
IDENTIFICATION AND FUNCTIONAL CHARACTERIZATION OF THE PALE YELLOW GENE IN TOBACCO

GRUNDMANN L., PRAMOD S., ADAMS A., FREDERICK J., KAENEL A., NOLL G., XU D., PRUEFER D. and LUSSO M.

The Pale Yellow Trait

- ✓ Found in accession TI1372
 - accelerated chlorophyll breakdown¹
- ✓ trait noticeable usually when plants flower and after topping¹
- ✓ introduced into several dark lines
- ✓ traditional breeding using phenotypic selection²
 - detached leaf ethephon treatment



¹ Chaplin James F.; 1969; *Inheritance and Possible Use of Pale Yellow Character in Tobacco 1*; Crop Science; 9 (2) p. 169

² Adapted from the LC Protocol;
<https://www.uky.edu/Ag/Tobacco/Pdf/LC-Protocol.pdf>

The Pale Yellow Trait – Pros and Cons

➤ Pros

- reduced curing time
- improved overall quality
- balance genetic impact affecting senescence and quality

➤ Cons

- reduced field harvest time window

Guidelines for Fire Curing Dark Tobacco*



Yellowing

- Ventilation as needed
- None or low heat
- Temp. not to exceed 100°F (37°C)
- 5 – 8 days

Color Setting

- Little or no ventilation
- Temp 100°F-115°F (37°C - 46°C)
- 7 – 14 days

Stem Drying

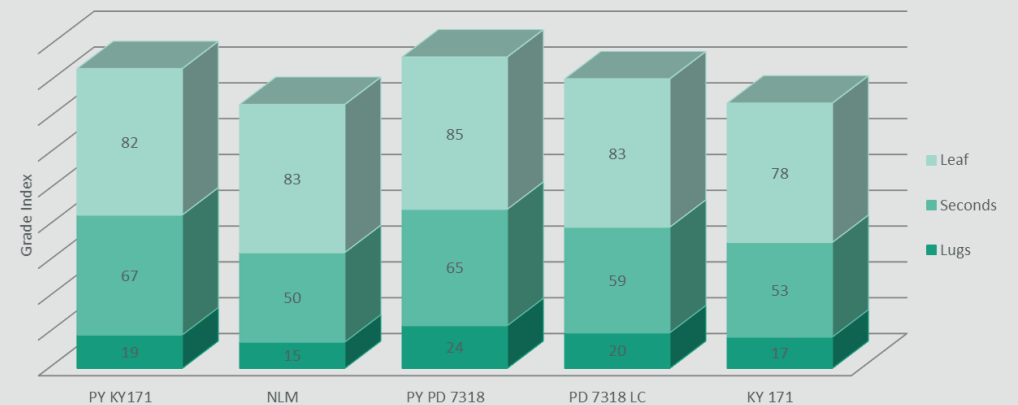
- Full ventilation
- Temp not to exceed 130°F (54°C)
- 4 – 8 days

Finishing

- No ventilation
- Temp not to exceed 120°F (48°C)
- 10 – 14 days

*Bailey, A., 2006. Harvesting, Curing, and Preparing Dark Fire-Cured Tobacco for Market. University of Kentucky – College of Agriculture, AGR152.

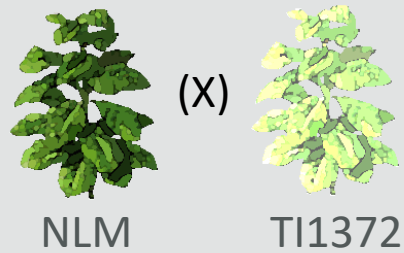
Grade Index (GI) Average of Two Locations in 2009: Blackstone, VA and Princeton, KY



Lusso M., Hayes A., Lion K., Davis G., Hart F., Morris J., 2014; *Methods of Reducing Tobacco-Specific Nitrosamines (TSNAs) And/Or Improving Leaf Quality in Tobacco*; US 2014/0076339 A1

Mapping the Pale Yellow Locus

F2 mapping population was grown in 2018



more information
https://www.coresta.org/sites/default/files/abstracts/2019_AP35_PramodAdams.pdf

all individuals were phenotyped by
a) visual observation at 4 wpt
b) ethephon screening of leaves at flowering



