Sorghum in the 21st Century
Global Sorghum Conference
Resiliency and Sustainability in the Face of Climate Change
June 5-9 2023 The Corum Event Center, Montpellier, France

Digging into the transcriptome of a developing sorghum grain to find the culprits of protein content and low digestibility

Nancy TERRIER

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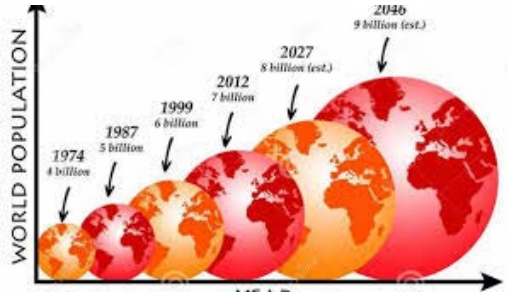
Amélioration génétique et adaptation des plantes méditerranéennes et tropicales

Sorghum in the context of climatic change

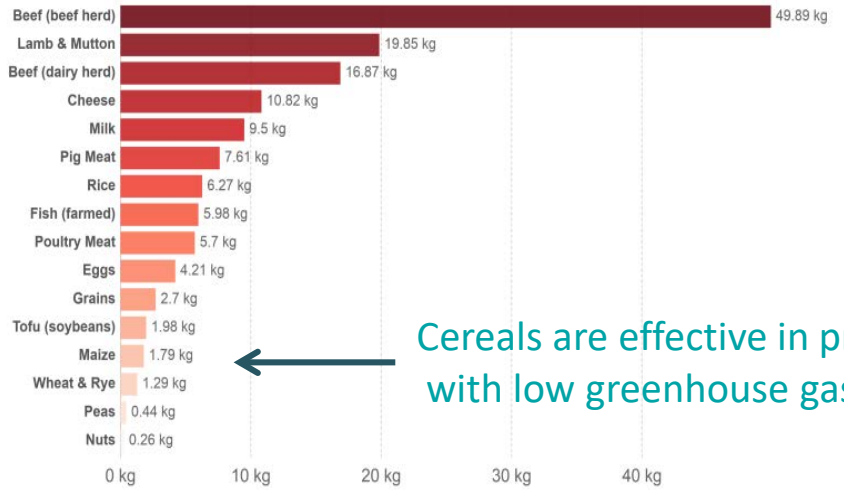
Context

and



A need to revise our protein sources

Greenhouse Gas emission / 100 grams of proteins

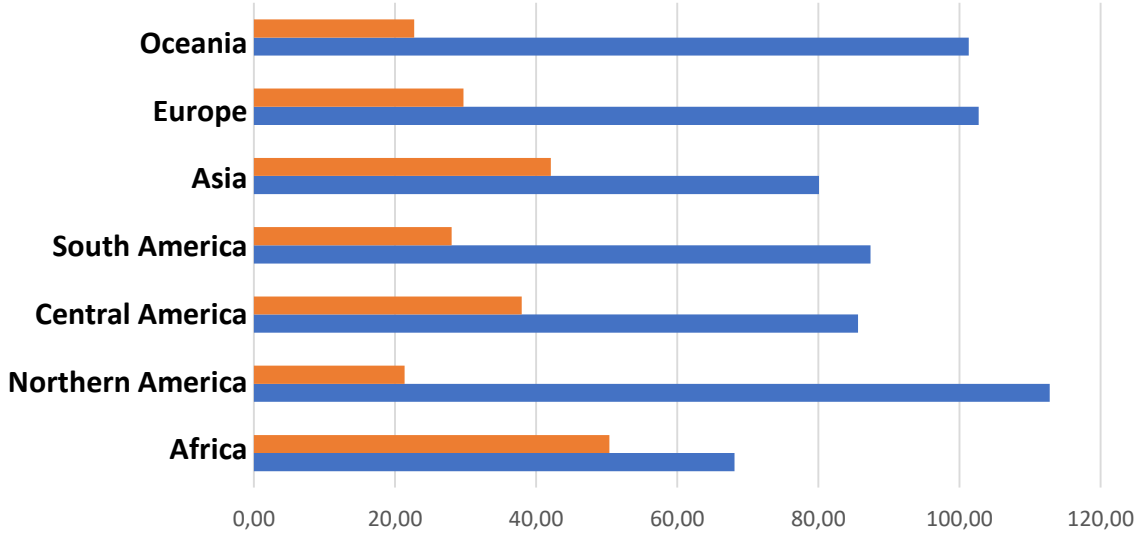


Source: Poore, J., & Nemecek, T. (2018). Additional calculations by Our World in Data.
Note: Data represents the global average greenhouse gas emissions of food products based on a large meta-analysis of food production covering 38,700 commercially viable farms in 119 countries.
OurWorldInData.org/environmental-impacts-of-food • CC BY

Cereals are effective in producing protein with low greenhouse gas emission

Poore J, & Nemecek T ,Science, 2018

Cereal proteins in human daily intake



Total protein intake (g/capita/d)

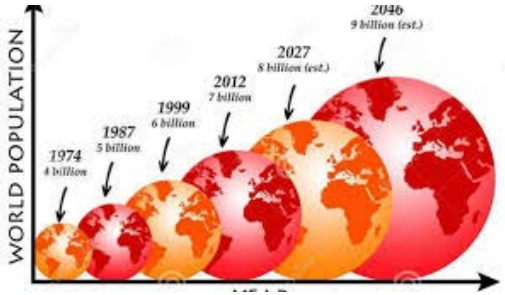
From cereal (%)

From Poutanen *et al.*, Nutrition Reviews, 2022

Sorghum in the context of climatic change

Context

and



A need to revise our sources of proteins

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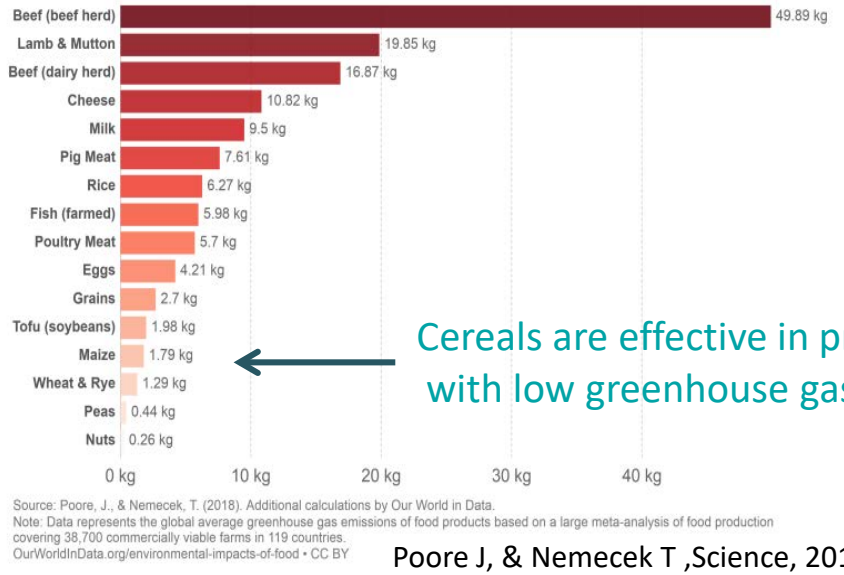

