The contribution of the International Rice Genebank to varietal improvement and farm productivity in Eastern India

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Highlights

- 20% of the improved varieties cultivated on 95% of rice area in Eastern India (10.8 million hectares during the 2015 wet season) had at least one direct parent from the IRG.

- Almost half (45%) of the genetic composition of these improved rice varieties came from accessions from IRG, based on Mendelian principles.

- The average Coefficient of Parentage (COP) among the top 10 improved rice varieties is 9.7% which implies high genealogical (latent) diversity in cultivated rice.

- A 10% increase in the definite genetic contribution of the IRG is associated with a 27% increase in rice yields.

Why we need the IRG

During the Green Revolution in 1960s, high-yielding rice varieties were introduced in response to the specter of famine as population densities rose and productivity stagnated. However, this remarkably successful event created an unintended consequence – crop diversity loss. Traditional varieties and the wild species of rice were rapidly replaced by new varieties.

To protect against the loss of rice diversity, the International Rice Research Institute (IRRI) initiated the collection of rice genetic resources in 1962 which eventually led to the establishment of the International Rice Genebank (IRG) in 1971.

Rice genetic improvement using IRG accessions was accomplished through IRRI's breeding program which produces improved cultivars for use as parents in national plant breeding programs or direct planting materials in farmers' fields.

Research objectives

- Assess the impact of genetic ancestry from IRG-distributed germplasm on rice productivity of farmers in Eastern India.
- Examine the ancestry of improved rice varieties grown by over 8000 farmers surveyed in 2016, characterizing the mostly widely used progenitors.
- Evaluate the genealogical (latent) diversity of the most widely grown, improved rice varieties using Coefficients of Parentage (COP).

Data and methods

We utilized data collected in 2016 by IRRI from 8,640 rice farmers in 720 villages and 4 states of Eastern India (Eastern Uttar Pradesh, Bihar, Orissa, and West Bengal) through the Rice Monitoring Survey (RMS) project funded by the Bill and Melinda Gates Foundation (BMGF).

To estimate the genetic contribution of germplasm from IRG, we –

- *identified the most popular improved rice varieties, covering 95% of the total area planted with improved rice varieties;*
- *conducted a pedigree analysis using Mendelgram to quantify the progenitor contribution of accessions from IRG to each improved rice variety;*
- *estimated a plot-level yield response function to test the effect of the genetic contribution of accessions from IRG to productivity;*
- *identified the country of origins of the accessions found in the ancestry of each variety and characterized 3 of the most popular progenitors;*
- *computed Coefficient of Parentages (COP) for the 10 most widely grown, improved rice varieties.*

The contribution of IRG genetic resources to farm productivity

Independent variables	Coef.
Fertilizer (InFer)	0.869**
Labor (InLab)	-0.673*
Power_cost (InPow)	0.139
Other_inputs (InOth)	0.206**
InFer x InFer	-0.034*
InLab x InLab	0.236**
InPow x InPow	-0.002
InOth x InOth	0.015**
InFer x InLab	-0.088*
InFer x InPow	0.027**
InFer x InOth	-0.040**
InLab x InPow	-0.055**
InLab x InOth	-0.034**
InPow x InOth	0.013**
Irrigation_percent	0.127**
Crop_establishment	0.315**
Submergence	-2.469**
Salinity	-1.279*
Drought	-1.247**
Age	-0.013
Age x Age	0.000
Education	-0.017
Education x Education	0.002
Access_input	-0.244*
Access_credit	0.305*
Access_extworker	-0.128
IRG_contribution	0.027**
i.State	included
Constant	4.764**

$$lny_i = \beta_0 + \sum_{i=1}^{n} \beta_i lnx_i + \frac{1}{2}\sum_{i=1}^{n}\sum_{j}^{n} \beta_{ij} lnx_i \, lnx_j + \sum_{j=1}^{n} \alpha_i z_i + \mu_i$$

The preferred translog model indicates that the coefficient of the definite IRG contribution is positive and significant. This result confirms that larger genetic contributions from IRG are associated with higher on-farm yields of improved rice varieties.

Type of IRG contribution	Mean contribution (weighted by area planted)
Definite	0.45
Possible	0.32
None	0.07
Unknown	0.16
Total	1.00

Photo from CGIAR Genebank Platform Flickr

This study identified 122 unique progenitors with definite and possible contribution of IRG from 18 countries of origin. Philippines has the highest (35), followed by India (30).
Peta, Dee Geo Woo Gen (DGWG), and Fortuna were the 3 most frequently used progenitors with definite IRG contribution.

IRG has contributed to both higher yields & higher diversity of rice on farms in Eastern India.

https://www.genebanks.org/resources/impacts/rice/