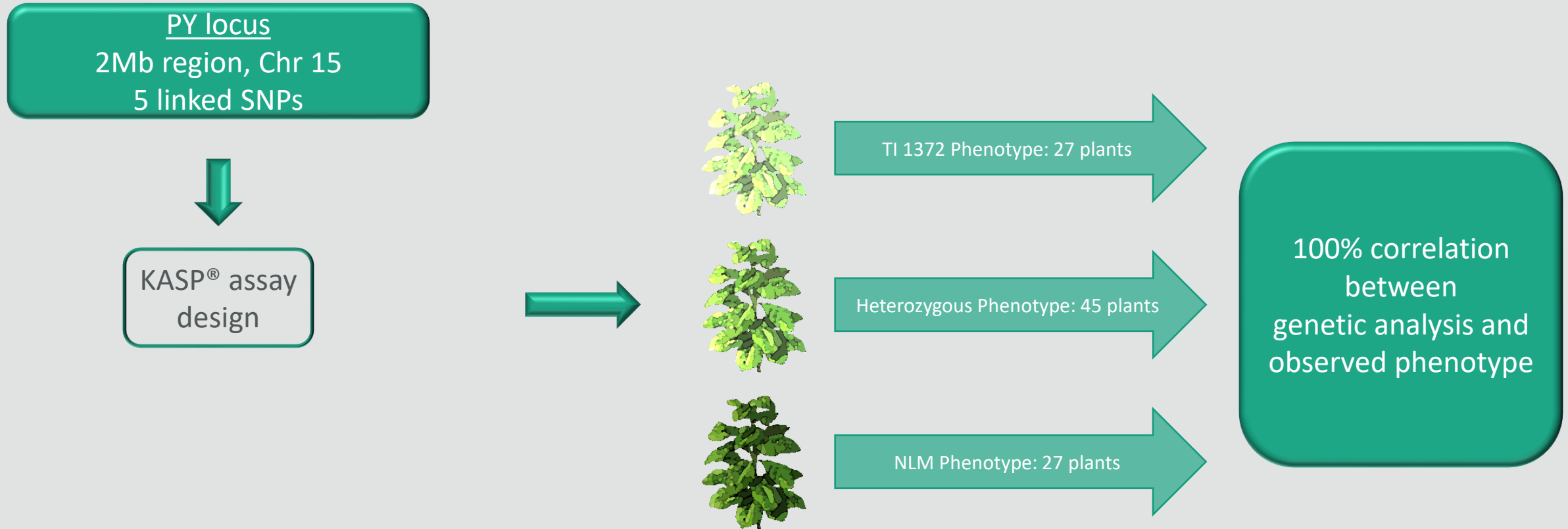
PY locus
2Mb region, Chr 15
5 linked SNPs

93 F2 individuals and parents genotyped on the ~178K SNP tobacco Axiom array



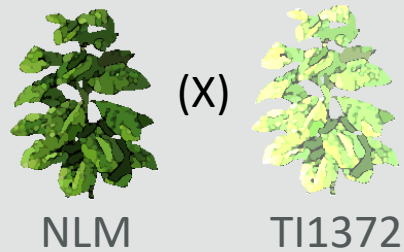
F2: (NLMxTI1372)xF2
wpt: weeks post topping
SNP: Single Nucleotide Polymorphism

QTL Analysis – Phenotypic Evaluation versus Genetic Analysis



Mapping the Pale Yellow Locus and QTL analysis

F2 mapping population was grown in 2018

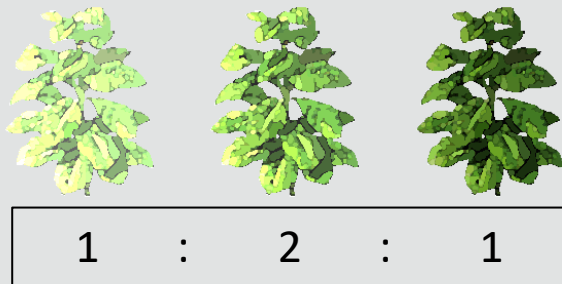


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PY locus
2Mb region, Chr 15
5 linked SNPs

58 genes in QTL

RNAseq

5 candidate genes

F2: (NLMxTI1372)xF2
wpt: weeks post topping
SNP: Single Nucleotide Polymorphism
QTL: Quantitative Trait Locus

PY: Pale Yellow

Verification of Identified Candidate Genes in (NLMxTI1372)xF2

- by quantitative real-time PCR
 - relative to NLM untopped (UT)

- g58899 expression is drastically reduced in TI1372 and F2 plants genotyped as homozygous for Pale Yellow (PY)



