# P.36 Non-destructive Near Infrared Reflectance Spectroscopic Technique for Selecting High Protein and Oil Soybean Lines

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## 고단백·고지방 콩 계통 선발을 위한 비파괴적 근적외 분광분석 기술

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**Objectives** : The objectives of this research were to study the potential of non-destructive NIR spectrocomputer system to estimate the protein and oil contents of intact soybean seeds and to provide the mass screening technique for selecting high protein and oil soybean breeding lines.

**Materials and Methods** :

Soybean samples : 299 soybean germplasms
Chemical analyses : Auto-kjeldahl and soxhlet system
Near infrared analysis : NIRSystem 6500 monochrometer NIRS(400~2500㎚)
Calibration and validation : Using the WinISI program, *Calibrate* and *Monitor*
Calibration method : MPLS, Sample cup : Small reflectance vessel(whole seeds)

**Results** : The 198 soybean samples were used for non-destructive NIRS equation development of protein and oil, and a total of 101 soybean sample set was used for prediction of developed NIRS equations. In the developed NIRS equations, the most accurate non-destructive NIRS equation condition of protein and oil were obtained respectively at 2, 8, 6, 1 and 2, 1, 20, 10(Mathematical derivative, Gap size, First smoothing point and Second smoothing point) math treatment condition with SNVD (Standard Normal Variate and Detrend) scatter correction method and entire spectrum (400~2498㎚) by using MPLS (Modified Partial Least Squares) regression. Validation of these NIRS equations showed very low bias (Protein : 0.060%, Oil : -0.017%) and standard error of prediction (SEP, Protein : 0.568%, Oil : 0.451%) and high coefficient of determination ($R^2$, Protein : 0.927, Oil : 0.906). Therefore, these non-destructive NIRS equations seem reliable for determination the protein and oil contents of intact soybean seeds, and non-destructive NIRS technique could be used as a mass screening method for selecting high protein and oil soybean breeding lines.

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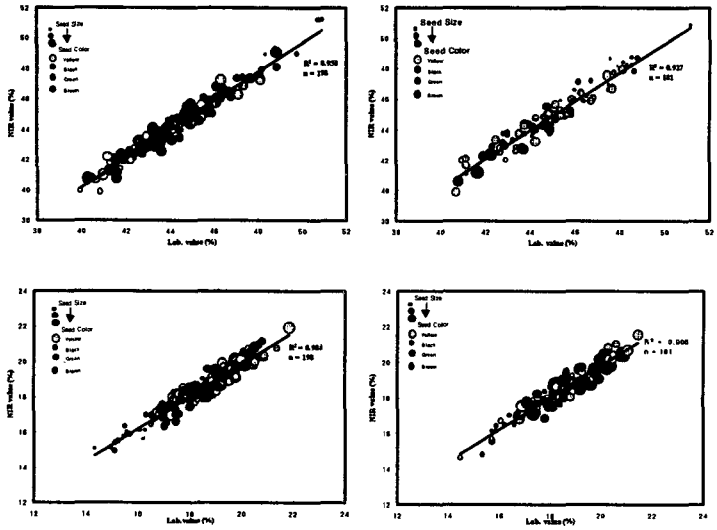

Fig. 1. Scatter plots of protein(upper) and oil(lower) contents by chemical value versus NIRS value for the calibration(left) and validation(right) sample set.

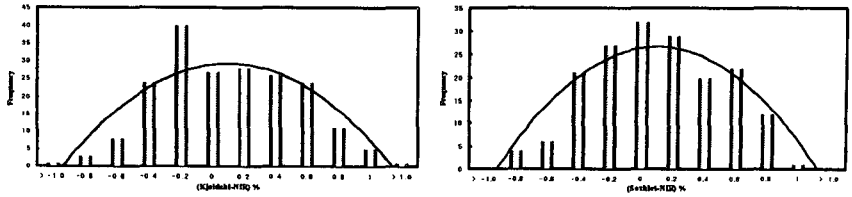

Fig. 2. Histograms of differences between standard chemical method and NIRS contents with a fitted normal distribution curve.

Table 1. Laboratory reference value statistics for protein and oil contents based on intact soybean seed samples.

| Sample set | | n | Mean | Range | SD |
|---|---|---|---|---|---|
| | | | | % | |
| Calibration | Protein | 198 | 44.36 | 39.92~50.90 | 1.98 |
| | Oil | 198 | 18.39 | 14.32~21.84 | 1.35 |
| Validation | Protein | 101 | 44.75 | 40.66~51.13 | 2.09 |
| | Oil | 101 | 18.37 | 14.45~21.42 | 1.48 |

Table 2. Statistics for optimal protein calibration and validation results in MPLS regression method.

| | Calibration$^{T}$ (n=198) | | | Validation (n=101) | | | | |
|---|---|---|---|---|---|---|---|---|
| Term | SEC | $R^2$ | 1-VR | SEP | $R^2$ | Bias | R. SD(%) | SEP/M(%) |
| 9 | 0.442 | 0.950 | 0.926 | 0.568 | 0.927 | 0.060 | 0.57 | 1.27 |

Table 3. Statistics for optimal oil calibration and validation results in MPLS regression method.

| | Calibration$^{T}$ (n=198) | | | Validation (n=101) | | | | |
|---|---|---|---|---|---|---|---|---|
| Term | SEC | $R^2$ | 1-VR | SEP | $R^2$ | Bias | R. SD(%) | SEP/M(%) |
| 9 | 0.418 | 0.904 | 0.795 | 0.451 | 0.906 | -0.017 | 0.45 | 2.45 |