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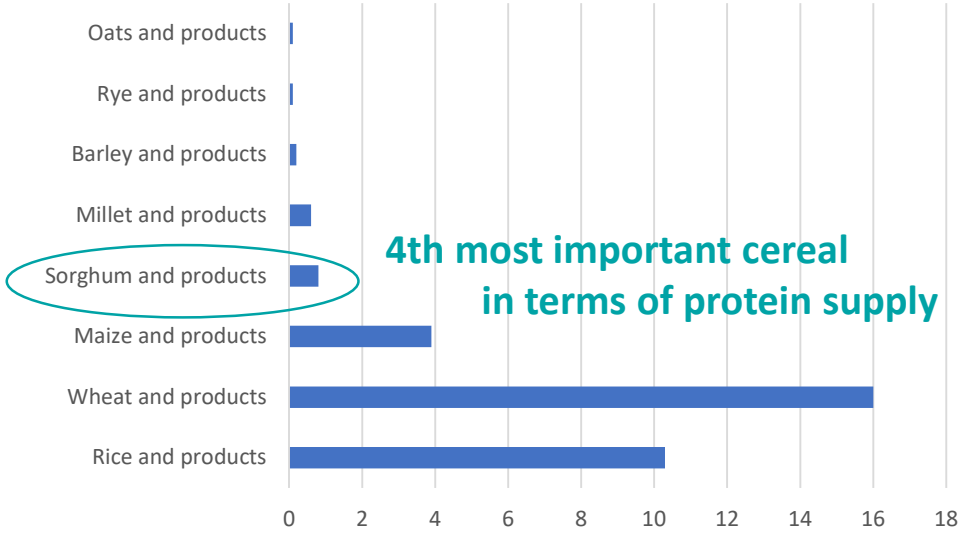
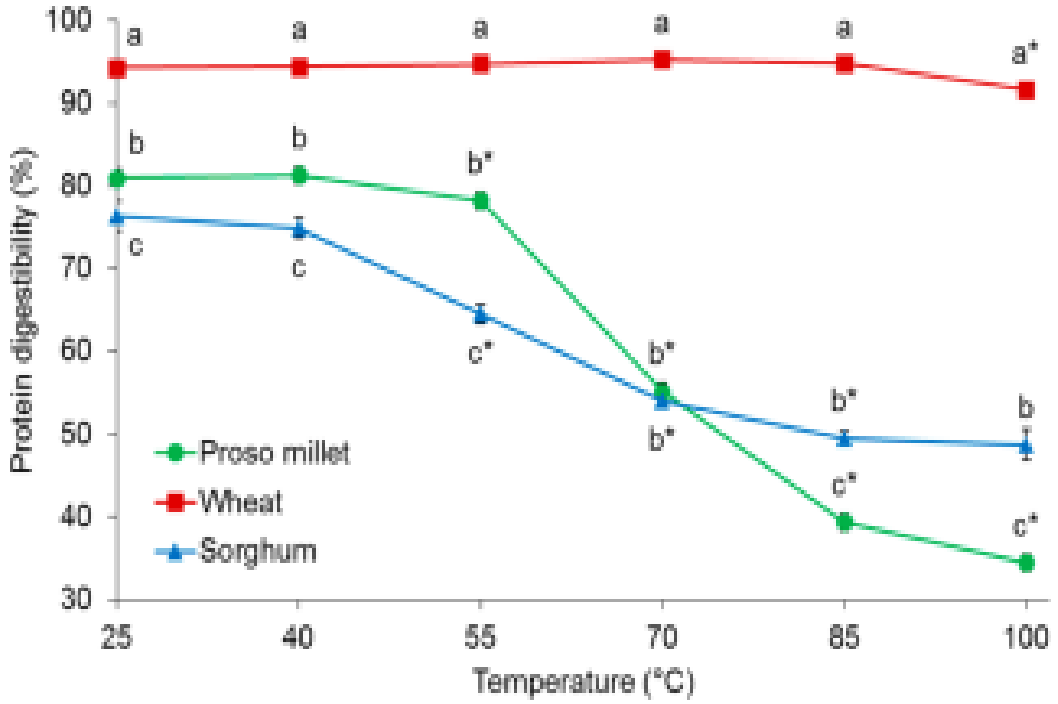


4th most important cereal in terms of protein supply

From Poutanen *et al.*, Nutrition Reviews, 2022

Main limits of sorghum regarding its use for feed and food

- Amino Acid disequilibrium
- Low digestibility (decreased with cooking)

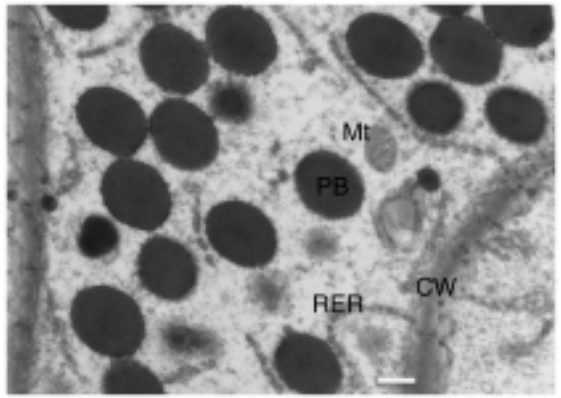


Gulati *et al.*, 2017

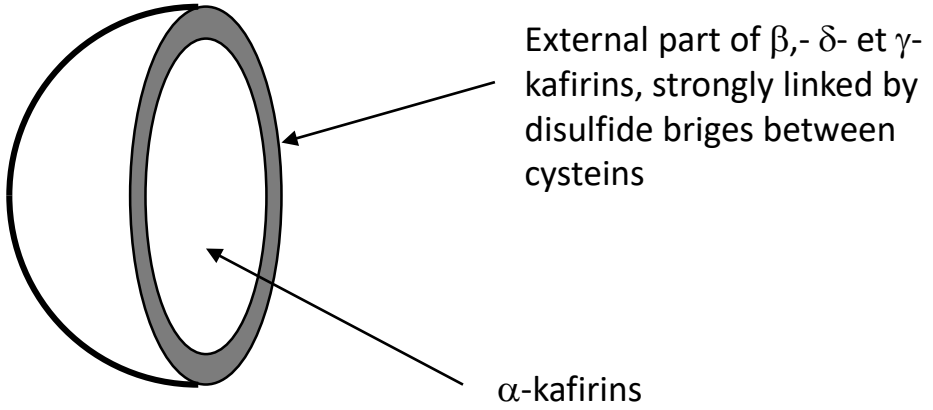
Protein low digestibility: several factors

- **Interaction between proteins and other compounds** :
  - Tannins
  - Starch
  - Cell wall components (see presentation of PhD student C. Costes, O87)

- **Storage structure of proteins :**
  - Reserve proteins (prolamin, called Kafirins) in protein bodies
  - Appearance of additional disulfide bridges during grain development (see presentation of H. Mameri O114) and cooking



Wu et al., 2013



Does solution exist to solve this problem ?