Characterization of g58899 overexpression lines – T₀



L3



L9

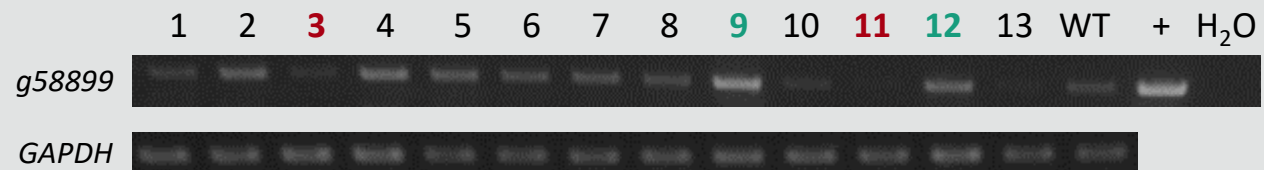


L11



L12

CaMV 35S-P::g58899

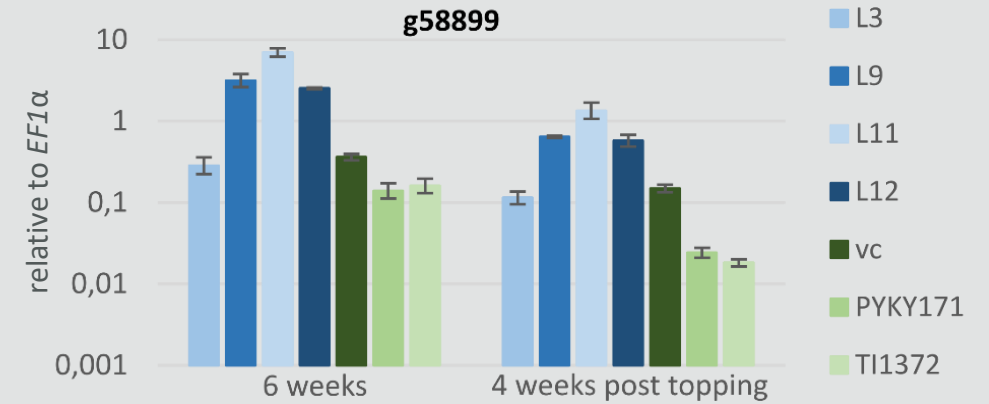


Characterization of g58899 overexpression lines – T₁



pictures taken 4 weeks post topping

➤ gene expression in medial leaves

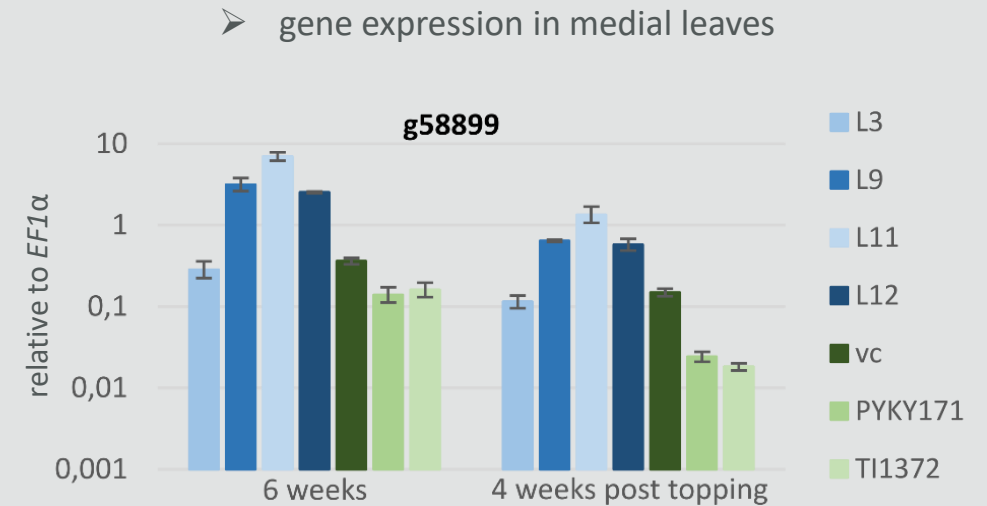
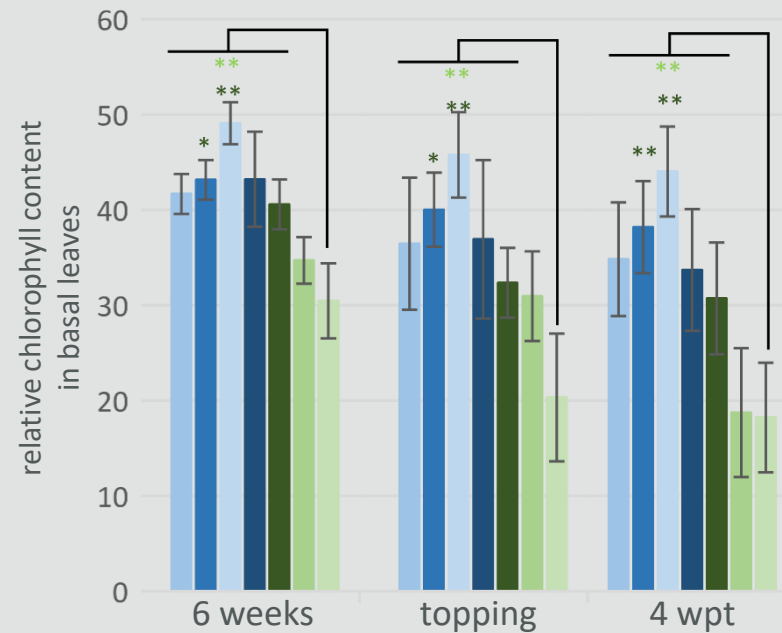


