

**Assessment of Genetic Variability and
Character Association of Myanmar Local Rice
(*Oryza sativa* L.) Germplasm**

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ABSTRACT

Forty-two Myanmar local rice genotypes were evaluated to estimate the magnitude of genetic variability, relationship of some agronomic traits and genetic diversity. Randomized Complete Block (RCB) design with three replications was used to design this experiment at the Department of Plant Breeding, Physiology and Ecology, Yezin Agricultural University in Myanmar, 2017 (dry season). STAR (Statistical Tool for Agricultural Research, version 2.0.1) statistical software for analysis of variance and genetic parameter, and SPAR 2 software for path analysis were used to obtain the optimal result in the collected data: plant height, effective tillers hill⁻¹, panicle/straw weight ratio, panicle length, filled grain percent, spikelet panicle⁻¹, 1000 grain weight, harvest index, yield plant⁻¹. Genotypes showed highly significant difference for all the traits studied, meaning that the genotypes constitute a pool of germplasm with adequate genetic variability. Genetic variance was higher than environmental variance and heritability were above 80 % in all characters, which ensures the predominance of the genetic components among genotypes. The slight difference between genotypic coefficient variation (GCV) and phenotypic coefficient of variation (PCV) in all characters indicated there is enough genetic variability for the traits to be facilitated selection. High heritability with high genetic advance for spikelet panicle⁻¹ and filled grain percent, their strong and positive correlation and the positive direct effect on yield plant⁻¹ indicated that these are important indicator characters and their manipulation through selection. These characters can be utilized as selection criteria for further breeding programs related to high yielding rice varieties.

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Keywords: correlation, genetic advance, heritability, path analysis and variability

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1. INTRODUCTION

Agriculture in Myanmar, dominated by rice cultivation, generates a direct or indirect economic livelihood for over 75% of the population. Rice is the principal human food resource and primary foreign exchange earner of Myanmar. It is an important crop for Myanmar, which has the highest per capita consumption of rice in the world: more than 210kg per person per year. In 2016, rice cultivation covers 7.21 million hectares and production was reached to 28.21 million metric ton (1).

The success of increasing the productivity of any crop through breeding largely depends on the presence of variability among the breeding materials (2, 3). Genetic variability can provides a different kind of genotypes that could be selected to develop new improved varieties (4). It is necessary to estimate heritability to make a plan of an efficient breeding programme (5). Knowledge about heritability can help plant breeders to predict the genetic

30 nature of the succeeding generation, to do an effective selection and to attain genetic
31 improvement through selection (6).

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33 Yield is a complex character and highly influenced by the environment. The direct selection
34 for yield alone limits the selection efficiency for the improvement of cultivars. Therefore,
35 indirect selection for yield components **could achieve** higher yield (7). The correlation
36 coefficients provide information about interrelationship among yield and its components. This
37 information is very helpful for the development of efficient selection strategy (8). Correlation
38 does not generally imply causation; however, the path analysis can applied cause and effect
39 of the related traits. Its application, however, is not limited to agriculture. Several authors
40 have discussed the use of path analysis in epidemiology (9-13) and in sociology (14-17).
41 Consequently, the contribution of each character to yield through path analysis could be
42 estimated for picking up appropriate traits for indirect selection.

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44 Therefore, path coefficient analysis is essential to gather information for optimum
45 combination of yield contributing characters and to know the implication of the
46 interrelationships of various characters in a single genotype (18). Knowledge based on direct
47 and indirect effect between grain yield and other characters can be helpful to plant breeder
48 in efficient selection of suitable cultivars of rice. Therefore, this study was conducted to
49 estimate the magnitude of genetic variability and relationship of some agronomic attributes
50 of Myanmar local rice genotypes.

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52 **2. MATERIAL AND METHODS**

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54 Forty-two Myanmar local rice genotypes were grown in Randomized Complete Block design
55 with three replications at the field of the Department of Plant Breeding, Physiology and
56 Ecology, Yezin Agricultural University, Nay Pyi Taw, Myanmar, in 2017 dry season (Appendix
57 1). The spacing was **20 cm x 20cm** and one seedling per hill was planted. The data were
58 collected on five randomly chosen plants from each genotype per replication for agronomical
59 traits. To obtain optimum performance, recommended cultural practices was followed
60 whenever needed. The data on days to flowering (days), plant height (cm), effective tillers hill⁻¹
61 (no.), panicle/straw weight ratio, panicle length (cm), filled grain percent, spikelet panicle⁻¹
62 (no.), 1000 grain weight (g), harvest index, yield plant⁻¹ (g) were collected according to the
63 Standard Evaluation System for Rice (19) released by International Rice Research Institute
64 (IRRI), Philippines. **The experiment site was situated at elevation 152.11m where has
65 subtropical climate and receiving the mean annual rainfall about 1257mm and the
66 temperature ranges from 21°C to 34°C.** Analysis of variance (ANOVA) was carried out on the
67 data to assess the genotypic effects for RCB design in STAR (Statistical Tool for Agricultural
68 Research, version 2.0.1) (20). Estimates of variance components were generated based on
69 mean squares values. Broad-sense heritability (H) was calculated as the ratio of the
70 genotypic variance to the phenotypic variance using the formula according to (21). Genetic
71 advance was calculated at 10% selection intensity (i=1.76). Phenotypic and genotypic
72 coefficients of correlation (PCV and GCV) and path analysis were computed using SPAR 2
73 software.

