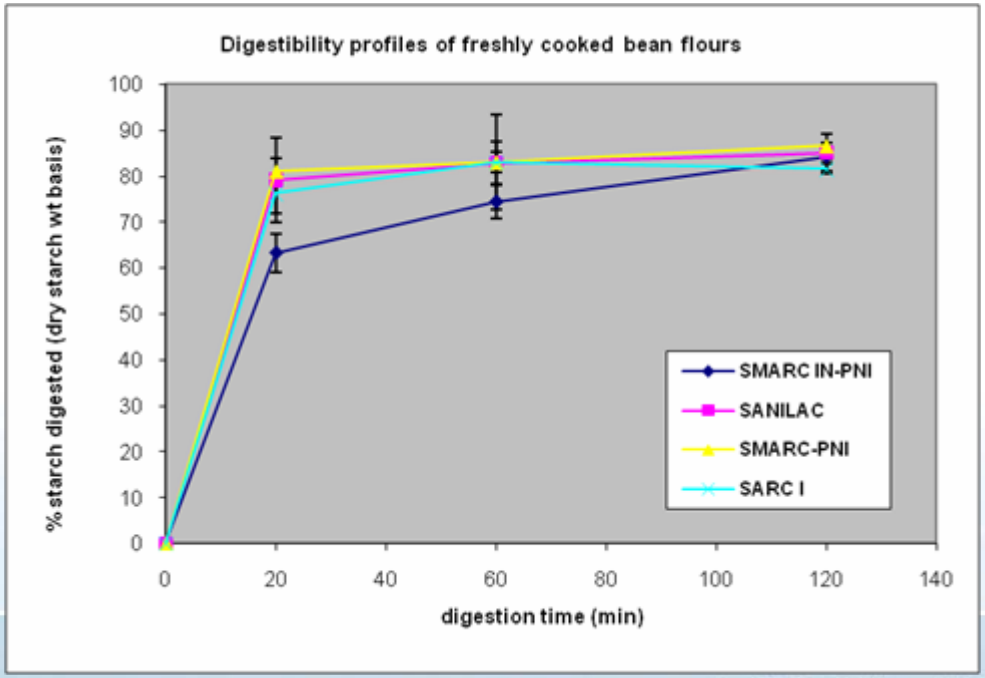
Genetics and breeding



- Protein composition of 185 lines determined (Aga Pajak)
- Analyze relationships between protein composition, concentration of essential sulphur amino acids and agronomic traits

Starch

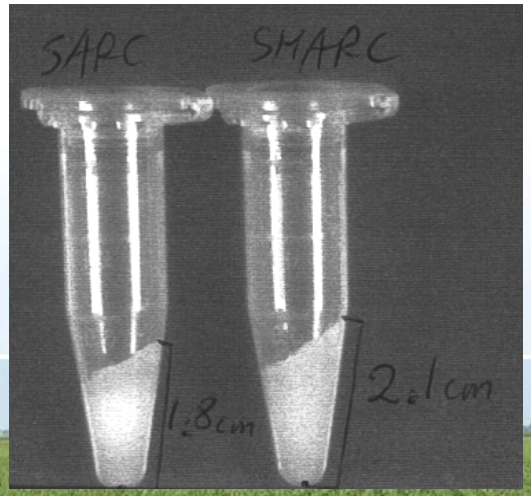
- SMARC1N-PN1 has increased concentration of slowly digestible starch in cooked flour – Qiang Liu, Guelph Food Research Centre



- Slowly digestible starch: 21% in SMARC1N-PN1 vs. 6% in other genotypes

Starch and Fiber

- Increased swelling of purified starch after gelatinization (Aga Pajak)
- Increased transcript expression of pectin acetylesterase by 15-fold (Dengqun Liao) – may alter digestibility and swelling (viscous fiber)