Characterization of g58899 overexpression lines – T₁

- leaves of transgenic lines stay green



pictures taken 4 weeks post topping



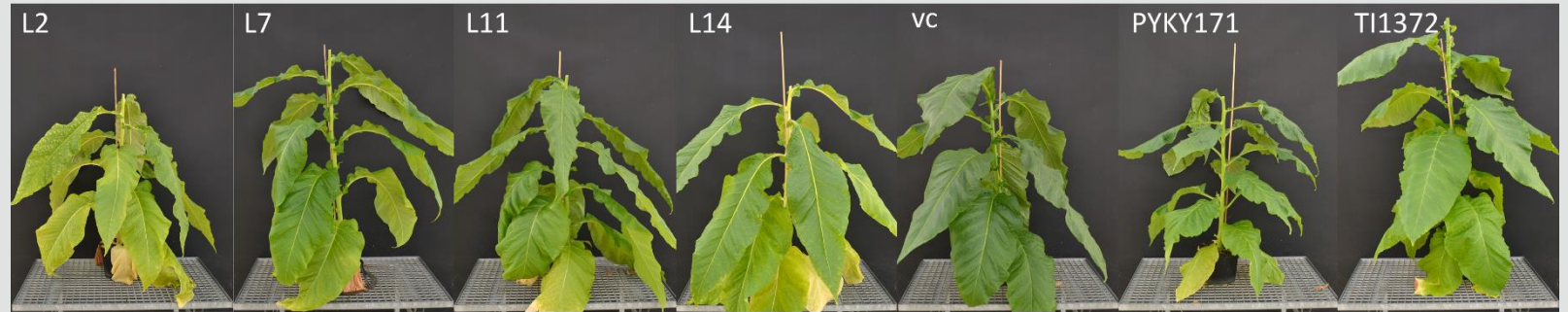
Characterization of g58899 RNAi lines – T₀

- pale yellow and whitish leaves even in tissue culture



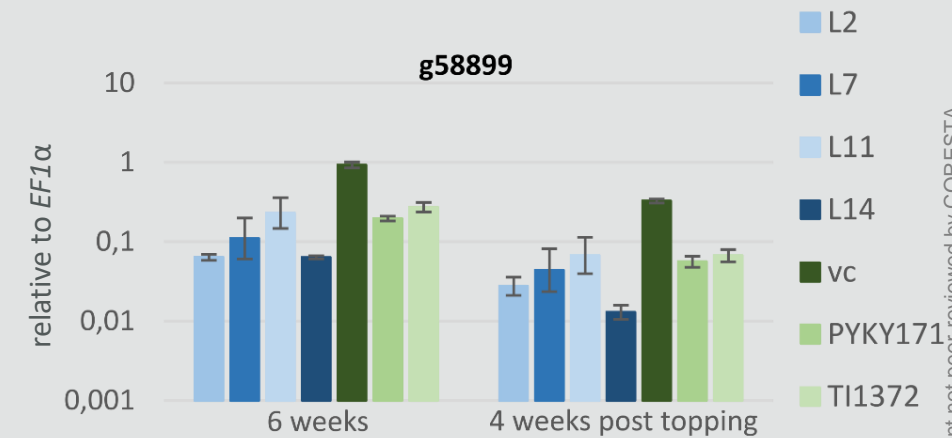
Characterization of g58899 RNAi lines – T₁