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75 **3. RESULTS AND DISCUSSION**

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77 **3.1 Evaluation of Agronomic Traits of 42 Myanmar Local Rice Genotypes**

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79 The mean square values due to genotypes **shows** highly significant differences (**P**
80 **value<0.01**) in days to flowering, plant height, effective tillers hill⁻¹, panicle/ straw ratio,
81 panicle length, filled grain percent, spikelet panicle⁻¹, 1000 grain weight, harvest index and
82 yield plant⁻¹ (Table 1). This result indicated that there was the high genetic variability within

83 the genotypes among all the significant agronomic traits and hence it would be beneficial for
 84 the improvement of the crop. Similar finding was found by Girma et al. [2018](22).and
 85 Shahriar et al. (23) for all the traits they studied.

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Table 1. Analysis of variance on agronomic traits of 42 local rice genotypes

| Source of variation | Mean Squares | | | Coefficient of Variation (CV) |
|--------------------------------------|--------------|------------|---------|-------------------------------|
| | Replication | Genotypes | Error | |
| Days to flowering | 13.883 | 496.163** | 4.309 | 2.04 |
| Plant height | 4.661 | 1180.330** | 9.377 | 2.40 |
| Effective tillers hill ⁻¹ | 0.372 | 36.129** | 1.901 | 10.55 |
| Panicle/Straw weight ratio | 0.003 | 0.246** | 0.003 | 14.31 |
| Panicle length | 3.369 | 22.613** | 2.437 | 6.76 |
| Filled grain percent | 158.030 | 1222.443** | 44.659 | 11.10 |
| Spikelets panicle ⁻¹ | 474.289 | 2472.382** | 173.790 | 15.35 |
| 1000 grains weight | 1.211 | 43.433** | 0.452 | 2.74 |
| Harvest Index | 0.0001 | 0.061** | 0.0006 | 9.77 |
| Yield plant ⁻¹ | 20.047 | 415.924** | 8.321 | 15.72 |

88 Significant at * $P < 0.05$; ** $P < 0.01$

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3.2 Genetic Variability Occurred in 42 Genotypes of Myanmar Local Rice

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92 Genetic variables of 42 genotypes of Myanmar local rice are presented in Table 2. The
 93 results revealed a wide range of variability among all tested genotypes for effective tillers hill⁻¹,
 94 panicle/straw weight ratio, harvest index, filled grain percent, spikelet panicle⁻¹ and yield
 95 plant⁻¹. The values of phenotypic variance (V_P) were higher than that of genotypic variance
 96 (V_G) in all traits. There is neglected amount of V_E in all traits, meaning that the variation
 97 occurred in all genotypes is be due to genetic effect rather than environmental effect.

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99 In all traits, the phenotypic coefficient of variation (PCV) was also higher than genotypic
 100 coefficient of variation (GCV). The highest PCV and GCV were recorded for the trait of
 101 panicle/straw weight ratio (75.81%, 75.36%) followed by yield plant⁻¹ (64.17%, 63.52%). In
 102 contrast, the lowest PCV and GCV belonged to the traits of panicle length (11.89%, 11.23%)
 103 followed by days to flowering (12.64%, 12.58%). It could be sure that all the traits in this study
 104 were mainly affected by genes and less affected by environment. This finding was the same
 105 with the result occurred by Devi et al, (24); Prajapati et al., (25); Sandhya et al., (26) and
 106 Onyia et al., (27). Therefore, selection on the basis of phenotype alone could be effective for
 107 the improvement of these traits. The slight difference between genotypic and phenotypic
 108 coefficients of variation (GCV and PCV) was observed in all traits revealed the presence of
 109 sufficient genetic variability for the traits which may facilitate effective selection.