Diversity in sorghum

✓ For protein content in grains
(Rami et al., 1998; Figueiredo et al., 2010; Rhodes et al., 2017;Kimani et al., 2020)

✓ For digestibility
(Hicks et al., 2002; Cremer et al., 2014 ; Impa et al., 2019; Duressa et al., 2020; Kardes et al., 2021; Diatta-Holgatte, 2022)

Objectives

Better understanding of the molecular and biochemical mechanisms leading to protein accumulation and their low digestibility

→ Which actors are involved in protein body establishment and modification ?

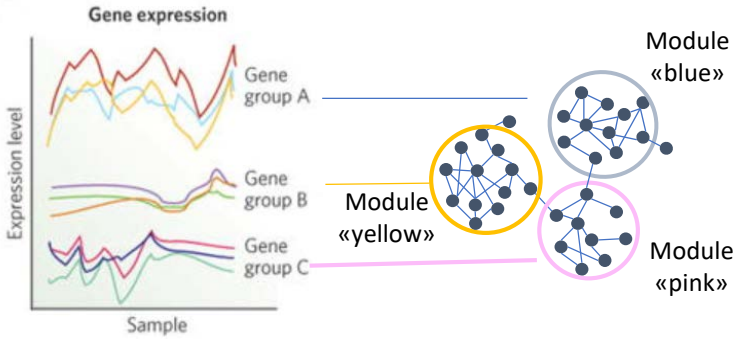
→ Are there variabilities that could modify these protein structures and digestibility ?

Transcriptomic analysis

- Macia genotype
- 10 developmental stages (Days After Anthesis+7 to DAF+40)
- 3 biological replicates in 2 years (2017, 2018)

RNAseq = 60 samples

Gene network analysis



Traits

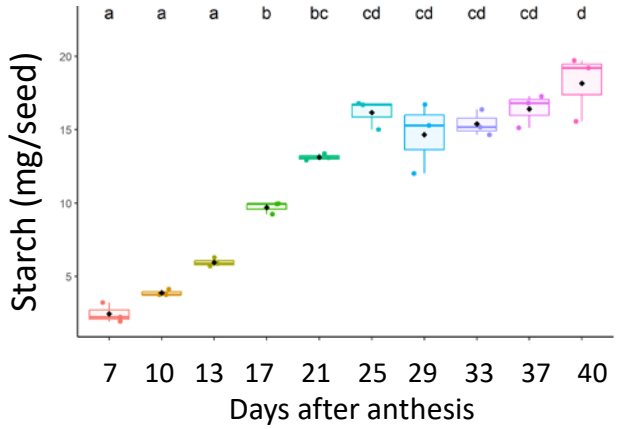
- ✓ **Protein Digestibility** (%)
- ✓ **Starch** (mg/grain)
- ✓ **Protein** (µg/grain)

Kinetics of those traits during grain development

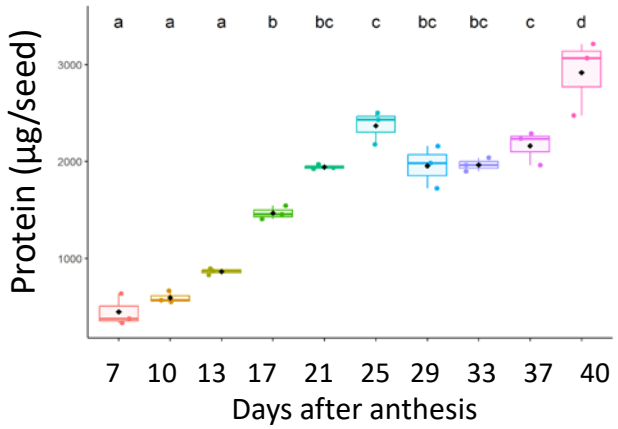
Poster of PhD student
Mamadou Sene (P69)