- pale yellow and whitish leaves even in tissue culture



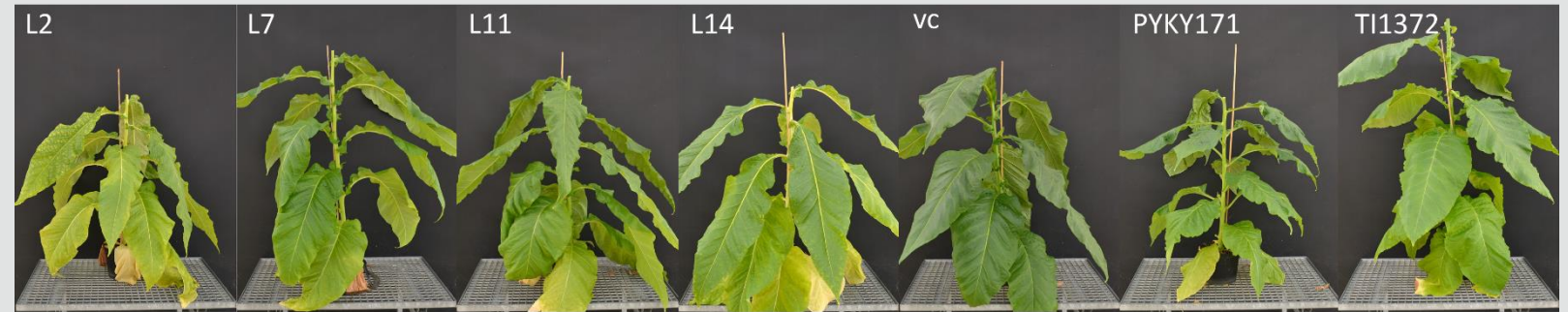
pictures taken 4 weeks post topping

- gene expression in medial leaves

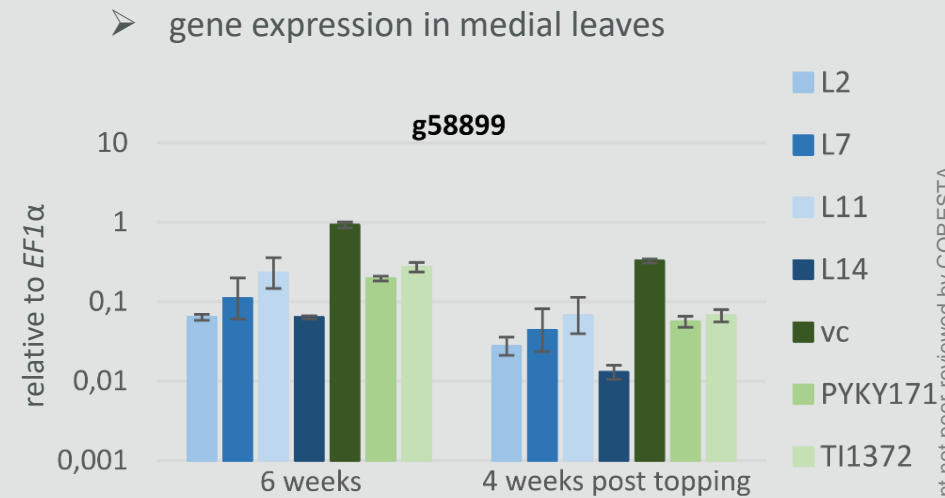
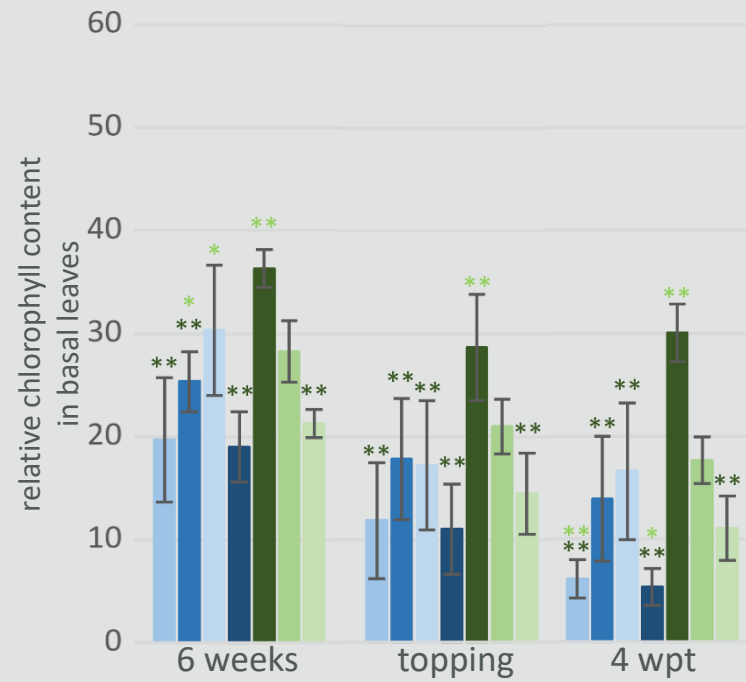


Characterization of g58899 RNAi lines – T₁

- pale yellow and whitish leaves even in tissue culture
- chlorophyll content is reduced

