

# PROCALIB : developing NIRS ADF Van Soest and Protein content models on two brands and a standardized network in France for hi-pro rapeseed

Vincent Jauvion<sup>1\*</sup>, Sylvain Tréguier<sup>1</sup>, Claire Reculé<sup>1</sup>, Audrey Gendron<sup>1</sup>, Jérémy Manzini<sup>1</sup>, Roland Welle<sup>2</sup>, Jean-Claude Pruvot<sup>3</sup>, Virginie Bortolussi<sup>4</sup>, Raphaëlle Girerd<sup>5</sup>

<sup>1</sup> Terres Inovia, 270 av. de la Pomme de Pin, Ardon, 45166 Olivet, France

<sup>2</sup> Corteva, Münstertäler Strasse 26, 79427 Eschbach, Germany

<sup>3</sup> Corteva, Epuisseau, 41290 Oucques, France

<sup>4</sup> Corteva, Route de Suisse, 160, 1290 Versoix, Switzerland

<sup>5</sup> Sofiproteol, 11 Rue de Monceau, 75008 Paris, France

[v.jauvion@terresinovia.fr](mailto:v.jauvion@terresinovia.fr)

## Background and Objectives

International rapeseed commercial transactions are usually done according to quality parameters such as water, oil and impurities content. Protein content (Nx6.25) is not commonly mentioned in contracts.

Although rapeseed main value is coming from the oil part, meals are key coproducts for feed. In order to increase the protein content while maintaining the oil content, new varieties of rapeseed are being bred for Hi-Pro / Low-fiber traits. As Molecular Assisted Breeding (MAB) is not possible for these complex traits therefore fast, efficient and non-destructive phenotyping is needed.

To offer a reliable and efficient method to determine Hi-Pro / Low-fiber traits, we aimed to use NIRS (near infrared spectroscopy) and chemometrics after wet chemistry. As breeders and companies are using different NIRS brand, we also aimed to develop models on two mainly used brands, Bruker and Foss, and organize a standardized equipment network in France.

## Materials and methods

200 rapeseed samples from Corteva covering a range of protein (Nx6.25) and ADF from 14.7 to 32.0% and 6.7 to 15.2%, respectively have been analyzed. These samples are from different European geographic origins.

Water content has been performed according to an internal method adapted from NF V03-909. Protein content has been determined by Dumas method according to NF EN ISO 16334-1 standard from dry seeds after water content analysis.

Prior to fiber analyses, samples have been grinded and defatted using a hexane solvent Soxhlet extraction, close to NF V03-908 method. After defatting, ADF content has been determined by Van Soest method according to NF V18-122 standard.

NIRS scans have been acquired with spectrometers from two brands, a Bruker Tango and a Foss DS3 (Figure 1). Multivariate analysis allowed us to develop PLSR (partial least squares regression) models for protein and ADF on both spectrometers.