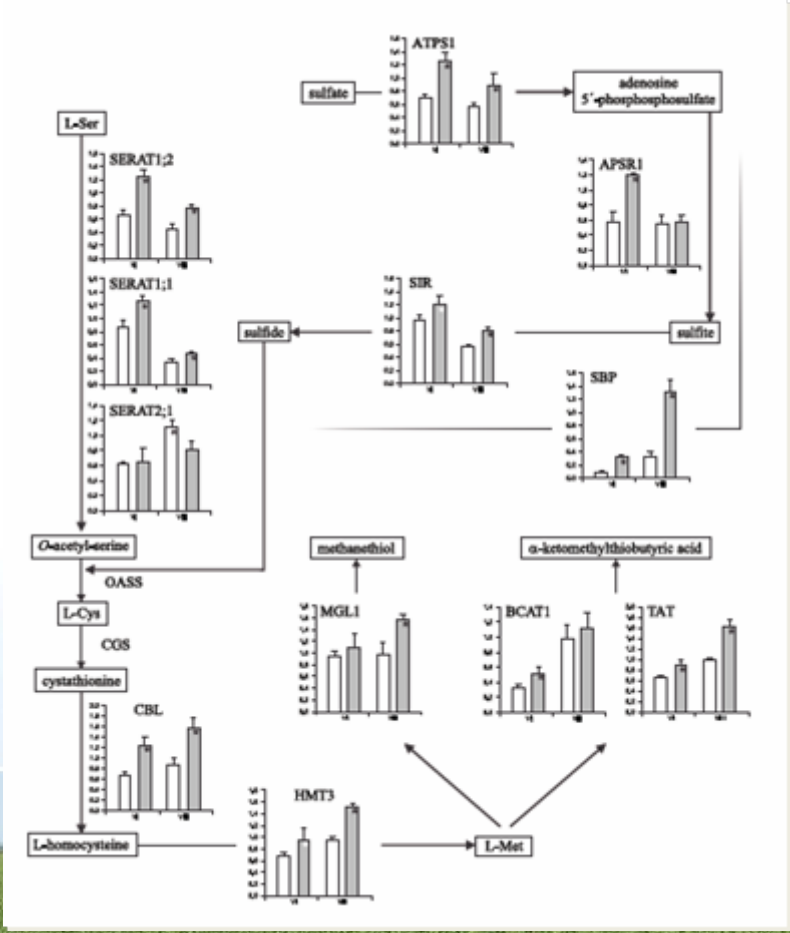


Genomics

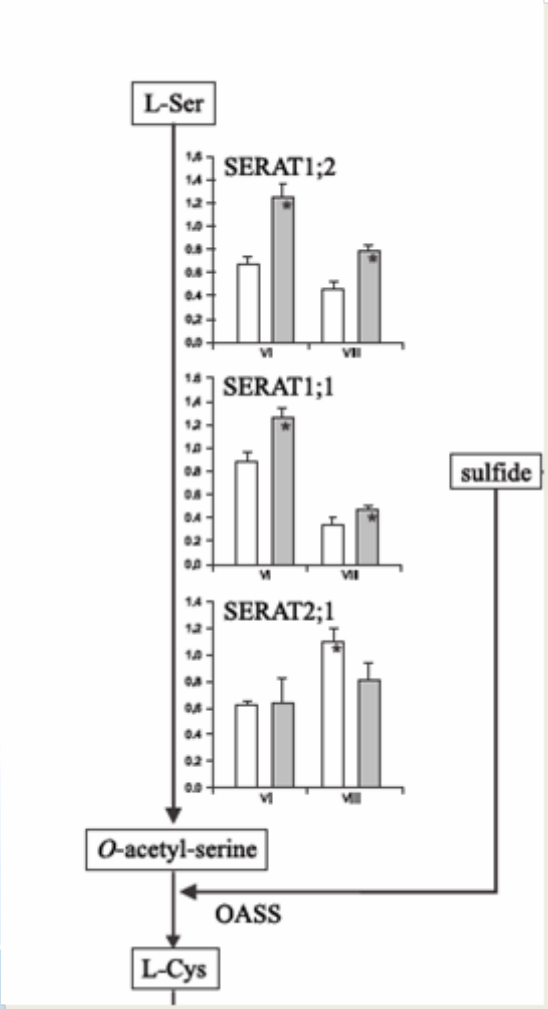
- Ontario Research Fund project led by Dr. Peter Pauls – Sudhakar Pandurangan
  - Genome sequencing of Sanilac, SARC1, SMARC1-PN1 and SMARC1N-PN1: nature of mutations at phaseolin and lectin loci?
  - Developed PCR genotyping assays for 7 different lectins genes and α-phaseolin
  - Models developed to explain origin and nature of variability in lectin and phaseolin genes at different loci

