

# Identification of K<sup>+</sup> Content QTL from High-throughput Phenotyping Data Using NIR Spectroscopy in Oil Palm

Sébastien Tisné<sup>1</sup>, Sandra Espéout<sup>1</sup>, Jean Ollivier<sup>2</sup>, Reinout Impens<sup>3</sup>, Florence Jacob<sup>4</sup>, Gilles Chaix<sup>1</sup> and Teresa Cuéllar<sup>1</sup>

<sup>1</sup>CIRAD, UMR AGAP Institut, F-34398 Montpellier, France, <sup>2</sup>CIRAD, UMR ABSYs, F-34398 Montpellier, France <sup>3</sup>SIAT, PRESCO-PLC, Benin city, Nigeria, <sup>4</sup>PalmElit SAS, Montferrier-sur-Lez, France. Correspondance: sebastien.tisne@cirad.fr - teresa.cuellar@cirad.fr

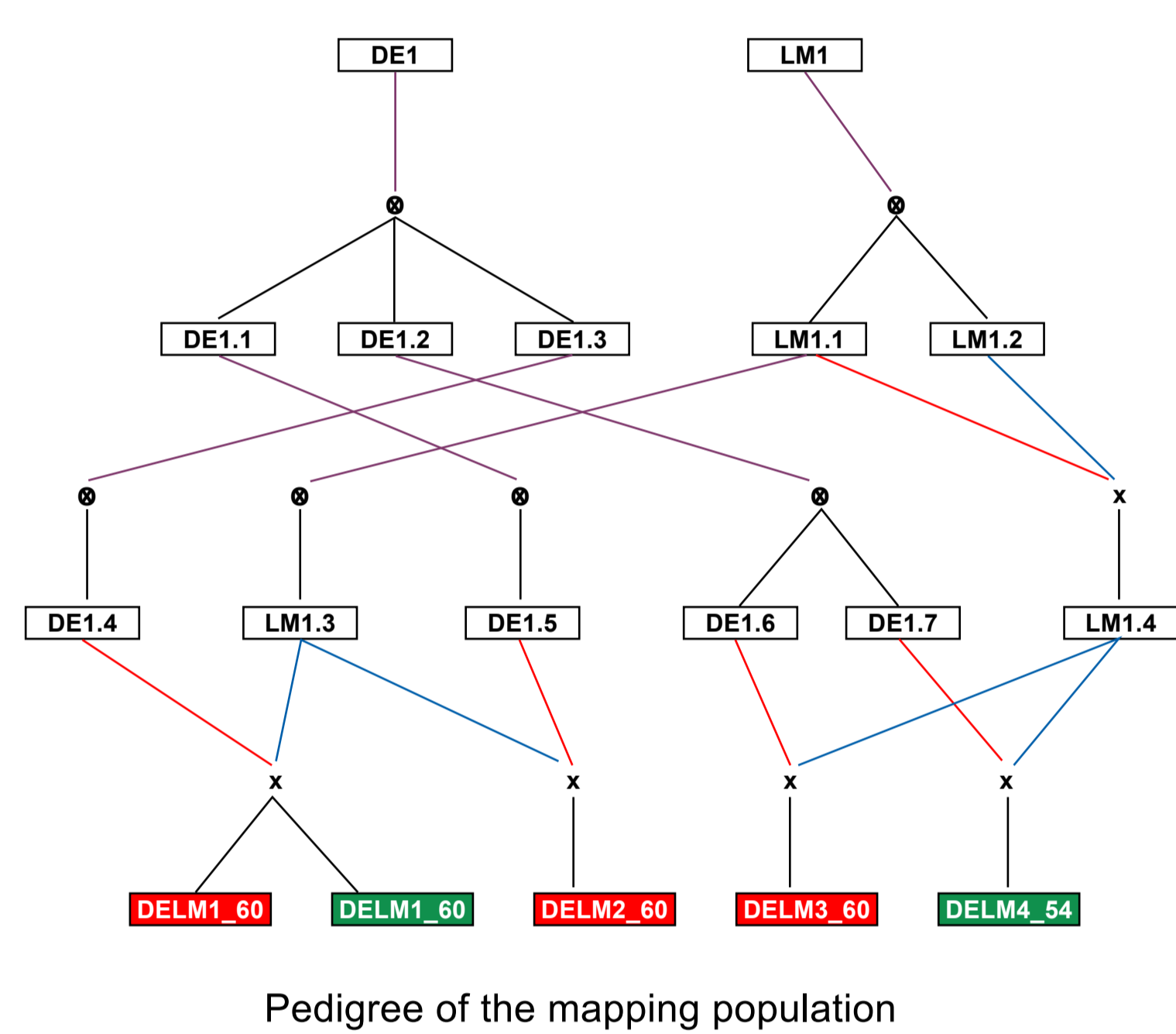
## Context

- Oil palms require large amounts of fertilizers with potassium (K<sup>+</sup>) playing the major role.
- The challenge is to maintain high yields while optimizing K<sup>+</sup> efficiency.
- Leaf analysis (LA) is currently used to monitor K<sup>+</sup> fertilization.
- LA is limited by its cost and time required, as well as by genetic factors influencing K<sup>+</sup> distribution in oil palm organs (Ollivier *et al.*, 2017).

>> Genetic determinism of K<sup>+</sup> levels in oil palm? Contribution of near infrared (NIR) spectroscopy as a low-cost and high-throughput phenotyping approach?