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111 High broad sense heritability (H) was found for all traits with the range from 89.22% to
 112 99.21%. The values of heritability over 99% were recorded for the traits of harvest index
 113 (99.02%), days to flowering (99.13%) and plant height (99.21%). It could be suggested that

114 these traits would highly respond to selection due to the presence of high genetic variability
 115 and heritability. High genetic advance was observed in spikelet panicle⁻¹ (46.97), plant height
 116 (34.63), filled grain percent (34.23) and days to flowering (22.44). Prasad et al., [2017] (28)
 117 and Yadav et al. [2018] (29) reported same findings in rice. Moderate genetic was observed
 118 in yield plant⁻¹ (20.31). Low genetic advance was found in harvest index (0.25), panicle/straw
 119 weight ratio (0.50), panicle length (4.31), effective tillers hill⁻¹ (5.79) and 1000 grain weight
 120 (6.63).

121 Occurrence of high heritability with high genetic advance for spikelet panicle⁻¹, plant height,
 122 filled grain percent and days to flowering indicated that additive gene action is controlling
 123 these traits. This pointed out that the less effect of environment in the expression of these
 124 traits and it can be amenable for simple selection. The traits with high heritability and
 125 moderate genetic advance found in yield plant⁻¹ and it could be governed by both additive
 126 and non-additive gene actions.

127
 128 **Table 2. Genetic parameters for yield and its component traits in 42 different local rice**
 129 **genotypes.**

| Traits | Mean | V _G | V _P | V _E | GCV (%) | PCV (%) | H (%) | GA (%) |
|--|--------|----------------|----------------|----------------|---------|---------|-------|--------|
| Days to flowering (day) | 101.76 | 163.95 | 165.39 | 1.44 | 12.58 | 12.64 | 99.13 | 22.44 |
| Plant Height (cm) | 127.63 | 390.32 | 393.44 | 3.13 | 15.48 | 15.54 | 99.21 | 34.63 |
| Effective tillers hill ⁻¹ (no.) | 13.07 | 11.41 | 12.04 | 0.63 | 25.84 | 26.55 | 94.74 | 5.79 |
| Panicle/Straw weight ratio | 0.38 | 0.0811 | 0.0821 | 0.0010 | 75.36 | 75.81 | 98.82 | 0.50 |
| Harvest Index | 0.25 | 0.0203 | 0.0205 | 0.0002 | 58.08 | 58.37 | 99.02 | 0.25 |
| Panicle Length (cm) | 23.09 | 6.73 | 7.54 | 0.81 | 11.23 | 11.89 | 89.22 | 4.31 |
| Filled grain percent (%) | 60.19 | 392.59 | 407.48 | 14.89 | 32.92 | 33.54 | 96.35 | 34.23 |
| Spikelet panicle ⁻¹ (no.) | 85.89 | 766.20 | 824.13 | 57.93 | 32.23 | 33.42 | 92.97 | 46.97 |
| 1000 grains weight (g) | 24.55 | 14.33 | 14.48 | 0.15 | 15.42 | 15.50 | 98.96 | 6.63 |
| Yield plant ⁻¹ (g) | 18.35 | 135.87 | 138.64 | 2.77 | 63.52 | 64.17 | 98.00 | 20.31 |

130 V_G= Genotypic variance, V_P=Phenotypic variance, GCV= Genotypic Coefficient of Variation,
 131 PCV= Phenotypic Coefficient of Variation, H= Heritability in broad sense, GA=Genetic
 132 advance
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134 3.3 Genotypic and Phenotypic Correlations among Traits

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 136 The relatedness of yield and its components traits can be identified by correlation analysis. It
 137 is important in indirect selection for higher yield improvement. The phenotypic and genotypic
 138 correlations for yield and its component traits are presented in Table 3. There was a
 139 significant and positive genotypic and phenotypic correlation of yield plant⁻¹ with effective
 140 tillers hill⁻¹ and panicle/straw ratio, harvest index, filled grain percent and spikelet panicle⁻¹.
 141 Therefore, this could be highlighted that these traits are major factors for improving grain
 142 yield. In addition, direct selection towards these characters would be effective for ensuring
 143 high grain yield in rice. These results collaborate with the finding of Ogunbayo et al. (30) who
 144 observed a positive and significant correlation between grain yield and number of
 145 panicle/m², Babar et al., (31) for the number of panicles per plant and Ramakrishman et al,

146 (32) for spikelet panicle⁻¹. Conversely, grain yield exhibited negative correlation with days to
 147 flowering, panicle length and 1000 grain weight, but not significant. Therefore, grain yield
 148 could be improved by selecting early flowering genotypes.
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153 **Table 3. Phenotypic (above diagonal) and genotypic (below diagonal) correlation**
 154 **coefficient among 10 quantitative traits of Myanmar local rice genotypes**