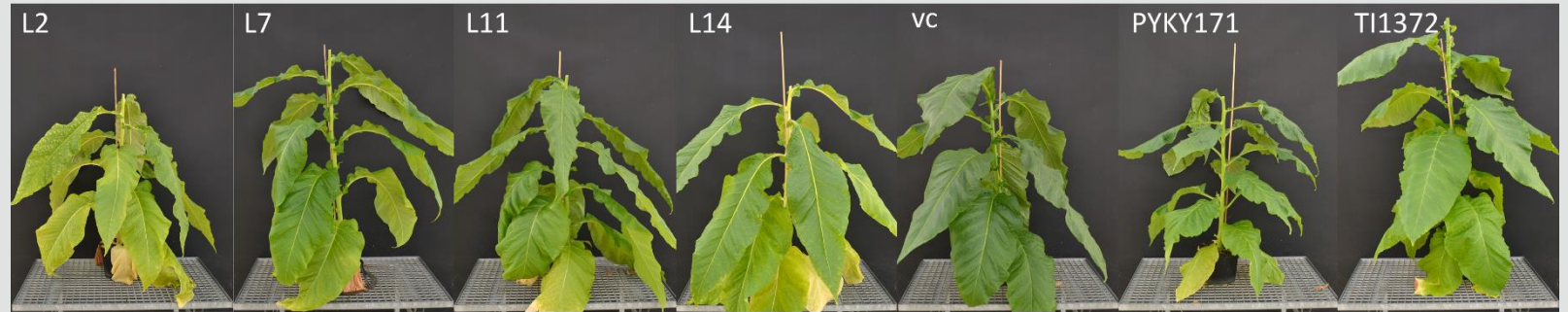


pictures taken 4 weeks post topping

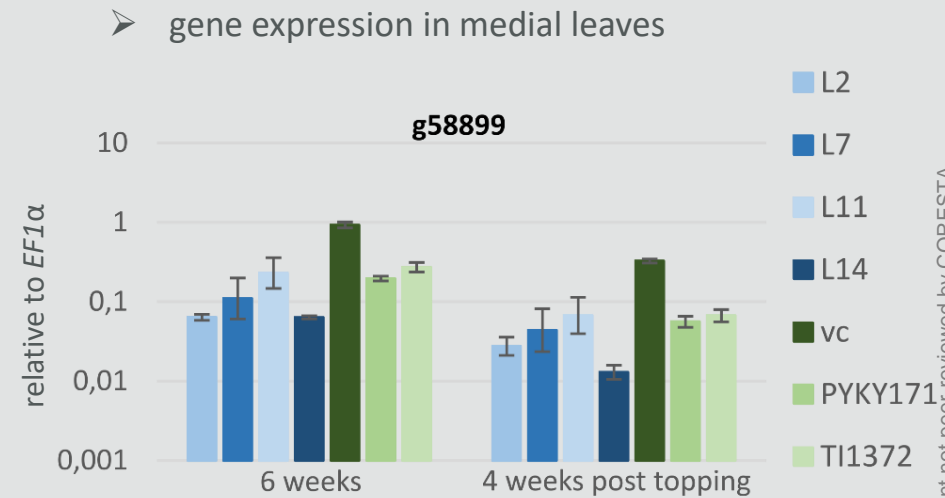
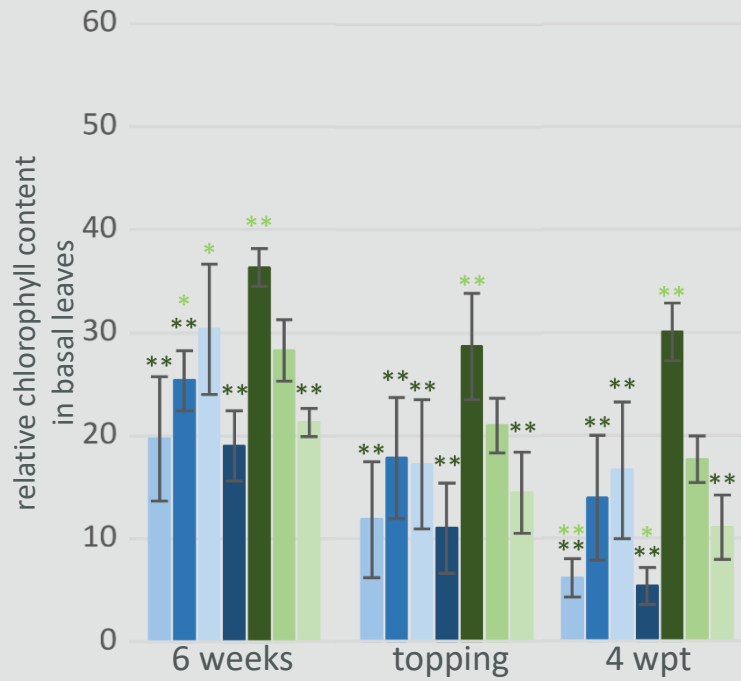
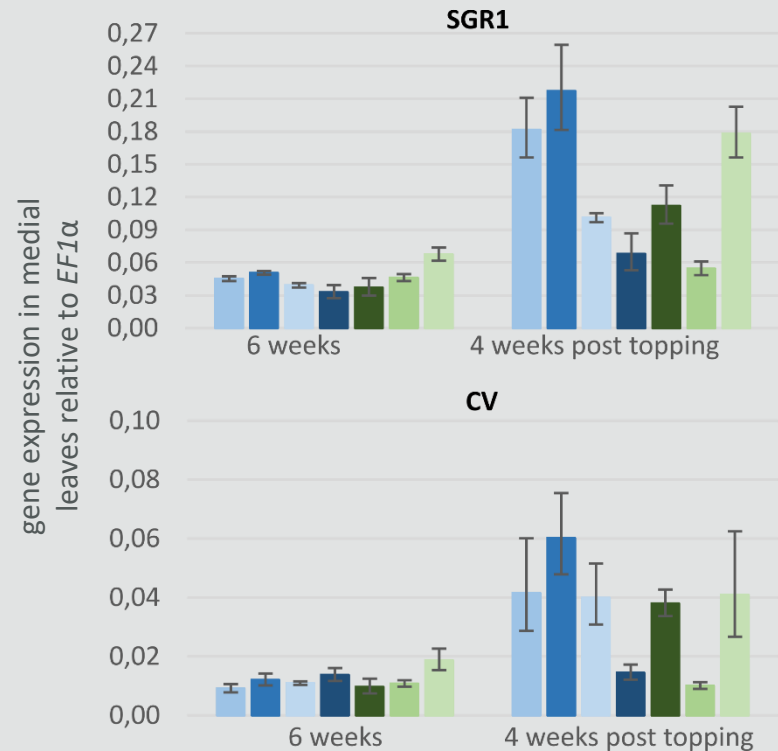


