**The BRRI stability trials**

Bangladesh Rice Research Institute (BRRI) have conducted multi-location rice variety trials since 2001. These trials were conducted in both the wet season (Aman dataset) and the dry season (Boro dataset). The Aman dataset contains the yields (t ha-1) up to 2017, while the boro dataset contains the yields up to the growing season in 2017-2018. In each location and in each year, the trials were laid out according a randomised complete block design with three blocks.

Currently, the plot data of the trials are divided into two series, ranging from 2001-2015 and from 2015-2017/2018, thus the data in 2015 occurs twice. The data of 2015 in the two series is, however, not consistent meaning that the two subsets of 2015 do not share the same locations and furthermore, the plot yields for shared locations differ in some cases. This needs to be checked in order to come up with a consistent set for 2015.

At the moment, the year 2015 was removed from the 2001-2015/2016 series. For the resulting combined series from 2001 to 2017/2018, the genotype-year combinations, and the location-year combinations are shown in Figures 1 and 2 in order to get an overview of the genotypes and locations tested in the different years.

The assessment of genetic gain requires the year of release of each genotype. For the new series form 2015-2017/2018, this information is, however, not contained in the data. Thus the year of release of genotypes that only occur in the series form 2015-2017/2018 was set to 2015 or 2016, according to Figures 1 and 2.

A last thing to note is that the categories of the growing duration differ between the series from 2001-2015 and from 2015-2017/2018, e.g. for Boro, genotype BR1 is listed as “short” in the data from 2001-2015 and as “medium” in the data from 2015-2017/18. For the Aman series, the group of genotype BR11 is “medium” for the series 2001-2015 and “long” in the series 2015-2017. Currently, the groups of the genotypes in the 2001-2015 series were chosen for the 2015-2017/18 series.

For the Aman series, the grouping of genotypes is not unique, meaning that two genotypes occur in different groups (“BRRI dhan53“ and “BRRI dhan57” are categorized as both “Short” and “Stress”). Those two genotypes were re-grouped to “Short”.

For the Boro series, some genotypes that only occur in the 2015-2017/18 series were grouped as “medium”. According to Table 1, this is not a valid group. Thus, the groups of these genotypes was chosen according to Table 1, using the estimated mean growth duration for these genotypes to determine the group.

So far, the analysis was done making the changes described above. Please be aware of that when looking at the results and please verify the changes concerning the year 2015, the registration years of genotypes occurring only in 2015-2017/18, and the genotype categories and send us updated data if necessary.



**Figure 1:** Classification of genotype-year combinations (left) and location –year combinations (right) for Aman Series. Cell colours indicate how frequently the combinations occur in the dataset (light grey: minimum frequency; dark grey: minimum to mean frequency; black: mean to maximum frequency)

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**Figure 2:** Classification of genotype-year combinations (left) and location –year combinations (right) for Boro Series. Cell colours indicate how frequently the combinations occur in the dataset (light grey: minimum frequency; dark grey: minimum to mean frequency; black: mean to maximum frequency)

**Table 1:** Categories of Boro and Aman rice varieties based on growth duration

|  |  |  |
| --- | --- | --- |
| **Category** | **Definition of category** | |
| **Boro** | **T. Aman** |
| Long duration (days) | More than 150 | More than 145 |
| Medium duration (days) | - | 135 to 145 |
| Short duration (days) | Less than 150 | Less than 125 |
| Stress condition | Tolerance capacity against different stresses | Tolerance capacity against different stresses |
| Aromatic | - | Premium quality |

Source: Plant Breeders of BRRI and BRRI (2017)

**Material and Methods**

**Analysis of trends**

***Analysis of genetic and non-genetic trends***

As there were no missing data and all trials had complete blocks, we estimated genotype means for each year-location combination (Figures 3 to 6). The model fitted in the second stage was (Piepho et al., 2014)

, (1)

where is the mean yield of the *i*th genotype in the *j*th location and *k*th year, is a fixed intercept, is the fixed slope for genetic trend, is the year of release for the *i*-th variety, is the fixed slope for non-genetic trend, is the calendar year, is the random main effect of the *i*th genotype, is the random main effect of the *j*th location, is the random main effect of the *k*th year, is the *jk*th random location-year interaction effect, is the *ij*th random genotype-ocation interaction effect, is the *ik*th random genotype-year interaction effect, and is a random effect comprising genotype-location-year interaction and experimental error. In model (1), the variance of is assumed to be known and equal to the variance of the corresponding genotype-location-year mean.

***Analysis of group-specific genetic trends***

In order to investigate if the genetic trend differs between category, we estimated category specific genetic trends. For this purpose model (1) was extended by a category specific intercept and slope.

(2)

This model allows to quantify the genetic trends for each category and to test if the trends differs between categories.

**Analysis of genotypic stability**

***Shukla’s stability variance model***

If (1) is extended by a random effect with genotype-specific variances we obtain a stability variance (Shukla 1972) based on the three-way interaction

(3)

where all terms but are defined as in (1).

**Results**

***Analysis of genetic and non-genetic trends***

The estimated genotype-location-year means are shown in Figures 3 to 6, where they are plotted against the trial year and the registration year. Table 2 shows the fixed effects (genetic and non-genetic trend) and the variance components estimated using model (1), revealing a significant genetic trend for the Boro series.

***Analysis of group-specific genetic trends***

The genetic trends for the different categories estimated by (2) are displayed in Table 3. For the Boro series, the standard errors of the group specific intercepts and the overall intercept are fairly large to those of the Aman series. Tables 4 and 5 show the differences of the genetic trends for each pair of categories and a test if the difference is significantly different from zero.