Biochemical parameters during grain development

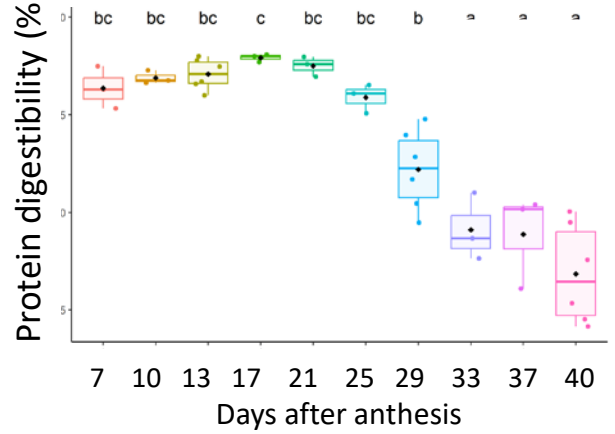
Starch



Protein

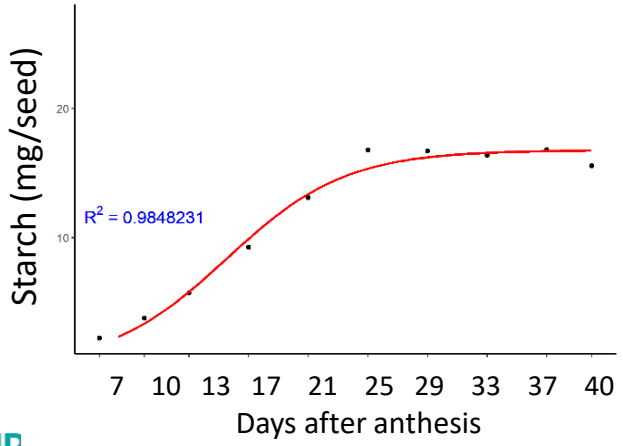


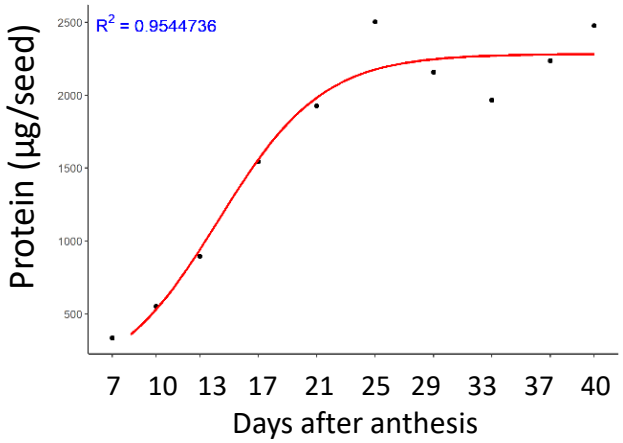
Protein digestibility



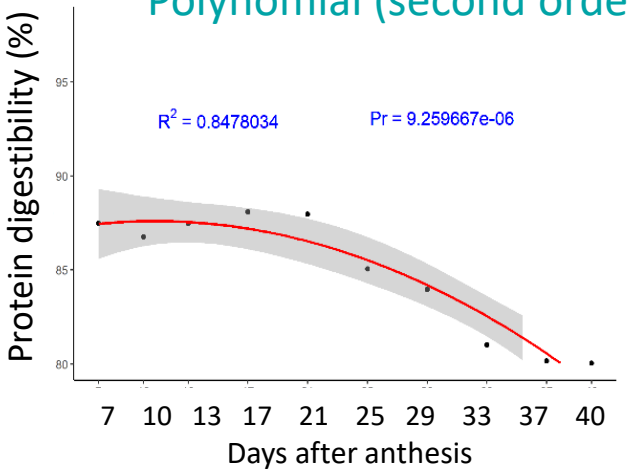
Curve fit

Sigmoïds



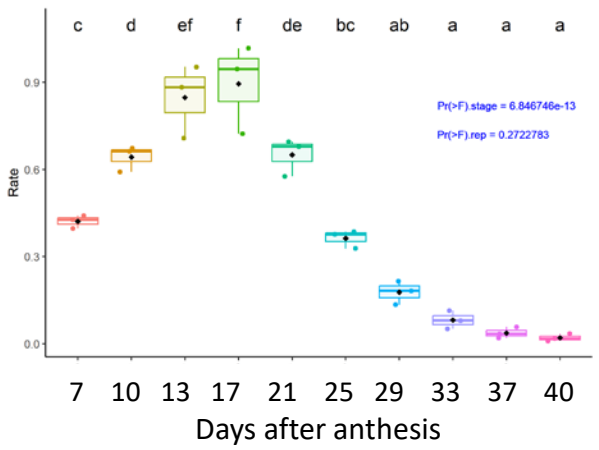


Polynomial (second order)

