

Evaluation of daily germination in two rice cultivars using linear regression

Evaluación de la germinación diaria en dos cultivares de arroz mediante regresión lineal

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ABSTRACT: Among the types of plant seed priming, hydropriming stands out with proven benefits in germination properties and is essential for standardizing germination in rice. The objective was to evaluate the daily dynamics of hydroconditioned germinated seeds of rice cultivars INCA P-5 and IACuba-41 (*Oryza sativa* L.) using a simple linear regression model. In January 2024, in Río Cauto, Granma, Cuba, the experiment was conducted with 200 rice seeds (100 per cultivar: INCA LP-5 and IACuba-41). The seeds, selected without defects and with moisture adjusted to 9-10%, were imbibed for 72 hours with irrigation water, dried for 48 hours in the shade, and sown in trays with local Vertisol soil. The number of germinated seeds was evaluated daily for 14 days. A simple linear regression model was applied (days as independent variable, germination as dependent) using ordinary least squares, with the slope (a), intercept (b) and their bootstrap confidence intervals with 1,999 repetitions and 95,0 percentile. Heteroscedasticity, autocorrelation of residuals, predicted values and their standard errors were also determined. The results confirm that the germinated seeds per day in both cultivars do not fit a linear regression model with asymmetric stages of dormancy breaking, germination peak and subsequent decline, with a slight lower dispersion or a more concentrated germination of the INCA LP-5 cultivar compared to IACuba-41

Keywords: Hydropriming, germination, rice, seeds, cultivars, linear regression.

RESUMEN: Entre los tipos de acondicionamiento de semillas de plantas se encuentra el hidroacondicionamiento con beneficios demostrados en las propiedades germinativas, e imprescindible para uniformar la germinación en arroz. El objetivo consistió en evaluar la dinámica diaria de semillas hidroacondicionadas germinadas de los cultivares de arroz INCA P-5 e IACuba-41 (*Oryza sativa* L.) mediante un modelo de regresión lineal simple. En enero de 2024, en Río Cauto, Granma, Cuba, se realizó el experimento con 200 semillas de arroz (100 por cultivar: INCA LP-5 e IACuba-41). Las semillas, seleccionadas sin defectos y con humedad ajustada al 9-10%, se imbibieron durante 72 h con agua de riego, se secaron 48 h a la sombra y se sembraron en bandejas con suelo Vertisol propio de la zona. Se evaluó la cantidad de semillas germinadas diarias durante 14 días. Se aplicó un modelo de regresión lineal simple (días como variable independiente, germinación como dependiente) mediante mínimos cuadrados ordinarios, con la pendiente (a), la ordenada al origen (b) y sus intervalos de confianza por bootstrap con 1 999 repeticiones y percentil 95%. Se determinó además la heterocedasticidad, autocorrelación de los residuos, valores predichos y sus errores estándar. Los resultados confirman que las semillas germinadas por días en ambos cultivares no se ajusta a un modelo de regresión lineal con etapas asimétricas de ruptura de la latencia, pico germinativo y posterior descenso, con una ligera dispersión menor o una germinación más concentrada del cultivar INCA LP-5 respecto a IACuba-41.

Palabras clave: Hidroacondicionamiento, germinación, arroz, semillas, cultivares, regresión lineal.

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INTRODUCTION

Hydropriming, or hydroconditioning in English, is a type of seed conditioning that transforms germination and initial establishment in plant species such as rice (*Oryza sativa* L.), sunflower (*Helianthus annuus* L.), lupin (*Lupinus albus* L.), and cotton (*Gossypium hirsutum* L.). It involves hydrating the seed in a controlled manner, which activates metabolism without causing radicle emergence. Mondo et al. (2016) demonstrated that this technique increases germination and vigor of upland rice without altering the cycle or grain yield, making it useful in agricultural systems under environmental pressure.

Hydropriming activates physiological, biochemical, and molecular networks that explain its favorable effect. Choi et al. (2024) observed that, in rice, this treatment stimulates plumule and radicle elongation, while also increasing the activity of antioxidant enzymes that reduce oxidative stress under water deficit.

Catiempo et al. (2024) used transcriptomic analysis in sunflower seeds and found that genes encoding cell expansion are key to improved germination after hydroconditioning. Priming strengthens tolerance to abiotic stresses. Khalequzzaman et al. (2023) observed that, in cotton, the treatment increased germination, yield, and water productivity under drought. Plažek et al. (2018) demonstrated that the combination of hydroconditioning with smokewater favored lupin (*Lupinus angustifolius* L.) germination at low temperatures, a valuable result for cold regions. Zhang et al. (2024) add that variables such as temperature and humidity regulate the germination of wild rice (*Oryza rufipogon* Griff.), and conditioning allows for fine-tuning these responses.