1. Spectrometers used for NIRS scans: (a) Bruker Tango ; (b) Foss DS3

## Results

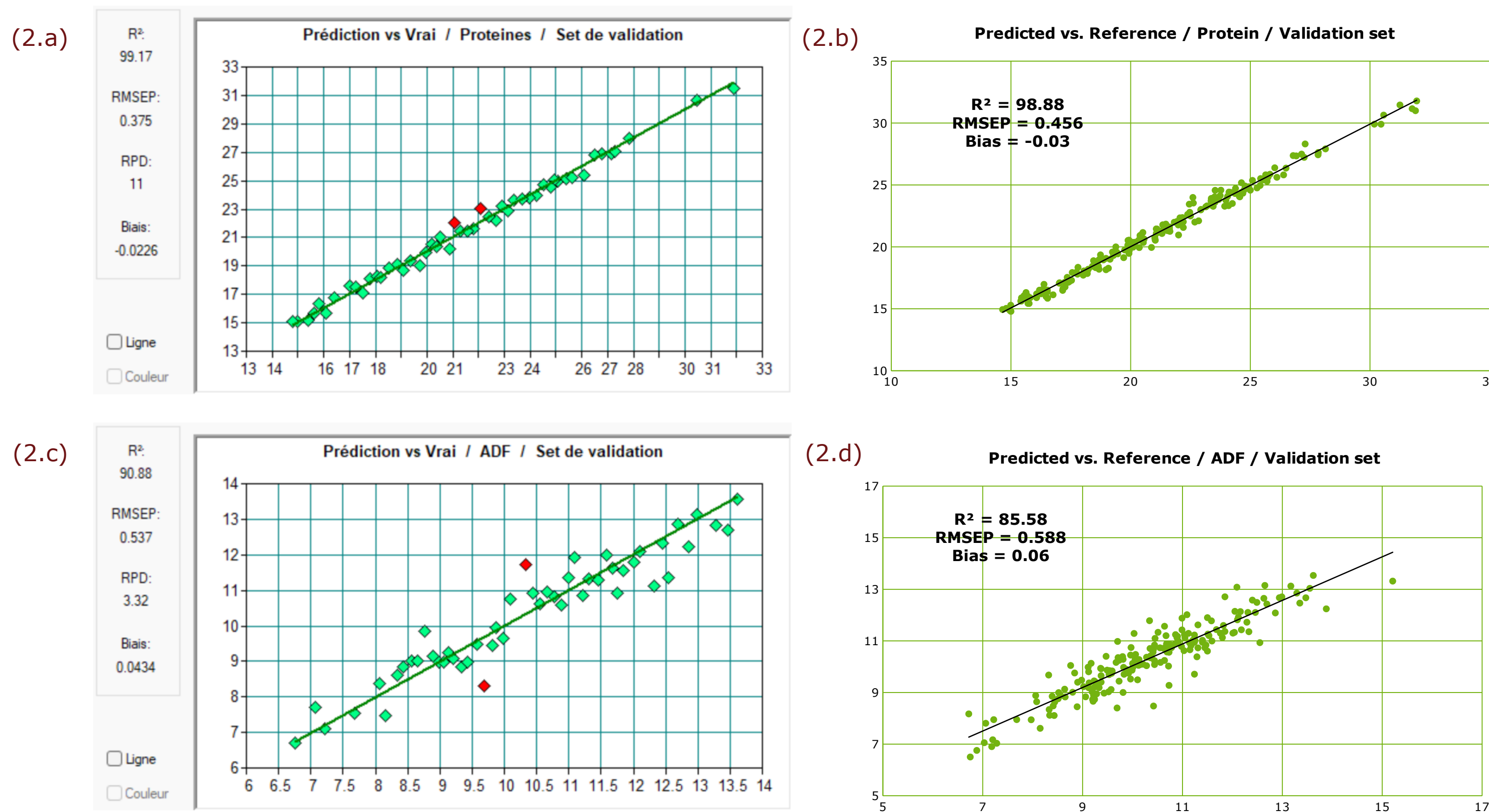
The predicted vs. reference values plots are displayed for the external validation of each PLSR model (Figure 2).

This validation set is composed of 20 to 25% of the whole dataset. The calibration set consist of the 75 to 80% remaining samples.

Spectra were pretreated using SNV (Standard Normal Variate) for protein models and using a combination of SNV and first derivative for ADF models.

Bruker Tango models were built using 12 factors. Foss DS3 protein model was built with 13 factors, while the ADF model was built with 6 factors.

Model performance is evaluated using several indicators: R-squared, RMSEP (root mean squared error of prediction) and bias.



2. Predicted vs. reference values plots for: (a) the Bruker Tango protein model; (b) the Foss DS3 protein model; (c) the Bruker Tango ADF model; (d) the Foss DS3 ADF model

## A future standardized network

The developed models are planned to be shared with other partners to allow fast and reliable screening of breeding material. To ensure the transferability of NIRS models on other spectrometers, performance indicators such as R-squared, RMSEP and RPD are assessed and compared for all partners on an independent validation set consisting of 20 samples.

After standardization, a proficiency test will be performed with 3 to 5 samples in order to verify predicted values from slave equipment in the network as well from master equipment and their performance compared to wet chemistry.

## Conclusions

Our work on wet chemistry and multivariate analysis to develop NIRS models allows rapid and efficient screening of the hi-pro rapeseed lines on two main NIRS brands for both protein and ADF contents in order to breed hi-pro rapeseed. Performance of models and of slave equipment prediction is ensured by a strong standardization process and monitored thanks to a proficiency testing.

These models will also allow the evaluation and benchmarking of available rapeseed varieties on the French market for protein and ADF contents, giving an opportunity to evaluate rapeseed varieties on protein and fiber content as well as other key criteria (oil content, glucosinolate content, yield, resistance...) and favor the feeding outlet for the meals, major oil extraction coproduct.