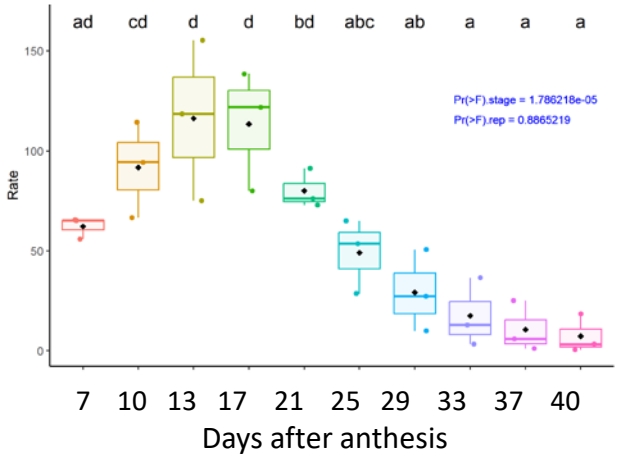


Kinetic parameters during grain development

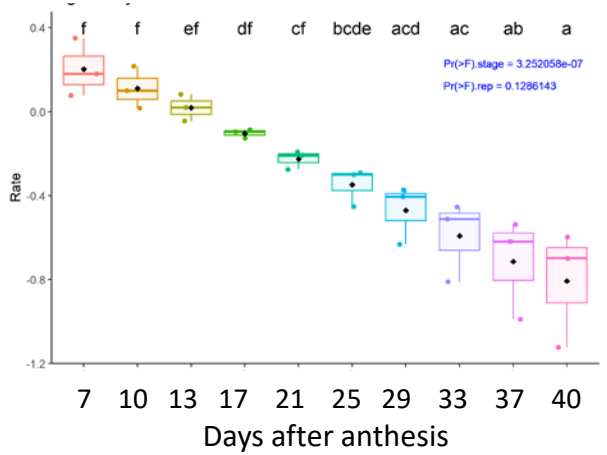
Starch accumulation rate



Protein accumulation rate

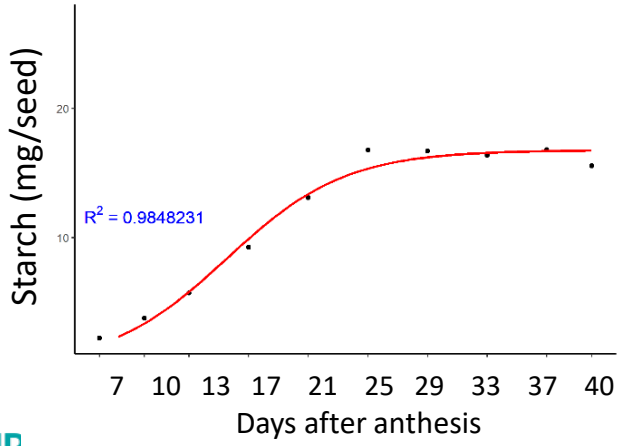


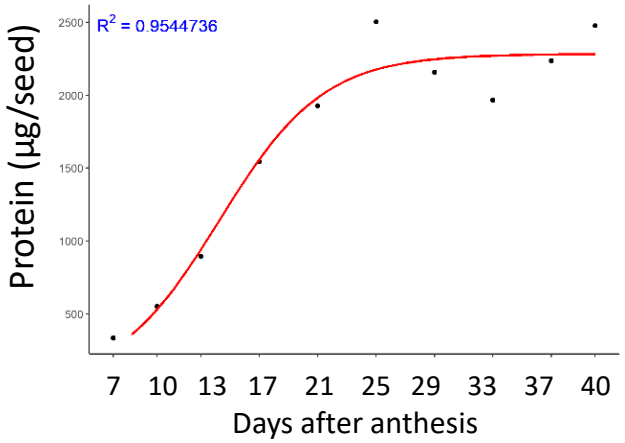
Protein digestibility decrease rate



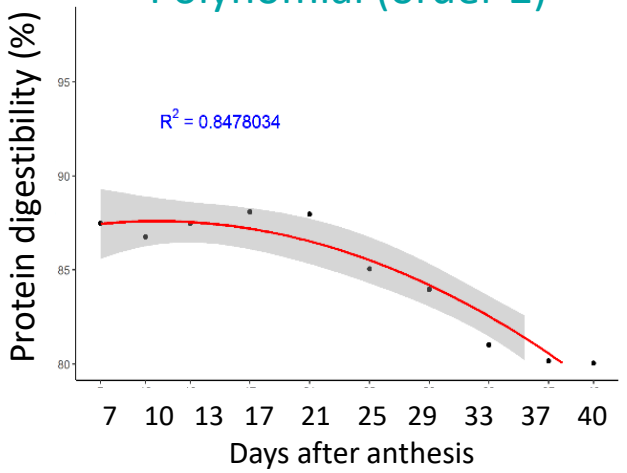
Derivative

Sigmoïds

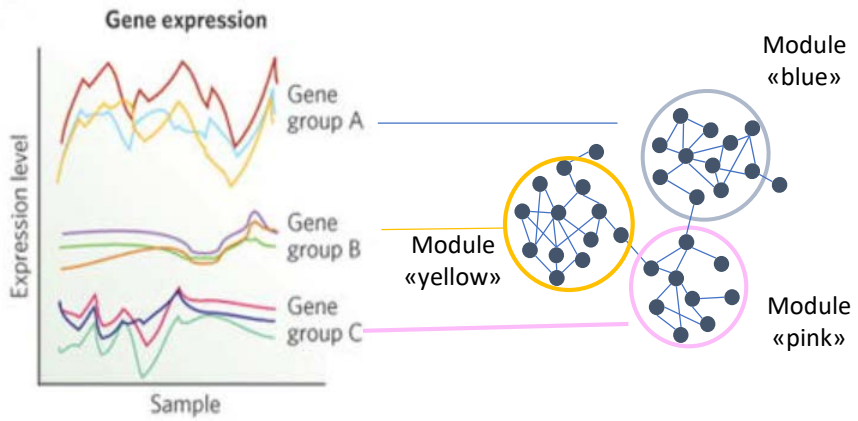




Polynomial (order 2)

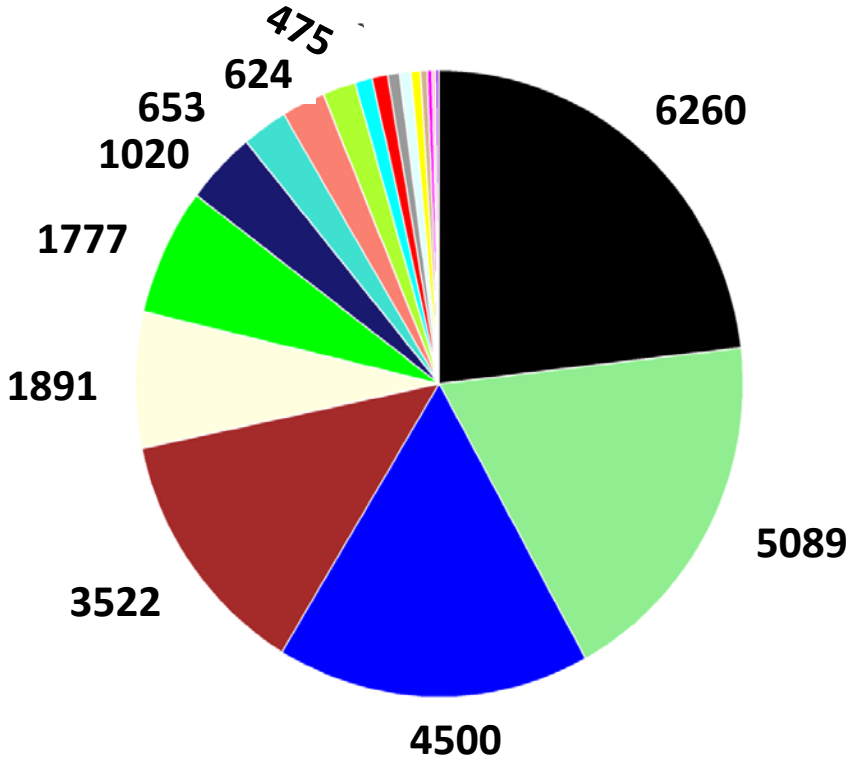


Gene network analysis



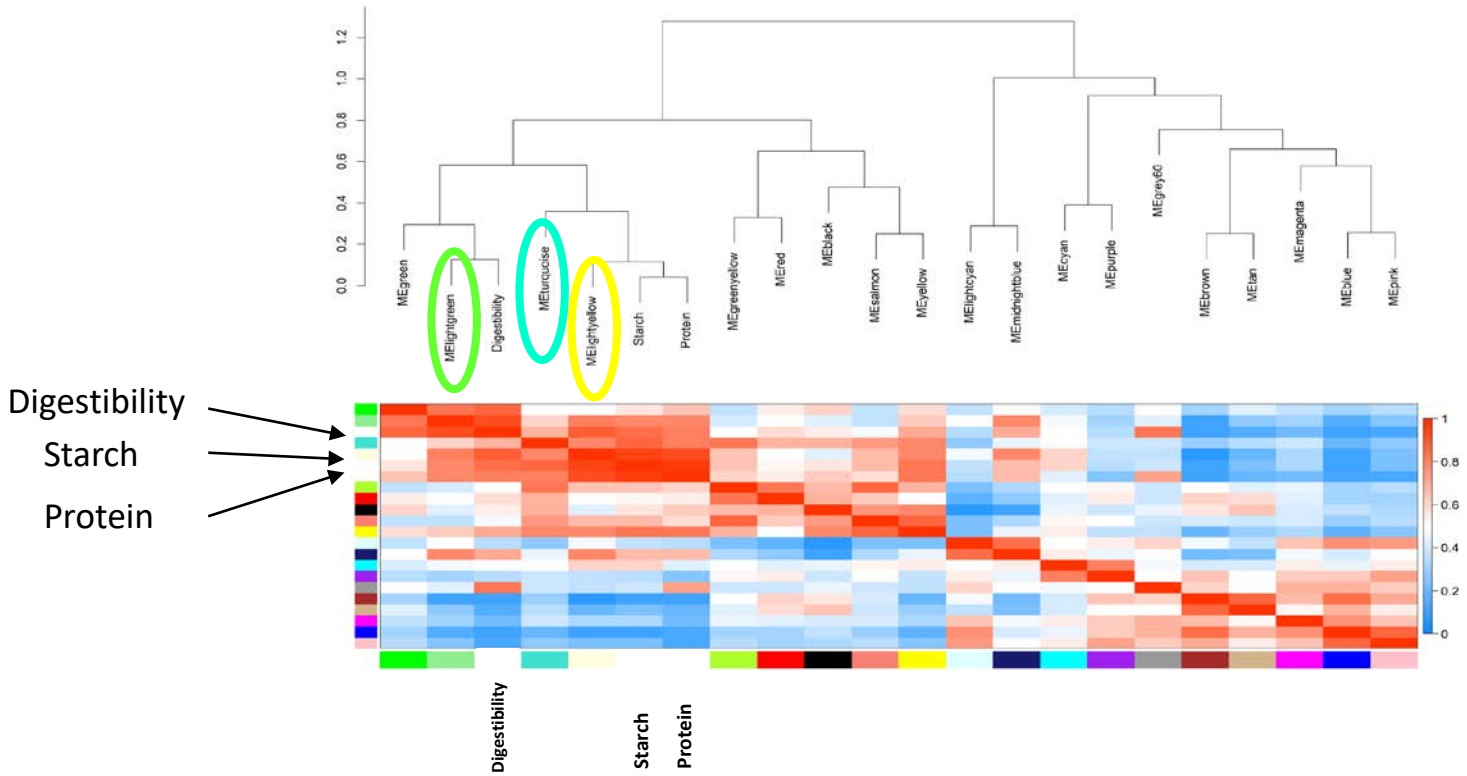
WGCNA

Langfelder et al., 2008



- ✓ 19 modules
- ✓ black, lightgreen, and blue ones contain the largest number of genes