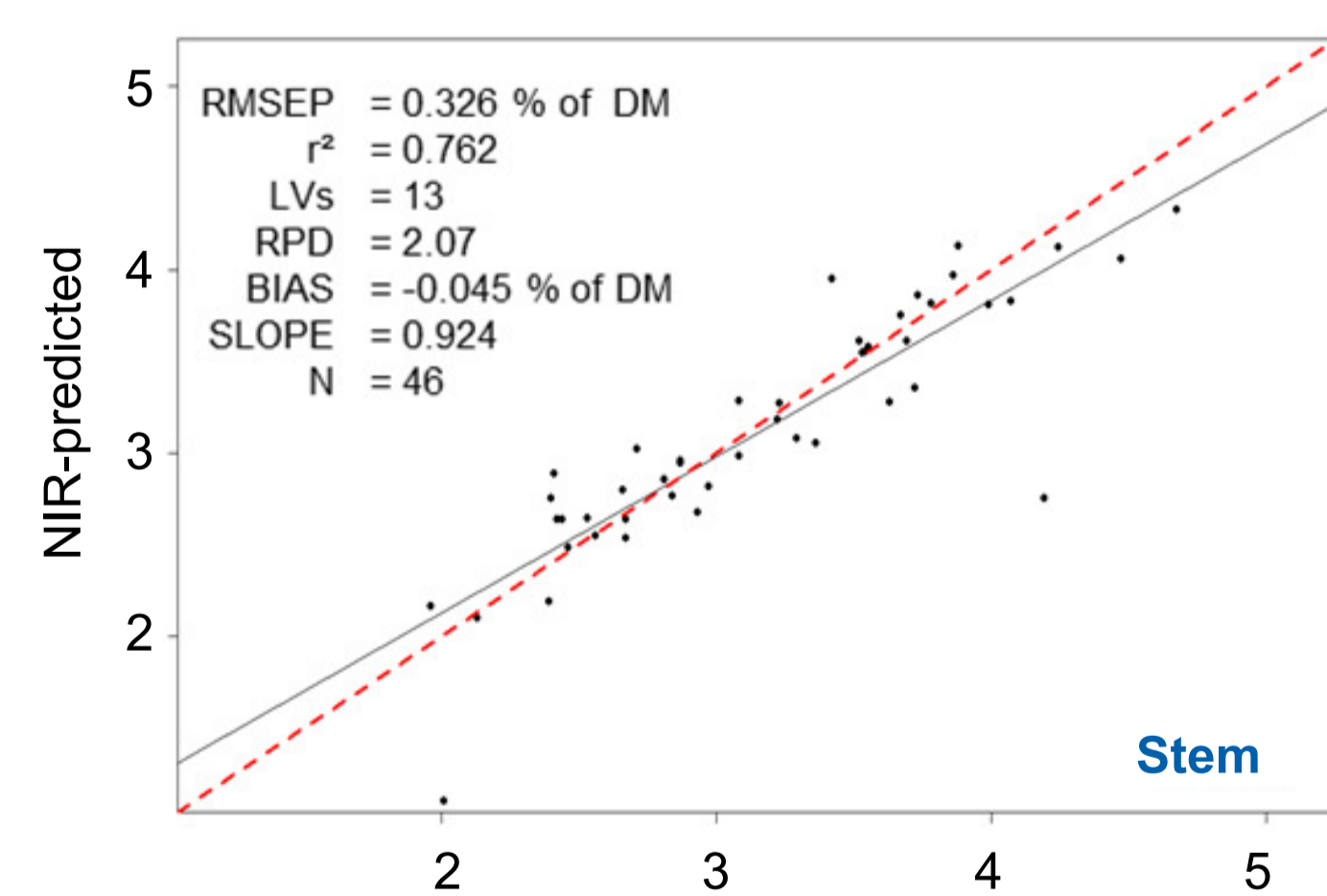