***Shukla’s stability variance model***

The Plots of the genotype specific variances based on Shukla’s stability variance model (3) are shown in Figures 7 and 8. These Figures clearly show that the standard errors of the variance components are generally large for genotypes that were only observed in a few years. For the Aman data, such genotypes are “BRRI dhan 66”, “BRRI dhan 70”, “BRRI dhan 71”, “BRRI dhan 72”, “BRRI dhan 73”, “BRRI dhan 75”, “BRRI dhan 76”, “BRRI dhan 77”.

For Boro, genotypes “BR26”, “BRRI dhan67”, “BRRI dhan68”, “BRRI dhan69”, “BRRI dhan74” have large standard errors.



**Figure 3.** Genotype means per environment of T. Aman seasons plotted against the calendar year of the respective trial. Colours indicate the year of release for the respective genotype.



**Figure 4.** Genotype means per environment of T. Aman seasons plotted against the year of release for the respective genotype. Colours indicate the calendar year of the respective trial.



**Figure 5.** Genotype means per environment of Boro seasons plotted against the calendar year of the respective trial. Colours indicate the year of release for the respective genotype.



**Figure 6.** Genotype means per environment of Boro seasons plotted against year of release for the respective genotype. Colours indicate the calendar year of the respective trial.

**Table 2**: Estimates of fixed effects (t ha-1) and variance components (t2 ha-2) using model (1).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Aman | | Boro | |
| Fixed effects | Estimate | Standard error (p-value) | Estimate | Standard error (p-value) |
|  | -56.0899 | 39.7316 (p = 0.1857) | -45.5913 | 39.6475 (p=0.2726) |
|  | 0.0053 | 0.0062 (p= 0.3946) | 0.01050 | 0.0035 (p=0.0027) |
|  | 0.0246 | 0.0188 (p= 0.1927) | 0.01502 | 0.0195 (p= 0.4411) |
|  |  |  |  |  |
| Variance components | Estimate | Confidence limits | Estimate | Confidence limits |
|  | 0.1952 | 0.1212-0.3659 | 0.076 | 0.0442-0.1619 |
|  | 0.1580 | 0.0655-0.7665 | 0.437 | 0.2060-1.4729 |
|  | 0.0674 | 0.0231-0.6820 | 0.067 | 0.0215-0.9191 |
|  | 0.5010 | 0.3892-0.6692 | 0.641 | 0.5089-0.8347 |
|  | 0.1690 | 0.1441-0.2011 | 0.147 | 0.1267-0.1747 |
|  | 0.0902 | 0.0775-0.1063 | 0.067 | 0.0579-0.0799 |

**Table 3**: Estimates of group-specific intercepts and slopes based on model (2) for both the Aman series and the Boro series.

|  | Aman | | | Boro | | |
| --- | --- | --- | --- | --- | --- | --- |
| Fixed effects | Estimate | Standard error | p-value | Estimate | Standard error | p-value |
|  | -67.6744 | 75.2722 | 0.3879 | 679.39 | 83257 | 0.9936 |
|  | 0.02430 | 0.01888 | 0.1982 | 0.01498 | 0.01946 | 0.4416 |
|  | -0.04355 | 32.1996 | 0.9989 | 0.01882 | 0.01005 | 0.0613 |
|  | 0.04898 | 32.1996 | 0.9988 | . | . | . |
|  | 0.03256 | 32.1996 | 0.9992 | -0.00763 | 0.01114 | 0.4935 |
|  | 0.05262 | 32.1996 | 0.9987 | . | . | . |
|  | 0.05136 | 32.1996 | 0.9987 | -0.00880 | 0.01187 | 0.4585 |
|  | 0.05510 | 32.1997 | 0.9986 | 0 | . | . |
|  | 11.1918 | 71.8102 | 0.8762 | . | . | . |
|  | 45.0095 | 67.8378 | 0.5071 | -726.19 | 83258 | 0.9930 |
|  | 5.0095 | 66.5431 | 0.9400 | . | . | . |
|  | 7.0100 | 72.3135 | 0.9228 | -724.02 | 83258 | 0.9931 |
|  | 0 | . | . | -741.62 | 83258 | 0.9929 |

**Table 4**: Differences of group-specific slopes based on model (2) for the Aman series.

| Difference | Estimate | Standard error | p-value |
| --- | --- | --- | --- |
|  | 0.01642 | 0.01746 | 0.3470 |
|  | -0.00364 | 0.01615 | 0.8216 |
|  | -0.00238 | 0.02152 | 0.9119 |
|  | -0.00612 | 0.03582 | 0.8644 |
|  | -0.02006 | 0.01103 | 0.0690 |
|  | -0.01880 | 0.01793 | 0.2946 |
|  | -0.02254 | 0.03381 | 0.5051 |
|  | 0.001262 | 0.01668 | 0.9397 |
|  | -0.00247 | 0.03316 | 0.9405 |
|  | -0.00374 | 0.03602 | 0.9174 |

**Table 5**: Differences of group-specific slopes based on model (2) for the Boro series.

| Difference | Estimate | Standard error | p-value |
| --- | --- | --- | --- |
|  | 0.001171 | 0.007979 | 0.8833 |
|  | -0.00763 | 0.01114 | 0.4935 |
|  | -0.00880 | 0.01187 | 0.4585 |

**second data inspection means aman shukla**

**Figure 7.** Shukla’s stability variances and their standard error for each genotype estimated via (3) for T. Aman seasons.

**second data inspection means boro shukla**

**Figure 8.** Shukla’s stability variances and their standard error for each genotype estimated via (3) for Boro seasons.

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