Gene co-expression network and kinetics

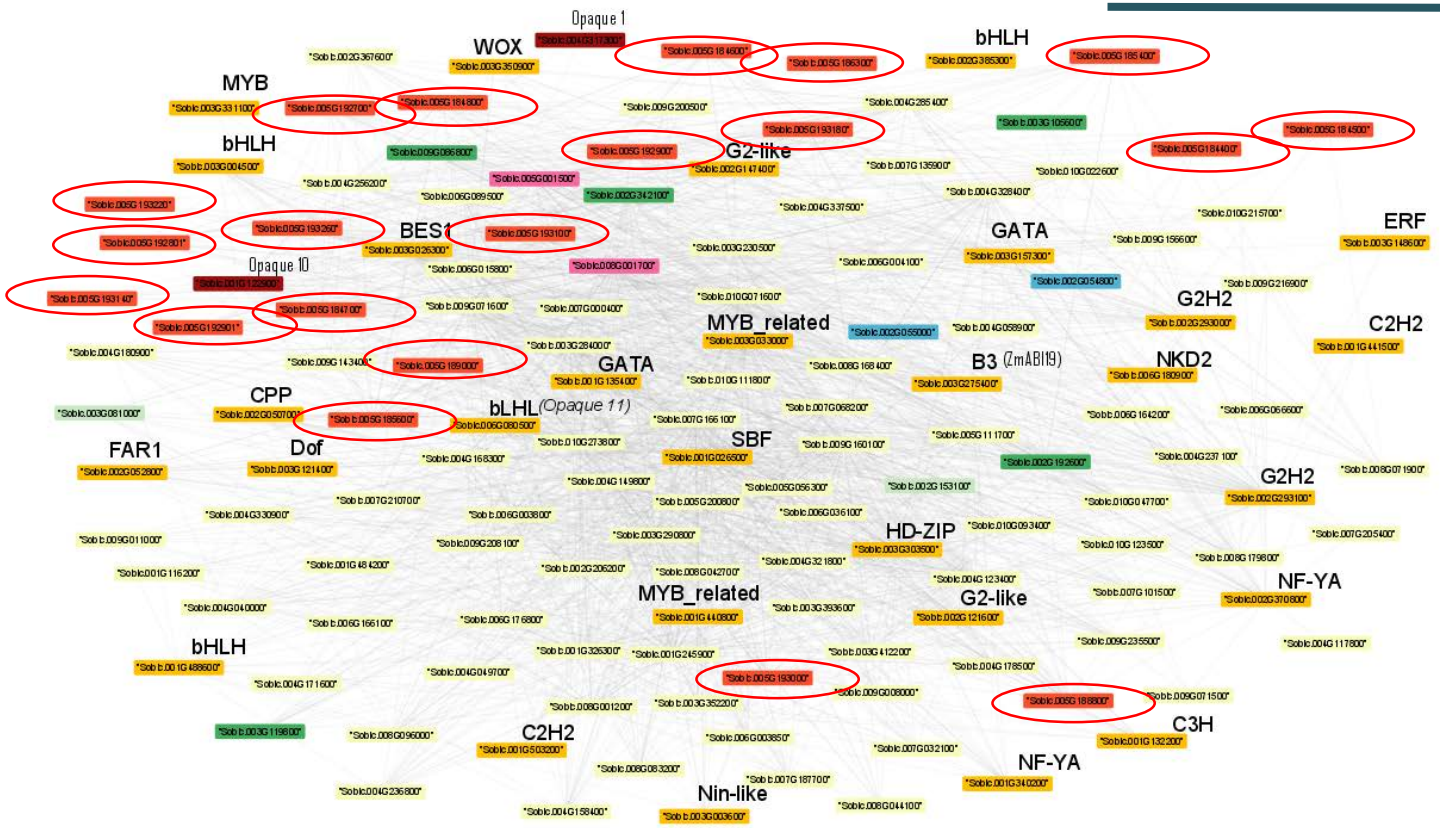


Starch, protein and digestibility kinetics are correlated with each other

Strong positive correlations observed between

- ✓ starch, protein, lightyellow and turquoise modules
- ✓ digestibility and the lightgreen module

Lightyellow module linked with protein accumulation rate



α-kafirins
Opaque2 (bZip)
PBF (Dof)
NAC
bZip
Other TFs
Other genes

✓ The majority (20) of genes coding for α-kafirin

Light yellow module linked with protein accumulation rate

Op2 and PBF regulate protein body structure, protein and starch synthesis , endosperm development

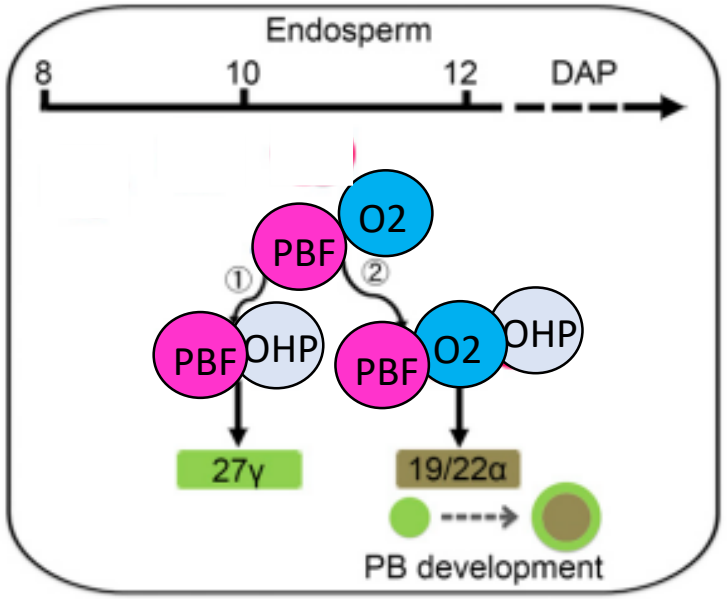


Figure 9. Hypothetical Model Depicting the Transcriptional Regulation of the 27-kD γ- and α-Zein Genes Mediated by O2, PBF, and OHPs.