Simple linear regression models germination by linking elapsed days with the percentage of germinated seeds, allowing for estimating rates and assessing uniformity. Bewley et al. (2013) used this technique with time-transformed (arcsine) data, after validating the independence of residues and calculating germination rates in alfalfa (*Medicago sativa* L.) and lettuce (*Lactuca sativa* L.) under controlled conditions.

However, there is a shortage of studies that use the dynamics of germinated seeds over time as a discrete quantitative variable, as opposed to the prevailing trend of evaluating germination parameters using calculated percentages and rates. The objective of this research was to evaluate the daily dynamics of germinated hydroconditioned seeds of the rice cultivars INCA P-5 and IACuba-41 (*Oryza sativa* L.) using a simple linear regression model.

MATERIALS AND METHODS

The experiment was conducted in the municipality of Río Cauto, Granma province, in January 2024. Two hundred rice seeds (*Oryza sativa* L.) were used, corresponding to the Cuban cultivars INCA LP-5 and IACuba-41,

with 100 units per cultivar. These cultivars emerged from the Cuban rice breeding program and are genetically uniform and have a registered category. They were obtained from the "La Gavina" Seed Unit, belonging to the "Fernando Echenique" Agroindustrial Grain Company in Granma, Cuba.

Seeds without visible defects, empty grains, insect damage, or malformations were selected. The moisture content was adjusted to a range of 9 to 10%, in accordance with international regulations (ISTA, 2022).

The seeds were sown in aluminum trays measuring 5 cm high, 20 cm wide, and 35 cm long. The trays were filled with Vertisol soil (Hernández et al., 2015).

Before sowing, the seeds were soaked in water from the irrigation canal used to flood the rice fields in that area for 72 hours. This is the usual practice in these productive areas, to ensure the results were as accurate as possible. This was not a limitation because the germination rate in the experiment for both cultivars exceeded 95.0%. After this time, the seeds were placed in the shade in an aerated area for 48 hours. They were then sown on the soil surface of the trays, and the soil was moistened with water without causing waterlogging. Each seed was sown in the trays in rows spaced three centimeters apart, with a 10 cm separation between rows.

The trays remained under ambient conditions in January 2024. The recorded temperatures were a minimum of 25°C, an average of 27°C, and a maximum of 29°C. The photoperiod was 12 hours, and the relative humidity was 80%. The number of germinated seeds per day was evaluated for 14 days, from sowing to day 14. Germination was considered when the radicle emerged (>2 mm).

A simple linear regression model was fitted to the data (days as the independent variable, germination as the dependent variable) using ordinary least squares. The slope (a), the intercept (b), and their confidence intervals were obtained by bootstrap resampling and the 95.0% percentile. The significance of the coefficients was verified with Student's t test and heteroscedasticity with the Breusch-Pagan test. Autocorrelation of the residuals was estimated using the Durbin-Watson statistic. The strength of the association was measured with the product-moment correlation coefficient (r) and the proportion of explained variance or adjusted coefficient of determination (adjusted R²). The p-value of the linear regression model was also determined by Fisher and by bootstrap with 9,999 permutations at 95.0% confidence interval.

For both cultivars (INCA LP-5 and IACuba-41), the residual (observed value - value predicted by the fitted line) and its standard error of prediction were calculated for each day. The simple linear regression equation $\hat{Y} = b_0 + b_1X$ was used. The predicted values came from the model, while the residuals arose from the difference between observed and predicted values. Likewise, the standard errors of the predicted values were estimated to assess the model's accuracy. The autocorrelation function of the residuals was analyzed using an autocorrelation function plot to determine the independence of the errors.

The residuals and their standard errors were plotted against the number of days elapsed to inspect homoscedasticity and the model's adequacy.

The probability of germinating seeds over time, estimated by Kaplan-Meier, log-rank, and Wilcoxon for survival analysis using nonparametric methods, was also determined for germination times T25, T50, and T75 (number of days required for 25.0, 50.0, and 75.0% of the total germinated seeds to germinate).

The analyses were performed in R software version 4.5.1 (R Core Team, 2025), with the packages boot for bootstrap, lmttest for diagnostic tests, car for statistical support, broom for tabulating results, and survival version 3.7-0 (Therneau, 2024) for survival analysis.