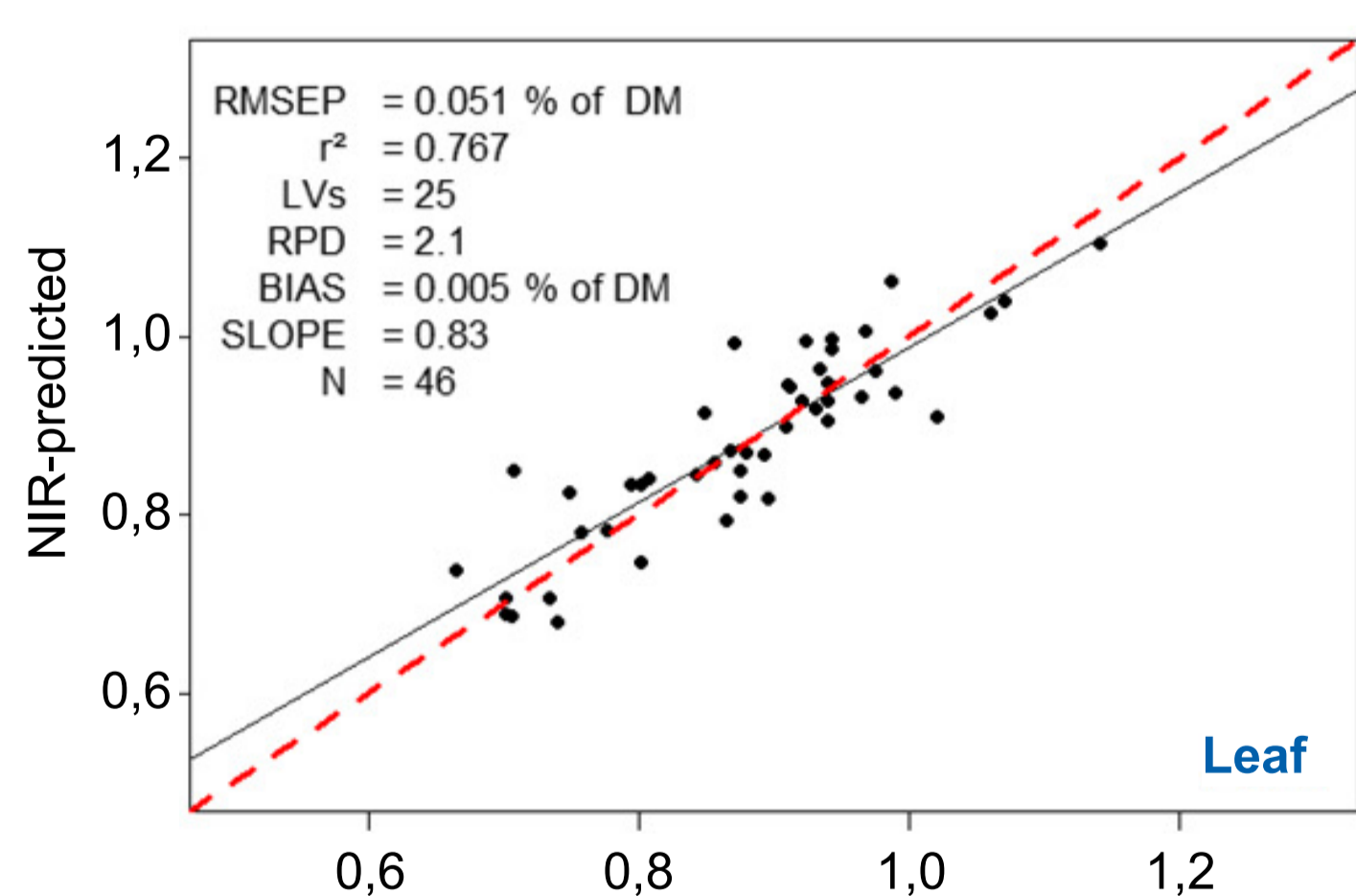
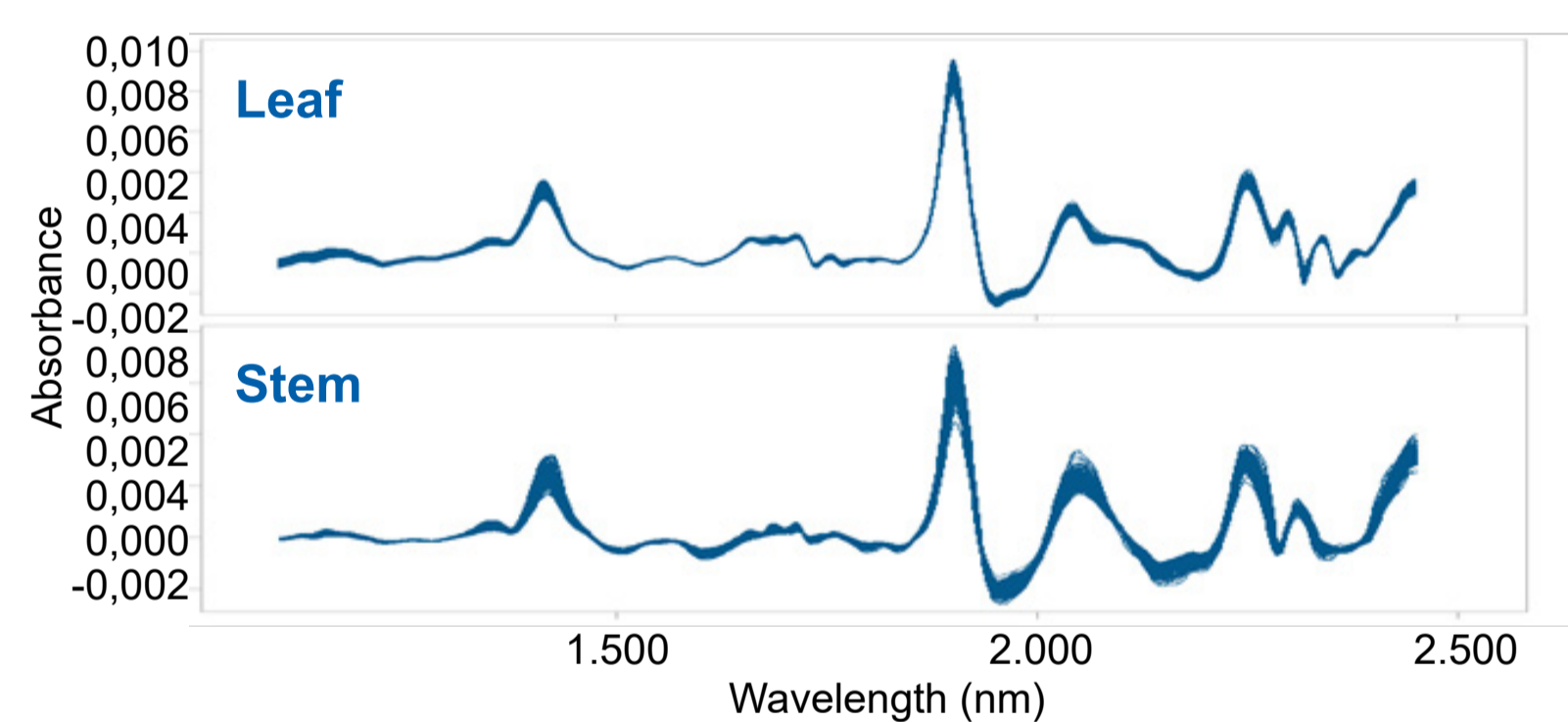
## Genetic material and molecular data