Genomics

- AAFC Crop Genomics Initiative project – Transcript profiling of sulphur amino acid metabolism, Dr. Dengqun Liao



Opposite regulation of cysteine and *S*-methyl-cysteine



Cytosol

O-acetylserine + sulphide → cysteine

Plastid

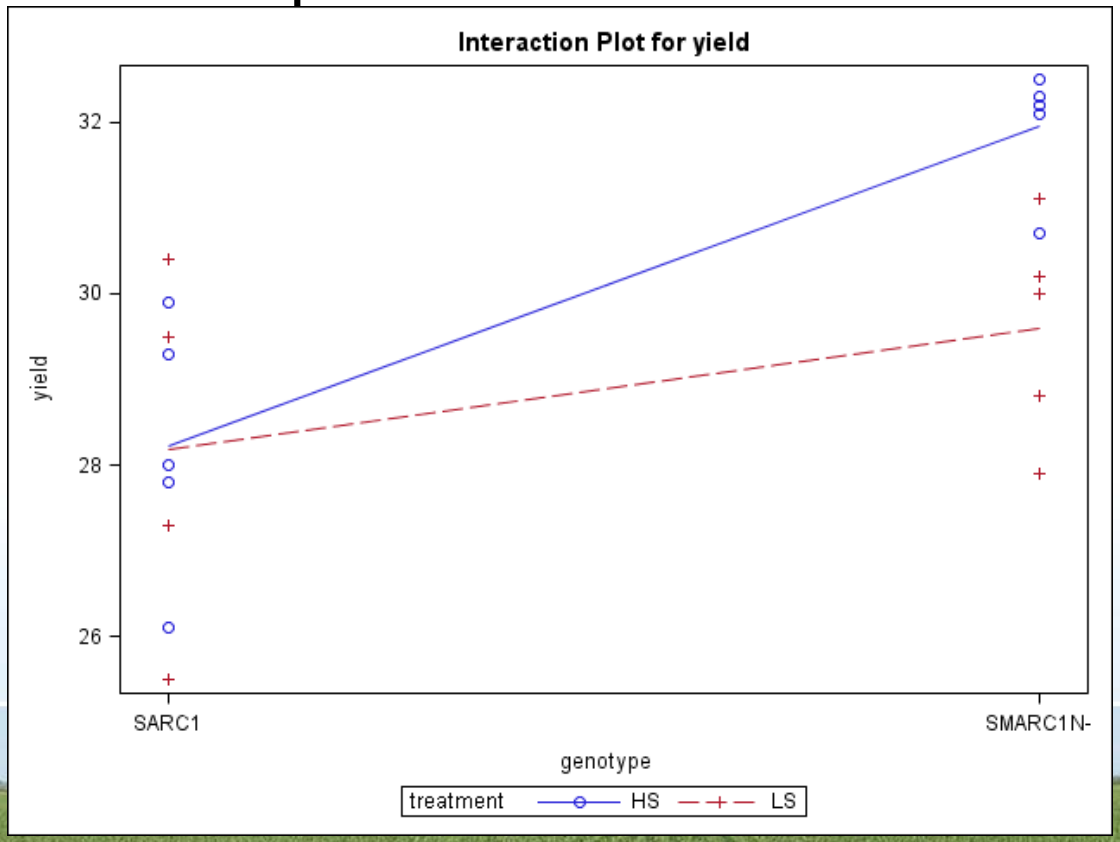
O-acetylserine + CH_3SH → *S*-methyl-cysteine