RESULTS AND DISCUSSION

The purpose of interpreting Table 1 is to compare the INCA LP-5 and IACuba-41 cultivars based on the simple linear regression parameters and their agronomic relevance.

Table 1. Statistical parameters of the linear regression: days vs. germination. *** $p < 0.001$ for both cultivars

Variable	INCA LP-5	IACuba-41
Pendiente (a)	0.369 ± 0.319	0.367 ± 0.337
IC 95 % Pendiente	-0.117 - 1.213	-0.108 - 1.284
Intercepto (b)	1.171 ± 2.443	1.114 ± 2.581
IC 95 % Intercepto	-2.005 - 5.529	-2.281 - 5.277
Correlación r	0.317	0.300
R ² ajustado	0.025	0.014
Error estándar	4.82	5.09
Durbin-Watson	0.473***	0.437***
Breusch-Pagan (p)	0.132	0.081
p Fisher modelo	0.270	0.265
p Bootstrap modelo	0.298	0.292

The slope (a), which indicates the daily change in germination, is 0.369 ± 0.319 for INCA LP-5 and 0.367 ± 0.337 for IACuba-41, showing similar rates between both cultivars. The standard error, slightly higher in IACuba-41, suggests greater variability due to a wider dispersion in its data. The 95% confidence intervals (-0.117 to 1.213 for INCA LP-5; -0.108 to 1.284 for IACuba-41) include zero, indicating the absence of a significant linear relationship. The similarity in germination rates favors planting planning and ensures uniform rice emergence, which is key to crop homogeneity. However, it is recommended to validate these results under various soil and climate conditions. The intercept, 1.171 ± 2.443 for INCA LP-5 and 1.114 ± 2.581 for IACuba-41, reflects high uncertainty and overestimates initial germination, which should be zero. The confidence intervals (-2.005 to 5.529 for INCA LP-5; -2.281 to 5.277 for IACuba-41) include zero, confirming low precision. This overestimation highlights a limitation of the linear model, especially at the beginning of the process.

The Pearson correlation (0.317 for INCA LP-5; 0.300 for IACuba-41) indicates a weak relationship between days and germination, slightly stronger in INCA LP-5, although not practically relevant. The adjusted R² (0.025 for INCA LP-5; 0.014 for IACuba-41) shows that the model explains only 2.5% and 1.4% of the variability, characteristic of a poor fit. The standard error (4.82 for INCA LP-5; 5.09 for IACuba-41) indicates greater dispersion in IACuba-41 and lower predictive accuracy.

The Durbin-Watson statistic (0.473 for INCA LP-5; 0.437 for IACuba-41, $p < 0.001$) reveals positive autocorrelation in the residuals, violating the independence assumption. This indicates that the model does not capture the temporal structure of the data, with a systematic dependence between consecutive observations, more pronounced in IACuba-41. The Breusch-Pagan test ($p = 0.132$ for INCA LP-5; $p = 0.081$ for IACuba-41), being non-significant, indicates the presence of homoscedasticity in the residuals in both cultivars.

The autocorrelation and low adjusted R² reinforce the inadequacy of the linear model, which does not represent the true kinetics of germination. Nonlinear or time-series approaches would allow for better modeling of the dependence between successive observations, offering greater precision for both cultivars. Residual analysis (Tables 2 and 3) identifies four distinctive phases in the germination dynamics of both cultivars: dormancy, exponential, deceleration, and plateau. These stages reflect patterns of overestimation and underestimation of the linear model, linked to key physiological processes. Their examination facilitates understanding of the differences between INCA LP-5 and IACuba-41, in addition to highlighting the limitations of linear fitting in describing rice germination.

The p-value for the linear regression model, calculated using Fisher's F statistic and bootstrapping for both cultivars, was greater than 0.05; therefore, the model is not statistically significant. This indicates that there is insufficient evidence to affirm that the number of seeds germinated per day follows a linear relationship.