- 294 individuals derived from a Deli (DE1) and a La Mé (LM1) parent, planted in two trials (red and green) in Presco, Nigeria
- Genotyping using an Axiom 67K SNP array.



## NIR spectroscopy calibration for K<sup>+</sup> content

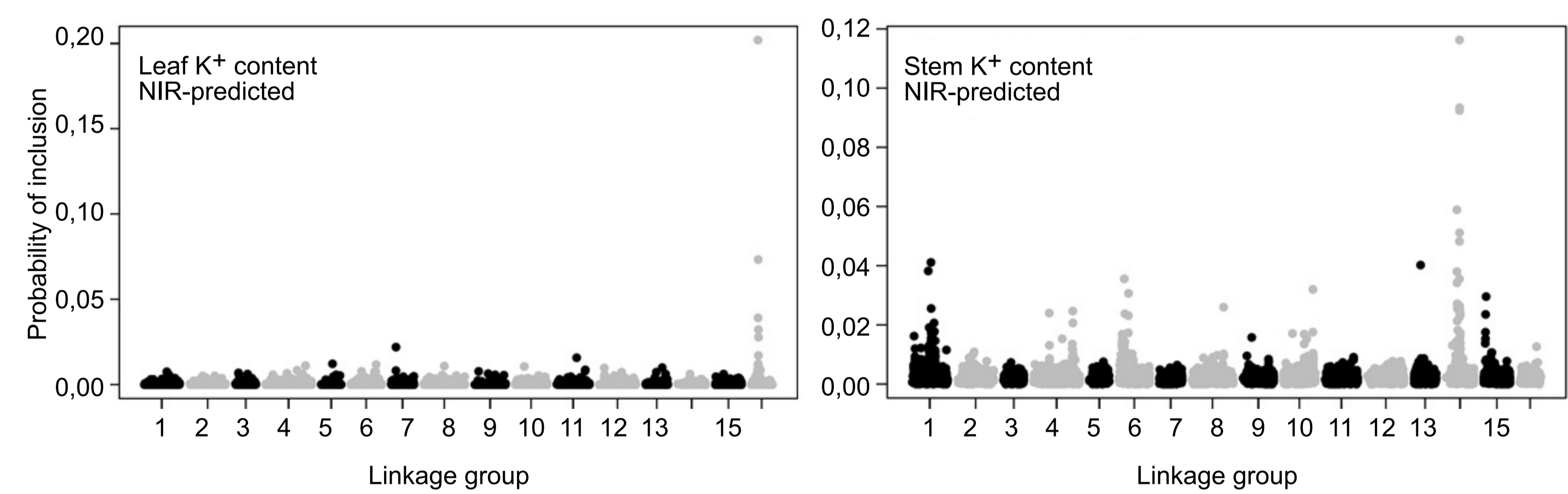
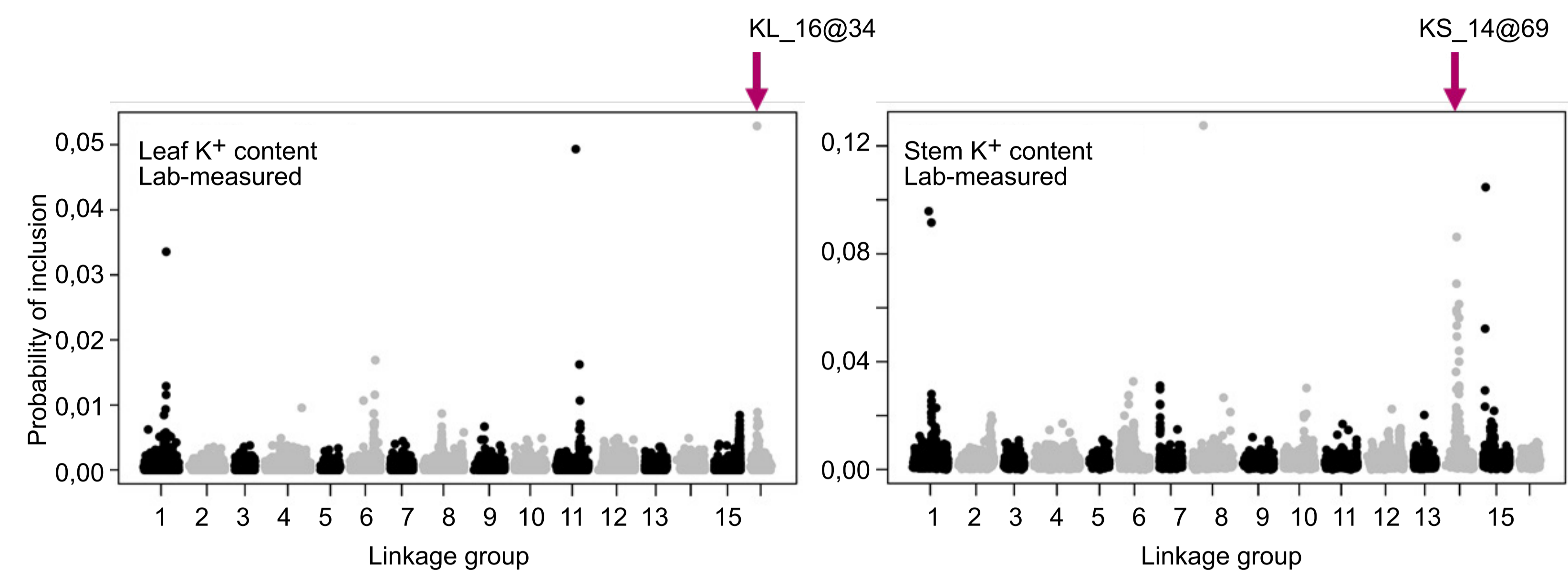
- 1.176 spectra obtained using ASD Labspec4 spectrometer (350-2500 nm): 294 individuals, 2 grounded tissues (leaf and stem), 2 repetitions per sample
- Development of leaf and stem K<sup>+</sup> content NIR prediction models based on K<sup>+</sup> concentrations from standard Cirad protocol using CP-OES Agilent 720-ES.