Transcript profiles - *Phaseolus vulgaris* and *Vigna mungo*

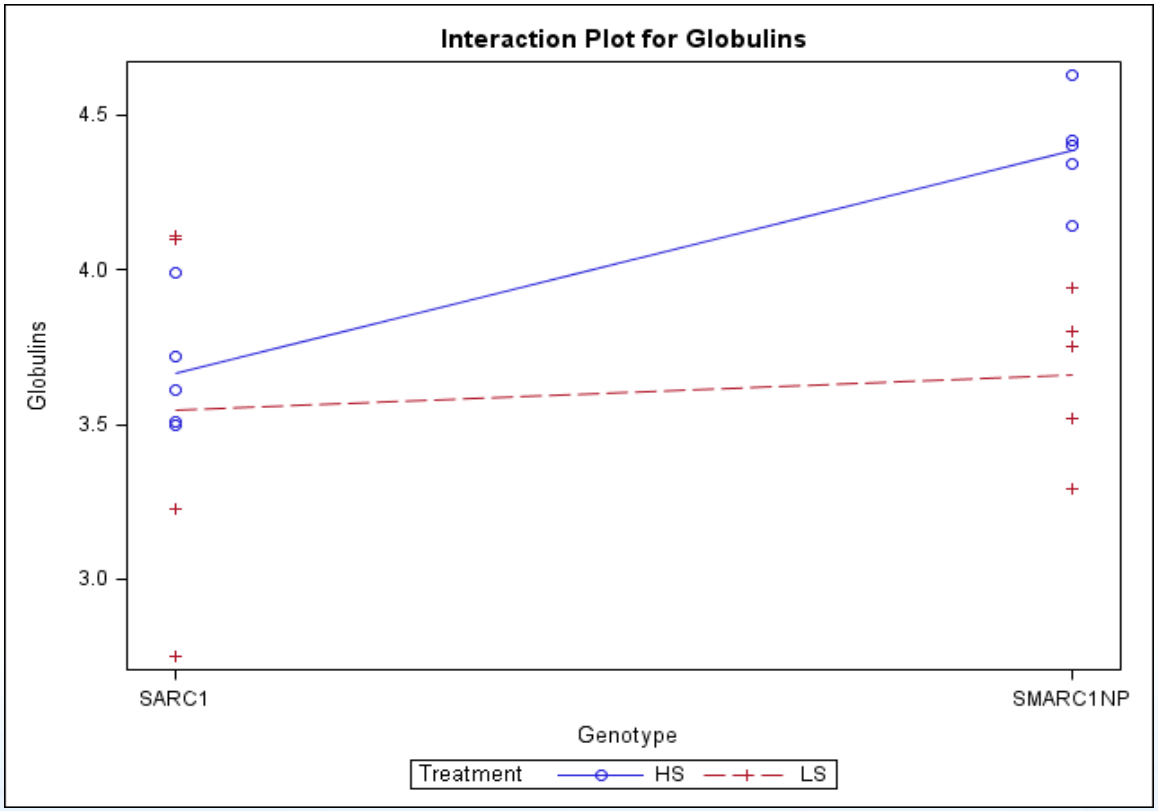
	P. vulgaris	*V. mungo*
S-Methyl-cysteine	Yes	No
Cytosolic serine acetyltransferases	68	13
Plastidic serine acetyltransferase	54	33
Plastidic *O*-acetylserine sulhydrylase	214	22

Response of SARC1 and SMARC1N-PN1 to sulphur nutrition – yield (Sudhakar Pandurangan)