Table 2. Observed, predicted and residual values for INCA LP-5

Days	Seeds Germinated	Predicted Value	Residual	Standard Error of Predicted Value
0	0	2.343	-2.343	4.885
1	0	3.081	-3.081	4.355
2	0	3.820	-3.820	3.859
3	0	4.558	-4.558	3.410
4	0	5.297	-5.297	3.030
5	2	6.035	-4.035	2.747
6	8	6.774	1.226	2.594
7	26	7.512	18.488	2.594
8	24	8.250	15.750	2.747
9	20	8.989	11.011	3.030
10	14	9.728	4.273	3.410
11	6	10.466	-4.466	3.8587

Table 3. Observed, predicted, and residual values for IACuba-41

Days	Seeds Germinated	Predicted Value	Residual	Standard Error of Predicted Value
0	0	2.229	-2.229	5.162
1	0	2.963	-2.963	4.603
2	0	3.697	-3.697	4.077
3	0	4.431	-4.431	3.602
4	0	5.165	-5.165	3.199
5	2	5.900	-3.900	2.902
6	8	6.633	1.367	2.741
7	18	7.367	10.633	2.741
8	28	8.101	19.900	2.902
9	26	8.835	17.165	3.199
10	14	9.569	4.431	3.602
11	2	10.303	-8.303	4.077
12	0	11.037	-11.037	4.603
13	0	11.771	-11.771	5.162

Residual analysis reveals a nonlinear pattern that can be grouped into phases of the germination process.

Dormancy-breaking phase (days 0-4): overestimation and differences in the magnitude of the initial delay

During the first five days of sampling, both cultivars exhibit increasing negative residuals. This indicates a systematic overestimation by the linear model. The cumulative magnitude of the error differs: INCA LP-5 accumulates 15.98 units on days 0-4, while IACuba-41 reaches 18.48 units.

This greater magnitude in IACuba-41 suggests a more pronounced initial delay, possibly due to a link with persistent residual dormancy or a slower initial imbibition rate, implying that IACuba-41 would require greater degree-days to surpass the physiological threshold for germination.

Exponential phase (days 5-8): amplitude and peak of underestimation

Between days 5 and 8, both cultivars move to positive residuals. This reflects the model's underestimation at the stage of maximum germination speed. The dynamics differ qualitatively: INCA LP-5 reaches its maximum positive residual on day 7 (18.49%), while IACuba-41 does so on day 8 (19.90%).

This lag indicates that IACuba-41 has a germination progression curve shifted to the right. The accumulation of positive residues in IACuba-41 is 49.66 units versus 35.27 in INCA LP-5, indicating a steeper germination rate.

Deceleration phase and loss of viability (days 9-13)

From day 9 onwards, both cultivars show a reduction in positive residues. INCA LP-5 changes sign on day 11 (-4.47), while IACuba-41 does so on day 10 (-8.30) and reaches an extreme negative residual on day 13 (-11.77). This greater amplitude in IACuba-41 (accumulated -31.11 units vs. -4.47 in INCA LP-5) indicates a more abrupt

deceleration and more rapid loss of viability, indicating that IACuba-41 has a germination amplitude that is less concentrated over time.

Predictive Accuracy and Residual Heterogeneity

The standard error of the residuals is greater in IACuba-41 (range 2.74-5.16) than in INCA LP-5 (2.59-4.89). This greater dispersion reflects greater residual heterogeneity in IACuba-41, attributable to intra-seed biological variability or sensitivity to environmental microvariations.

From a statistical perspective, the wider confidence intervals for the IACuba-41 residuals reinforce the fact that its germination curve is more difficult to predict with a simple linear model. Although both cultivars challenge the validity of the linear model, there are nuances that allow us to distinguish their physiological behavior. INCA LP-5 exhibits earlier and more stable germination, with a lower residue range and superior fit. This makes it more robust under marginal conditions or with intensive agronomic management.

IACuba-41 shows delayed germination but is explosive once initiated, with an abrupt plateau and high residual variability. These characteristics would make it more suitable for homogeneous and stable environments where concentrated emergence is a competitive advantage. The graph shows the residuals (Fig. 1a) of the model (y-axis) according to the number of days elapsed (x-axis), with error bars reflecting the standard errors of the predictions. From a statistical perspective, this allows for assessing violations of the assumptions of linearity (systematic patterns in residues), homoscedasticity (constant variance, indicated by similar error bars), and independence (temporal clustering). The red line at $y=0$ serves as a reference to verify whether the residuals are randomly distributed, which would suggest an adequate model fit.

In IACuba-41, the residuals show a curvilinear pattern: negative on days 0-4 (<-10), positive on days 8-9 (>15), and negative on days 11-13 (<-10), indicating nonlinear dynamics. The linear model underestimates early and late germination but overestimates the intermediate phase. The error bars, wider at the extremes, confirm heteroscedasticity, reflecting biological variability in seedling emergence, influenced by imbibition or reserve depletion. The linear model does not capture the nonlinear kinetics of this cultivar adapted to tropical conditions.