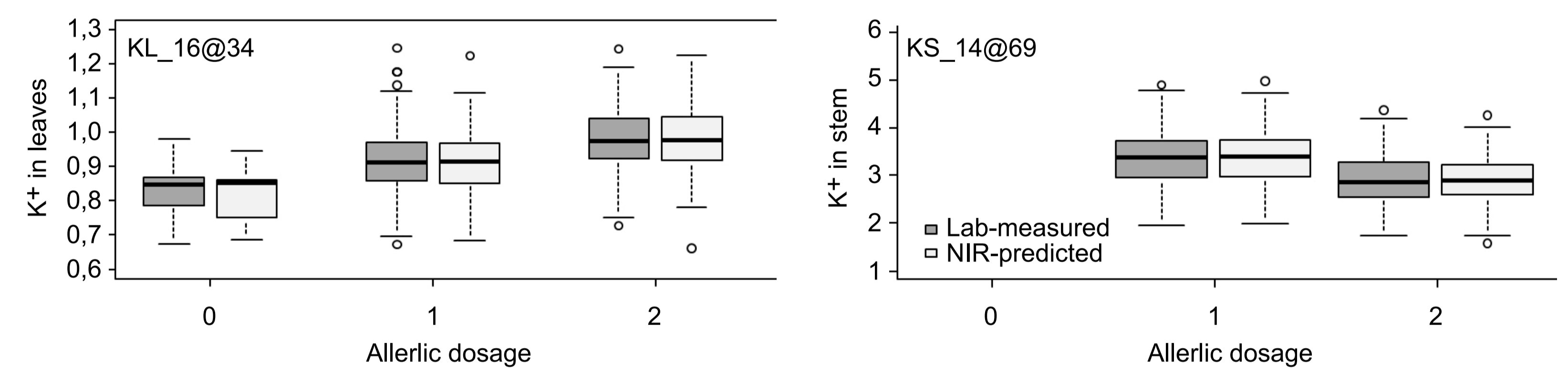
Lab-measured vs NIR-predicted K<sup>+</sup> contents using prediction models

## Results

- QTL analysis performed using a Bayesian variables selection approach implemented in R/BGLR package (Pérez and de los Campos, 2014).
- QTL patterns are consistent between Lab-measured and NIR-predicted phenotypic data.
- Strong QTL were obtained in both organs but in different genetic locations depending on the organ considered.



Manhattan plots for QTL detection of K<sup>+</sup> content. Higher probability of inclusion indicates higher probability of QTL presence. Largest QTL are indicated by arrows at their genetic positions.



Boxplot of K<sup>+</sup> content in individuals from the mapping population depending on their SNP alleles at the largest QTL in leaves (left) or stem (right).

## Conclusions

- This work provides an initial insight into the genetic determinism of important traits related to K<sup>+</sup> nutrition and its distribution in the plant.
- NIR phenotyping is validated for K<sup>+</sup> content in oil palm organs (Shen *et al.*, 2021) and will enable the scope of genetic analyses to be extended at reasonable cost.

>> These results open up new perspective for reducing K<sup>+</sup> fertilizers by using marker-assisted selection (MAS) for K<sup>+</sup> use efficiency in breeding programs.

## Bibliographic references

- Ollivier, J. *et al.* (2017) Journal of Plant Nutrition 40, no 4 : 558-73  
 Pérez, P., de los Campos, G. (2014) Genetics 198, 483-495.  
 Shen J. *et al.* (2021) Applied Science, 11, 5103  
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