# Application of stepwise multiple regression to predict shoot nitrogen content around panicle initial stage of rice using canopy reflectance data

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## **Objectives**

Shoot N uptake (NUP) at panicle initiation stage (PIS) of rice is an important indicator for yield and protein prediction and N topdressing prescription for rice. Therefore, this study intended to apply stepwise multiple regression to predict NUP around PIS by canopy reflectance (CR) data.

## Materials and Methods

Data of CR and NUP used in this study were collected in two experiments at Experimental Station, Seoul National University, Suwon, Korea in year 2004. The main objectives of the experiments were to determine effect of different N application dates around PIS (exp.1) and variable N rates at PIS (exp.2) on yield, yield components and milled rice protein content. Canopy reflectance was measured by GER 1500 (wavelength range of 300-1100 nm with step of 1.55 nm).

162 observations measured on July 3, July 9 and July 29 in exp.1 were randomly separatedinto two sub-datasets for model calibration (calibration set, 113 observations) and model validation (validation set, 49 observations). Before model calibration, CR was transformed into log form and outliers were removed. The same procedure was applied for validation, test1 and test2 sets except outlier removal. The model was calibrated by stepwise regression with forward selection at P<0.05. The calibrated model was validated by validation set, tested by data in exp.2 measured on July 3 (test1 set) and on July 9 (test2 set). The model quality was examined by coefficient of determination (R<sup>2</sup>), root mean square of error in prediction (RMSEP) and relative error in prediction (REP) that was recommended by Hansen and Schjoerring, 2003.

#### Results and Discussion

Calibrated stepwise regression model to predict NUP by CR was:  $NUP = -2.17 + 7.7CR_{637} + 16.6CR_{958} \quad 23.6CR_{723} \qquad (R^2 = 0.89) \qquad (Eq.1)$ 

Where number followed by CR was wavelength  $\pm$  1.55 nm at which CR was recorded. Canopy reflectance at 637 nm and 723 nm (belonged to red and red edge regions) was related to chlorophyll and N concentration and content (Hansen and Schjoerring, 2003) and at 958 nm (near infrared) was related to biomass, LAI and canopy water content (Thenkabail et. al., 2000). However, the parameters of each CR at a selected waveband did not reflect real relationship between the CR at this waveband and NUP due to normalizing among CRs. For instance, parameter of 7.7 for CR<sub>637</sub> does not mean that there was positive correlation between CR<sub>637</sub>and NUP. The correlation coefficients between NUP and CR at 637, 723, and 958 nm were -0.88, -0.77, and0.70, respectively. Although there was a little bit lower model R<sup>2</sup>and higher REP in test1 and test2 sets than those of calibration set (Table 1 and Fig.1), 13% of relative error in NUP prediction of the test sets promises potential application of the predicted NUP at PIS for prediction of yield and protein content and prescription of N topdressing rates at PIS

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#### **Key references**

Hansen P.M and J.K. Schjoerring, 2003. J. Remote Sens. of Environ. 68: 542-553. Thenkabail P.S., R.B. Smith and E.D. Pauw. 2000. Remote Sens. Environ. 71: 158-182.

Table 1. Summary statistics and predicted model quality parameters of shoot N uptake in calibration, validation, test1 and test2 sets.

Crop variables -	Summary statistics						Model quality		
	n	Mean	SD <sup>\$</sup>	CV	Min	Max	R <sup>2</sup>	RMSEP	REP
Calibration set	105	7.03	2.24	31.9	3.15	13.20	0.89	0.74	10.5
Validation set	49	7.01	2.46	35.1	3.59	15.12	0.88	0.85	12.1
Test1 set	54	5.38	1.72	31.9	2.76	10.15	0.36	0.72	13.5
Test2 set	54	6.21	1.74	28.1	3.60	10.85	0.78	0.81	13.0

SD: Standard deviation, CV: coefficient of variation, R<sup>2</sup>: coefficient of determination, RMSEP: root mean square in prediction (g m<sup>-2</sup>), REP: relativeerror in prediction (%).

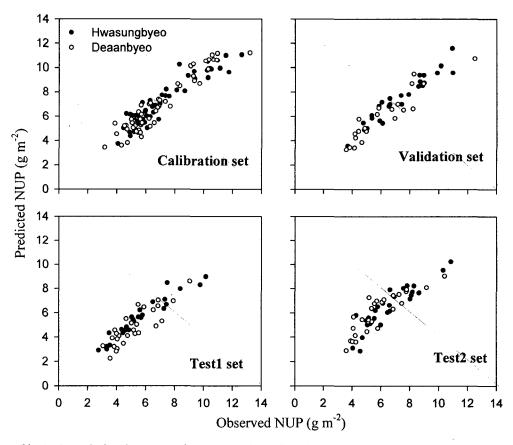


Fig.1. Correlation between observed and predicted shoot N uptake (NUP) in calibration, validation, test1 and test2 datasets. Solid line is 1:1 line.