IACuba-41 presents larger residuals (>19 vs. >18 in INCA LP-5) and wider error bars ($SE \approx 5.16$ vs. ≈ 4.89), indicating greater variability and lower predictive accuracy. The autocorrelation is more pronounced in IACuba-41, suggesting stronger temporal dependencies.

In INCA LP-5 (Fig. 2a), the residuals are negative on days 0-5 (≈ -5), positive on days 7-9 (>15), and negative on days 11-13 (<-10), with less pronounced curvature. Heteroskedasticity indicates lower accuracy at the extremes, with initial and late underestimation and central overestimation.

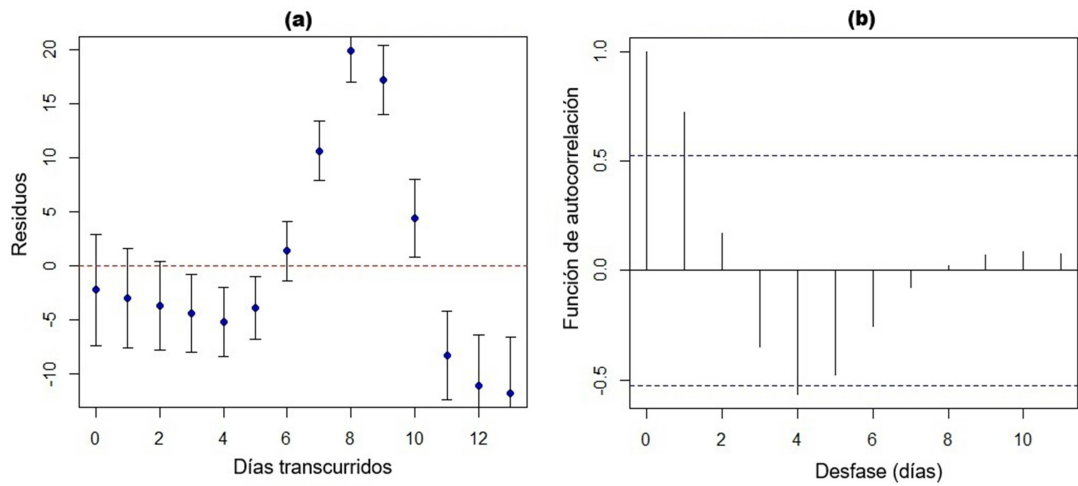


Figure 1. Residuals with their standard errors (Figure 1a) and autocorrelation (Figure 1b), cultivar IACuba-41.

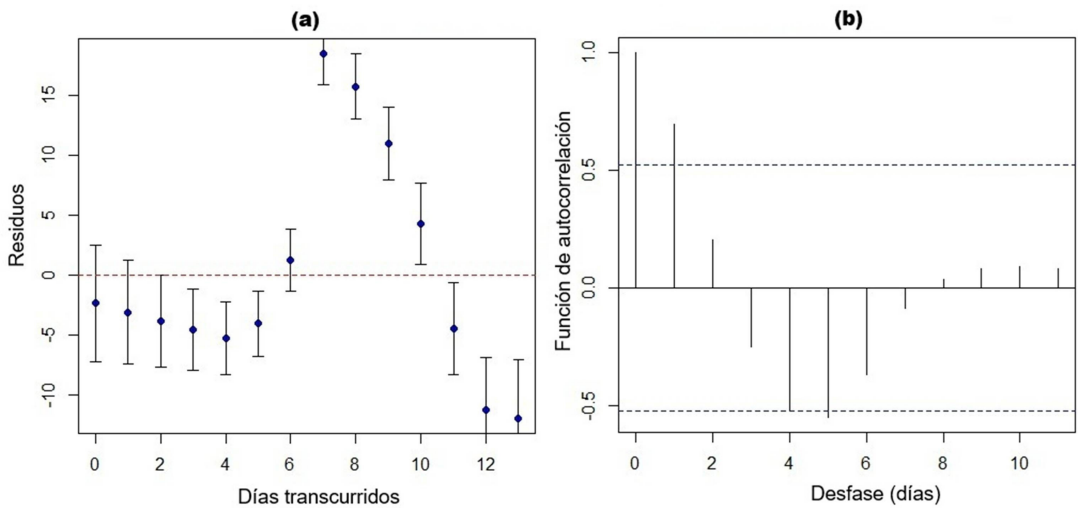


Figure 2. Residuals with their standard errors (Figure 2a) and autocorrelation (Figure 2b), INCA LP-5 cultivar.