Zhang *et al.*, 2015

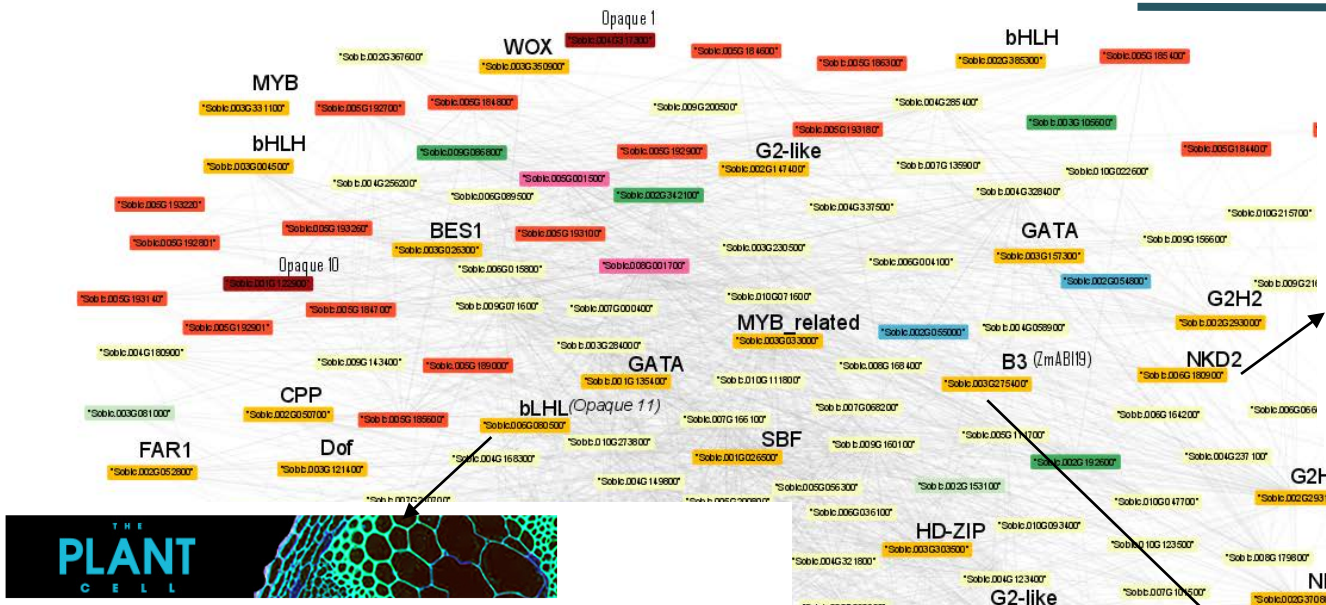
O2=Opaque2, bZip

PBF=Prolamine-box binding factor, DOF
(DNA-binding with one finger)

OHP=Opaque heterodimerizing protein, bZip

hang et al., 2015)

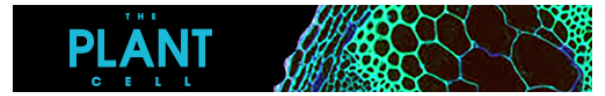
Lightyellow module linked with protein accumulation rate



Plant Cell. 2018 Feb; 30(2): 375–396.
Published online 2018 Feb 7. doi: 10.1105/tpc.17.00616
PMCID: PMC5868688
PMID: 29436476

OPAQUE11 Is a Central Hub of the Regulatory Network for Maize Endosperm Development and Nutrient Metabolism[OPEN]

Fan Feng,[a] Weiwei Qi,[a] Yuanda Lv,[b] Shumei Yan,[a] Liming Xu,[a] Wenyao Yang,[a] Yue Yuan,[a] Yihan Chen,[a] Han Zhao,[b] and Rentao Song[a,c,1]

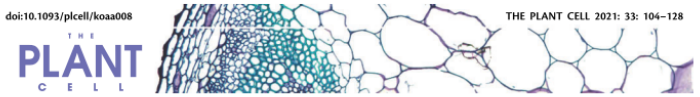


JOURNAL ARTICLE

NKD Transcription Factors Are Central Regulators of Maize Endosperm Development FREE

Bryan C. Gontarek, Anjanasree K. Neelakandan, Hao Wu, Philip W. Becraft
Author Notes

The Plant Cell, Volume 28, Issue 12, December 2016, Pages 2916–2936,

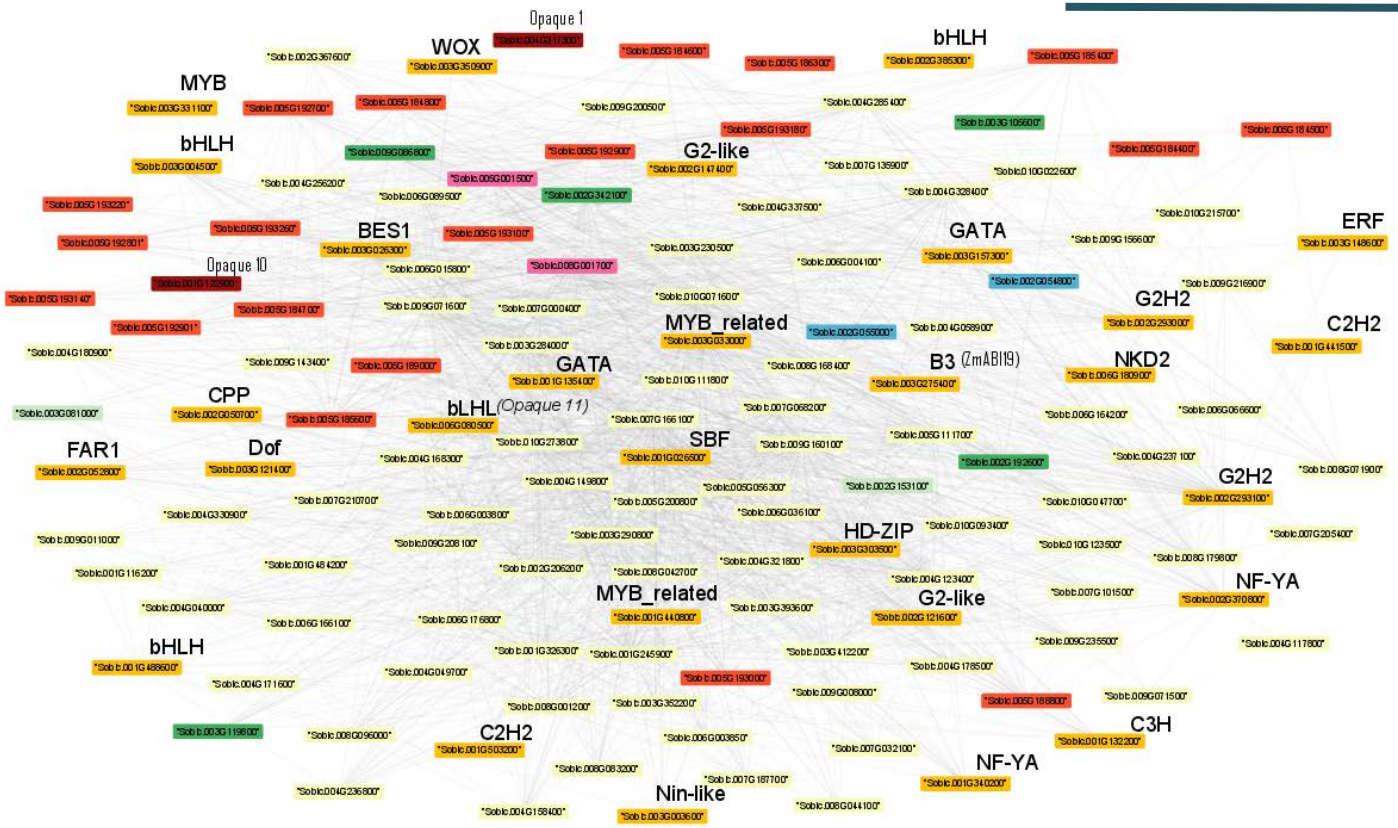


The B3 domain-containing transcription factor ZmABI19 coordinates expression of key factors required for maize seed development and grain filling