Characterization of g58899 RNAi lines – T₁

➤ leaf senescence-related gene expression is increased



pictures taken 4 weeks post topping



Characterization of g58899 in tobacco

- ✓ overexpression → stay green
- ✓ RNAi → pale yellow
- g58899 shares ~64 %/58 % identity with AtBCM1/2

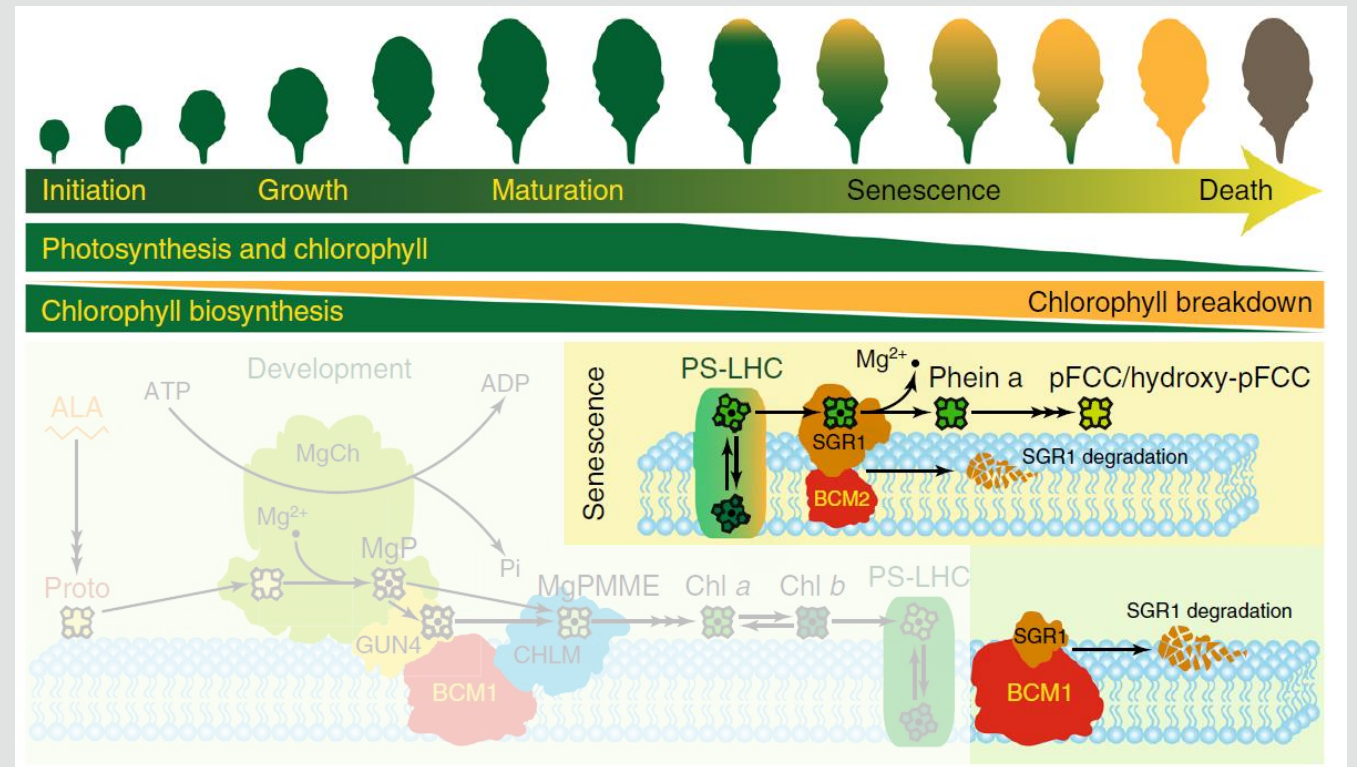


BCM2	MGLPLLSCSSTRVTLSSSSSSSWCSSGSGGFRSSSKLFDS PACSRSDLKKRSGKRNSRLN	60
BCM1	MELPLLSYASSASF---SRTGLCSSSS---SSTSIYEFERRRSLKLFNGGGE-----	48
g58899	MEVPLVARCNTPT----T-----SFLG---CKVSLFDFPIRRKLNKRNYKAKF-----	42
	::*:. : * : * :	
BCM2	GLSLEKLRSIKASSSSAGQSSSEVIDDGDAARGLAVTSGDVTSVGFSGGFVAGAGSGG	120
BCM1	-----RSRSVIA-----SAERSSEGIKTT-----DTVGGGGGGGAGR	81
g58899	-----SVLRVKA-----MAERTST-----EASADARERESGG	69
	: * : : : : : *	
BCM2	LAGPSGEVTSVG-EFVGGSGGDFKDWDKIGAVRLSYGIGIYCGMAVAGRFICEVAGIDY	179
BCM1	FAGTAMEVTTLDRGFANSTTVDFPIWDKIGAVRLTYGIGIYGMAMAVAGRFICSVTGIDS	141
g58899	YTGTTMEVTTFNQSFSD--AQLPVWEKIGAVRLSYGIGIYGMALAGFICSMGTGIDC	126
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BCM2	TGGFNASLDTIIAGLGYASPPIMALLFILDDEVVKLSPHARAIRDVEDELRFQGMSPA	239
BCM1	SGGFDPSLDALLAGLGYATPPIMALLFILDDEVVKLSPHARAIRDVEDELRSFFFGMSP	201
g58899	TGGFSPSLDAIVEGLGYAAPPIMALLFILDDEVVKLSPHARAIRDVEDELRFQGMSP	186
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BCM2	WQFILVVTASSVGEELFYRAAFQALADIFLRGTDLISDSRGMVALTGLLPPFVPPAQVF	299
BCM1	WQFILIVAASSIGEELFYRVAVQALSDIFLKGTLMTDSRGMASLTGVFPFVPPAEVF	261
g58899	WQFILIVAASSVGEELFYRAAFQALADIFLRGSGFVTDARGMASLTGVLPPYVPPAQVF	246