The autocorrelation plot (Fig. 1b) shows the serial correlation of residuals, with values between -1 and 1. The x-axis represents the lags, and the y-axis represents the autocorrelation function. Dashed blue lines mark significance thresholds ($\pm 2/\sqrt{n}$, $n=14$).

Autocorrelation assesses serial dependencies, where bars exceeding thresholds violate error independence, increasing the variance of estimators. In germinal data, this reflects inherent temporal dependencies.

In IACuba-41, the autocorrelation at lag 1 (≈ 0.6) is significant and declines at higher lags, indicating an AR(1) process. An AR(1) process (autoregressive of order 1) is a statistical model in which the value of a variable at a given time depends linearly on its value at the immediately preceding time, plus a random error term. This implies that the residuals are not completely random, but rather have a temporal structure where each residual is influenced by the previous one, and suggests carryover effects, such as timing of emergence or environmental factors like temperature.

The rapid decay implies that the linear model does not capture the temporal structure. Models with autoregressive errors or GAM could improve the fit of nonlinearities.

In INCA LP-5 (Fig. 2b), the autocorrelation at lag 1 ($\approx 0.5-0.6$) is significant but less intense, with decay at later lags, and suggests less serial dependence. This violates independence and affects tests such as Durbin-Watson ($\approx 0.4-0.5$). This may be attributed to cumulative effects, such as inhibitor release or metabolite accumulation. INCA LP-5 shows greater genetic evenness or lower environmental sensitivity.

IACuba-41 presents larger central positive residuals, although it presents greater uncertainty in the early and late phases. This characteristic could imply greater vulnerability to abiotic stresses, such as initial drought. INCA LP-5, on the other hand, shows more gradual transitions, indicating greater germination stability, which is useful in diversified cropping systems.

Both rice cultivars show similar violations of the linear model assumptions: nonlinearity (curvilinear residuals), heteroskedasticity (wider errors at extremes), and positive autocorrelation, low explanatory power (adjusted $R^2 \leq 0.025$), confidence intervals that include zero, and significant residual autocorrelation (Durbin-Watson < 0.5) coincide with problems described by Sileshi (2012) and Carvalho et al. (2018),

who warn about underestimation of the standard error and inflated significance by ignoring the binomial nature and temporal correlation of the data.

This limitation was highlighted in the study by Scott et al. (1984) with *Solanum lycopersicum* L., where it was shown that the estimation of mean germination time and conditional probability of germination (risk) is biased if survival models or cumulative distribution functions are not incorporated.

Another problem arises when germination data are expressed cumulatively, a situation that breaks the independence of observations. In this context, Hay et al. (2014) recommend analyzing proportions using probit or logit models (binomial GLM). These authors also warn that the arcsine transformation, common in studies on germination percentage, does not correct for heteroskedasticity and can even exacerbate the lack of normality, as demonstrated by Ahrens et al. (1990).

The variability in the proportion of germinated seeds is not always constant across genotypes. In the cultivar IACuba-41, marginal heteroskedasticity was observed ($p = 0.081$), indicating that the variance depends on the level of the mean. This behavior has been described by Scott et al. (1984) and Sileshi (2012), who showed that the variance follows a quadratic function with respect to the mean.

Given this limitation, the use of more flexible models is recommended. Generalized linear mixed models (GLMM) and beta-binomial regressions allow for the incorporation of associated random effects. This feature improves the representation of the hierarchical structure of the data. Bolker et al. (2009) and McNair et al. (2012) highlight that these approaches offer more reliable inferences when the variance is not constant.

For other regression analysis alternatives, Jiang et al. (2020) applied stepwise regression analysis to select minimum soil quality indicators in deltaic wetlands, with a high correlation coefficient of determination ($R^2 > 0.85$). This method allows for optimizing resources for a data set without sacrificing precision and is applicable to variables and parameters related to germination.

When comparing cultivars, it is essential to consider that seed physiological parameters such as base temperature (T_b) and base water potential (ψ_b) vary between genotypes. Bradford (2009) and Ali and Ullah (2022) recommend estimating them simultaneously using hydrothermal models. This procedure avoids biases that arise from assuming fixed values or fitting linear slopes separately.

The distribution of germination times rarely conforms to the normal model, especially in the presence of censoring or skewness. Watt et al. (2011) and Mesgaran et al. (2013) have shown that these alternatives reduce prediction error.

An additional robust approach is the use of conditional survival models. Scott et al. (1984) emphasize that they allow analysis of time to germination without assuming normality. This method has been validated in *Solanum lycopersicum* L. by Scott and Jones (1982).