Tao Yang [1,†] Liangxing Guo [1,2,†] Chen Ji [1,2] Haihai Wang [1] Jiechen Wang [1] Xixi Zheng [1,2] Qiao Xiao [1,2] and Yongrui Wu [1,*]

- ✓ The majority (20) of
- ✓ Orthologs of maize Op2 and PBF (Fenf et al., 2018; Gontarek et al., 2016; Zhang et al., 2015)
- ✓ Other known TFs : bHLH, ZmABI19, NKD, etc (Yang et al., 2021; Zhang et al., 2019; Zhang et al., 2015

Lightyellow module linked with protein accumulation rate



α-kafirins
Opaque2 (bZip)
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NAC
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Other TFs
Other genes

- ✓ The majority (20) of genes coding for α-kafirin
- ✓ Orthologs of maize Op2 and PBF (Fenf et al., 2018; Gontarek et al., 2016; Zhang et al., 2015)
- ✓ Other known TFs : NAC, ZmABI19, NKD, etc (Yang et al., 2021; Zhang et al., 2019; Zhang et al., 2015)
- ✓ Genes and TFs not yet identified

Take-home messages

→ Which actors are involved in protein body establishment and modification ?

Several putative actors identified.

-some are orthologs of already known actors in other plants (good news !)

-some are new candidates

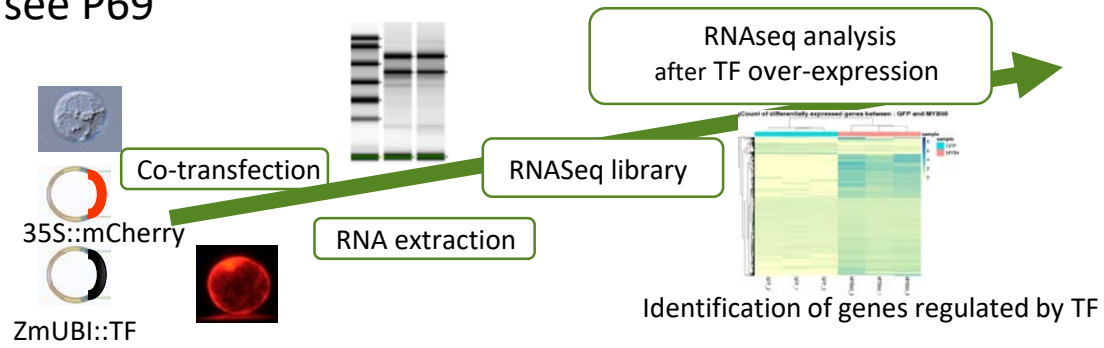
Investigate other modules (digestibility), see P69

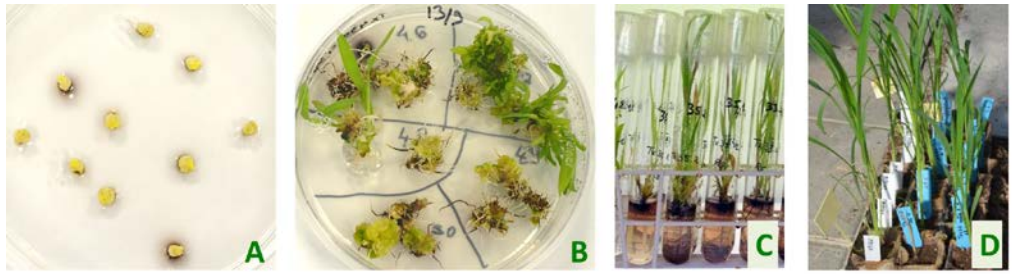
Validate their functions

-transient Over-Expression in protoplast

Poster F. Richaud and C. Calatayud P19

-stable transformation





Perspectives

→ Are there variabilities that could modify these protein structures and digestibility ?

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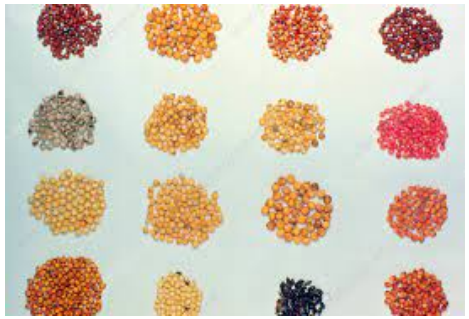
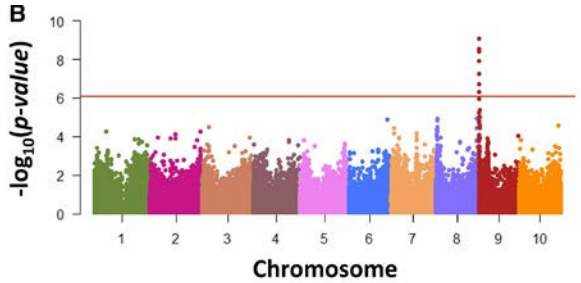
AVEC LA CONTRIBUTION FINANCIÈRE DU COMPTE D'AFFECTATION SPÉCIALE DÉVELOPPEMENT AGRICOLE ET RURAL

Jan.2022-June 2025



European commercial and
World-wide diversity
Protein/Digestibility



-GWAS
-genomic prediction
-phenomic selection

-animal growth, well-being
-meat quality
-proteomics

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Amélioration génétique et adaptation des plantes méditerranéennes et tropicales

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L'INSTITUT TECHNIQUE DES FILIÈRES AVICOLE, CUNICOLE ET PISCICOLE

UMRBOA
Biologie des Oiseaux & Aviculture

Thanks !


M. Séne


A. Berger

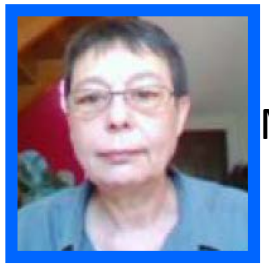

F. De Bellis


F. Richaud


M. Rios


C. Calatayud


D. Pot


J. Bonnicel


M.H. Morel


H. Mameri

Funding: SOKAFI from INRAE

PhD grant for M. Séne INRAE and cirad