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BCM2	AATITAALTGSLYYIAASPKDPTYIMAPVLKTR SARDELKCLFAAWYERRQMKKIYSPLL	359
BCM1	AAVITATLTGSLYFLAASPKDPTYIVAPVLR--RRDDFKLLSAWYERQMKKIYSPLL	319
g58899	AAVITAALTGSLYYMAASPKDPTYVAPVVKSHSGREDLKKLFAAWYERRQMKKIYSPLL	306
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BCM2	EGLLGLYLGFEWQTNLNLAPIITHGIYSAVVLGNLWKLHGHQRLRLRVQKLETEGDN	419
BCM1	EGLLALYLGFEWQTDNLIAPMMTHGIYSAVILGHGLWKIHDHRRRLRRRIEHIRSEATD	379
g58899	EAMLALYLGFEWQTNNIFAPIITHGIYSAVILGHGLWKIHDHRRRLHQRILKQEGNN	366
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BCM2	NSR*-	422
BCM1	KLI*-	382
g58899	SRNL*	370

Model for the concurrent regulation of Chl biosynthesis / catabolism by BCMs

✓ AtBCMs target SGR1 (involved in chlorophyll breakdown) for degradation

- down-regulation of BCMs (and probably g58899) prevents degradation of SGR1
- chlorophyll breakdown is induced earlier



Conclusion and Outlook

- ✓ low expression of g58899 = PY phenotype → identifying a key target gene for breeding
- ✓ PY KASP[®] assay → demonstrating the utility of a high-density SNP array for mapping of traits
- more precise and faster breeding of the PY trait in commercial tobacco cultivars
 - ❖ loss of function mutants from EMS populations will be analyzed
 - ❖ development of PY lines and agronomic evaluations in progress

THANK YOU

QUESTIONS?

lena.grundmann@ime.fraunhofer.de
sreepriya.pramod@altria.com