The application of simple linear regression in INCA LP-5 and IACuba-41 reproduces the systematic errors identified for more than four decades in the specialized literature: violation of independence, heteroskedasticity, and underestimation of error. The transition to probit/logit, hydrothermal, and survival models is not only advisable but necessary to obtain valid estimates and reliable comparisons between cultivars.

In both cases, it is advisable to move toward nonlinear models for germination curves or incorporate autoregressive terms, such as ARIMA models, to improve the fit and inferences about seed viability and potential yield. Future research could integrate environmental variables to unravel these dynamics and optimize planting practices in the context of tropical agronomy and the pressures of climate change.

Although germination slopes are very similar between cultivars (0.369 vs. 0.367), IACuba-41 reached a higher peak (14 vs. 13 seedlings on day 8). This difference could be attributed to higher initial viability or lower dormancy levels. These traits are relevant in breeding programs, where establishment is The rapid and uniformity of the crop directly impacts final yield.

In recent years, conditioning has evolved beyond its traditional use. Kharb et al. (2023) demonstrated that this technique, which includes the inclusion of iron, not only improves germination and growth in rice but also increases the iron content in seedlings. This evidence opens a promising avenue for crop biofortification, especially in regions with nutritional deficiencies.

However, this technique is not without risks. Ren et al. (2023) warn that certain seed conditioning methods can accelerate the deterioration of rice seeds. This effect is linked to an increase in the production of reactive oxygen species, elevated respiration, and premature starch degradation. These processes compromise long-term viability, requiring careful protocol design.

Environmental contaminants represent an emerging challenge for seed germination. Recent research reveals that microplastics such as polyethylene, polypropylene, and polystyrene adversely affect the early development of rice plants (Iswahyudi et al., 2024) and limit the effectiveness of conditioning in contaminated soils. Despite scientific progress, notable limitations remain. The lack of standardized protocols, including hydration times and substance concentrations, hampers the comparability and reproduction of results.

Our understanding of regulatory pathways remains incomplete. While studies have made progress in identifying essential genes and metabolites (Catiempo et al., 2024; Liu et al., 2023), integrating these elements into functional models requires further development. Another critical obstacle is the paucity of information on the long-term effects of conditioning on grain yield and quality, as most research focuses exclusively on germination and early growth. The extensive application of these techniques in commercial agricultural systems faces logistical and economic barriers.

Genotypic specificity in conditioning responses restricts its universal applicability. As Barik *et al.* (2022) point out, this variability demands research focused on the genetic diversity of crops.

On the other hand, Ranmeechai *et al.* (2022) found that hydroconditioning significantly improves germination and vigor in Philippine rice varieties after extended storage periods. This ability to counteract the effects of aging enables its use in systems where access to fresh seeds is limited. Thus, conditioning is consolidated as a strategic tool, provided that efficacy and preservation of seed quality are balanced.

Germination modeling using simple regression is an essential tool. These models make it possible to analyze responses to variables such as temperature, salinity, and water stress, in order to optimize agricultural conditions for rice, sesame, *Foeniculum vulgare* (Mill.), *Vigna radiata* (L.) R. Wilczek, and *Allium cepa* L. crops. The characterization of the germination response of *Secale montanum* Guss. to different temperatures allowed the identification of optimal thresholds using nonlinear models (Ansari *et al.*, 2017).

The analysis of interactions with stressors has been simplified by simple regression. When evaluating the joint effect of salinity and water conditioning on *Foeniculum vulgare* Miller, Kiani *et al.* (2013) observed an increase in tolerance that opens up possibilities for degraded soils. In an emerging scenario, Kumar and Thakur (2025) described, using nonlinear regression, the dose-dependent phytotoxicity of hematite nanoparticles in *Vigna radiata* (Linnaeus) Wilczek and *Allium cepa* Linnaeus, which projects sustainable uses of nanotechnology.

When data become complex or unbalanced, simple regression is combined with advanced methods to overcome its limitations. In rice seedling classification, Mara *et al.* (2025) integrated artificial intelligence and a linear component to refine accuracy, while Cheng *et al.* (2022) employed low-field nuclear magnetic resonance and machine learning, using linear regression to interpret vigor. Both works suggest a transition toward hybrid models and non-destructive techniques.