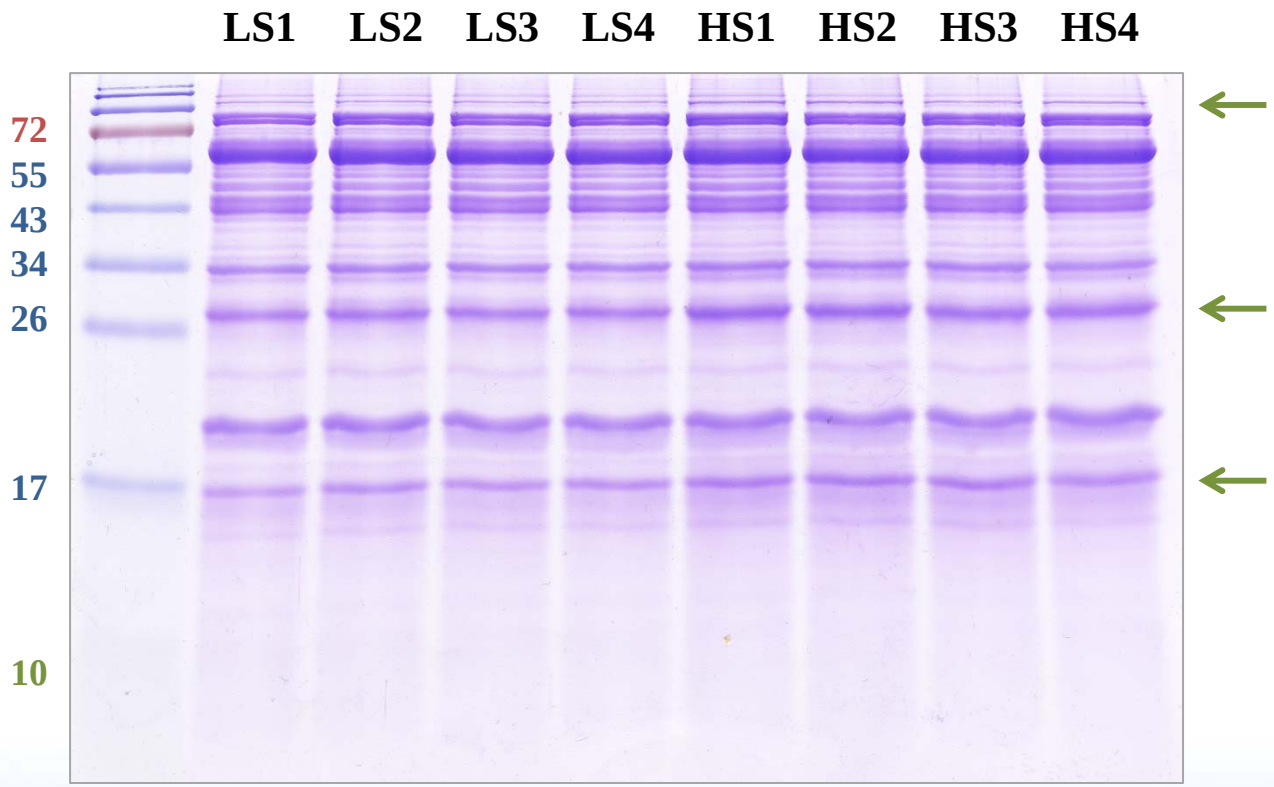
- Sulphur, sulphate, cysteine, and *S*-methyl-cysteine concentration respond to the treatment



Sulfur nutrition – globulin concentration



Globulin profile – SMARC1N-PN1



- Sulfur trial to be performed under field conditions at Morden Research Station

Summary

- Genetic analysis of protein quality improvement – breeding
- Analyzing different properties of starch, possibly pectin (viscous fibre)
- Genomic analysis of storage protein deficient lines
- Functional genomic discovery of sulphur amino acid regulation, biosynthesis of *S*-methyl-cysteine
- Performance of line with high cysteine and methionine concentration under sulphur deficiency

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Thank you!

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