In the genetic and production fields, Sales *et al.* (2017) applied linear regression in a genome-wide association study to locate loci related to cold tolerance in rice germination in japonica subspecies. Meanwhile, Sairdama *et al.* (2025) also used linear regression to identify factors that influence rice production, such as planted area and fertilizers, to demonstrate the usefulness of simple models in large-scale agricultural decisions.

Significant gaps remain. Research using nonlinear regression, such as that by Ansari *et al.* (2017), Pedroso *et al.* (2019), and Puteh *et al.* (2010), is conducted under controlled conditions and requires validation in real fields. Furthermore, simple regression, whether linear or nonlinear, requires support such as machine learning to capture multifactorial interactions, as noted by Cheng *et al.* (2022) and Mara *et al.* (2025).

Integration with omics data is also limited; although Sales *et al.* (2017) make progress in genetics, simple models do not reveal complex regulatory networks.

Studies such as those by Kiani *et al.* (2013) assume simple patterns and show sensitivity to extreme values, suggesting the suitability of robust or Bayesian approaches. Finally, the lack of standardized protocols and interspecies validation limits generalization. Overcoming these gaps will allow simple regression to be used with greater confidence in precision agriculture and climate resilience strategies.

The comprehensive review of analytical and graphical methods for analyzing seed germination data highlights the need to handle qualitative responses of individuals and population distributions over time, including censored data (viable seeds that do not germinate during the trial). Scott *et al.* (1984) present this analysis in their article.

Among the analytical methods, simple linear regression is widely applied for quantitative treatments, as is the case with germination percentage analysis. Linear regression after arcsin transformation is used to partition effects into linear, quadratic, or orthogonal components, facilitating treatment comparisons. Similarly, it is also used for germination index and germination rate coefficients to describe responses to continuous variables such as temperature, with analysis of covariance to test for homogeneity of coefficients and detect interactions such as genotype-temperature (Scott *et al.*, 1984).

The relationship between germination rate (the reciprocal of time up to a fixed percentage) and temperature is modeled using simple linear regression. Covell *et al.* (1986) extrapolated daily data and analyzed residuals to ensure independence in legumes such as chickpea (*Cicer arietinum* L.) and soybean (*Glycine max* (L.) Merr.).

These studies underscore the versatility of simple linear regressions in capturing daily germination progression, although they emphasize the need for transformations and validations to manage variability and meet statistical assumptions in agricultural contexts.

The results in Figure 3 demonstrate the high germination percentages achieved, the absence of significant differences ($p > 0.05$) between the germination patterns of both cultivars in the Log-rank ($p = 0.939$) and Wilcoxon ($p = 0.895$) tests, and that the small variations observed in the germination curves are due to chance and not to biological differences, water quality, or seed quality between the genetic materials. This statistical equivalence is reinforced by the exact coincidence in the germination times T25, T50, and T75 (8, 9, and 10 days, respectively, for both cultivars).

However, Mamani *et al.* (2024) found different significance values for both nonparametric statistical tests in germination parameters of *Cecropia pachystachya* Trécul and *Jacaranda caroba* (Vell.) A.H. Gentry.

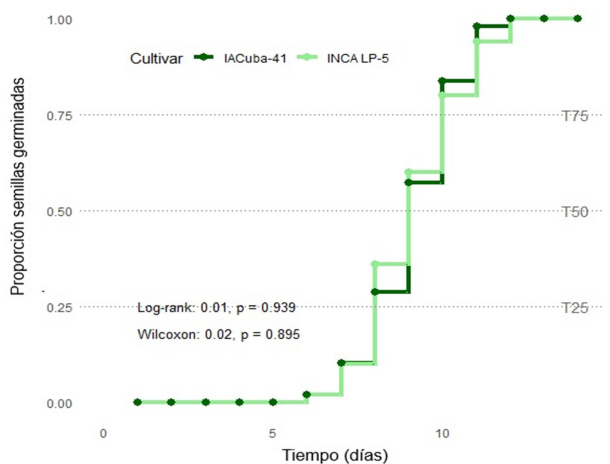


Figure 3. Probability of hydroconditioned seeds germinating as a function of time, estimated by Kaplan-Meier and Wilcoxon methods. T25, T50, and T75 are the germination times. P values > 0.05 indicate the absence of significant differences.

CONCLUSIONS

The Cuban rice cultivars INCA LP-5 and IACuba-41 exhibit similar germination dynamics, with INCA LP-5 showing lower residual dispersion and greater stability. However, the linear model does not adequately represent the process of germinated seeds by days due to its sigmoidal nature, with asymmetric stages of dormancy breaking, peak and decline in germination, autocorrelation, and low explanatory power.

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