| | DTF | PHt | EffT | PSR | HI | PLen | FGP | SPP | TGW | YPP |
|------|---------|----------|---------|----------|---------|---------|---------|---------|---------|---------|
| DTF | | 0.340* | -0.149 | -0.229 | -0.278 | 0.234 | -0.356* | 0.022 | -0.091 | -0.126 |
| PHt | 0.347* | | -0.297 | -0.440** | -0.38* | 0.456** | -0.298 | -0.112 | 0.498** | -0.204 |
| EffT | -0.176 | -0.337 | | 0.740** | 0.759** | -0.175 | 0.566** | 0.426** | -0.335* | 0.748** |
| PSR | -0.233 | -0.456** | 0.675** | | 0.982** | -0.178 | 0.679** | 0.640** | -0.164 | 0.820** |
| HI | -0.284 | -0.392* | 0.693** | 0.983** | | -0.171 | 0.734** | 0.685** | -0.144 | 0.857** |
| PLen | 0.279 | 0.520** | -0.141 | -0.229 | -0.215 | | -0.295 | 0.068 | 0.207 | -0.068 |
| FGP | -0.384* | -0.320* | 0.667** | 0.718** | 0.775** | -0.335* | | 0.499** | -0.203 | 0.805** |
| SPP | 0.035 | -0.111 | 0.599** | 0.718** | 0.767** | 0.048 | 0.600 | | -0.161 | 0.802** |
| TGWt | -0.100 | 0.511 | -0.356* | -0.167 | -0.146 | 0.248 | -0.218 | -0.184 | | -0.168 |
| YPP | -0.136 | -0.212 | 0.819** | 0.853** | 0.891** | -0.092 | 0.846** | 0.853** | -0.182 | |

155 DTF = Days to flowering, PHt = Plant Height, EffT = Effective tillers hill⁻¹, PSR =
 156 Panicle/Straw weight ratio, HI = Harvest Index, PLen = Panicle Length, FGP = Filled grain
 157 percent, SPP = Spikelet panicle⁻¹, TGWt = 1000 grains weight, YPP = Yield plant⁻¹
 158 Significant at * $P < 0.05$; ** $P < 0.01$
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161 3.4 Path Analysis

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 163 Path analysis allows separating the direct effect and their indirect effects through other
 164 attributes by apportioning the correlations for better interpretation of cause and effect (8).
 165 Path analysis has been conducted by taking grain yield per plant as dependent variable.
 166 Effective tiller plant⁻¹ had highest direct effect on yield plant⁻¹ followed by filled grain percent,
 167 spikelet panicle⁻¹ (Table 4). These characters had also positive and highly significant
 168 correlation with yield plant⁻¹. This indicated that the correlation revealed the true relationship
 169 and direct selection of these characters is likely to be effective in increasing yield plant⁻¹.
 170 Results on importance of direct effect of effective tiller plant⁻¹ were reported by several
 171 researchers (33-37). The spikelet panicle⁻¹ had positive direct effect on the yield plant⁻¹ was
 172 also reported by Akanda and Mundt, Chaturvedi and Gupta, Dofing and Knight, Gebeyehou
 173 et al., Gracia de Moral et al., Shahid et al. and Sharma and Rao (38-45).
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175 Panicle/straw weight ratio and panicle length has high indirect effect via effective tillers hill⁻¹
 176 and filled grain percent. Filled grain percent and spikelet panicle⁻¹ has also highly contributed

177 indirectly via effective tillers hill⁻¹. These indirect effects had not only supported the low
 178 magnitude direct effect but also resulted in high significant positive correlation with grain
 179 yield. Panicle/straw weight ratio exhibited high negative direct effects on yield plant⁻¹. **Similar**
 180 **finding was reported by Panwar and Ali (46)** for effective tillers plant⁻¹.

181

182 The residual effect determines how best the causal factors account for the variability of the
 183 dependent factor such as standard evaluation score. The residual effect was 0.1676 at
 184 genotypic level. This indicated that the characters which are selected in this study
 185 contributed 84% of variability.

186

187 **Table 4. Path coefficient analysis showing direct and indirect effects of various traits**
 188 **on yield plant⁻¹ in Myanmar local rice genotype**

| | DTF | PHt | EffT | PSR | HI | PLen | FGP | SPP | TGW | r _g with YLD |
|-------------|---------------|---------------|---------------|---------------|--------------|---------------|--------------|---------------|---------------|-------------------------|
| DTF | 0.0501 | 0.0174 | 0.0117 | 0.0142 | 0.014 | -0.0088 | 0.0192 | 0.0017 | -0.005 | -0.136 |
| PHt | 0.0223 | 0.0643 | 0.0293 | 0.0252 | 0.0335 | -0.0217 | 0.0206 | 0.0071 | 0.0329 | -0.212 |
| EffT | 0.1225 | 0.2392 | 0.5247 | 0.5159 | 0.1202 | 0.3885 | 0.3768 | 0.3766 | -0.0876 | 0.819** |
| PSR | 0.1171 | 0.1618 | 0.4053 | 0.4122 | 0.0886 | -0.3129 | 0.3194 | 0.3163 | 0.0603 | 0.853** |
| HI | 0.0165 | 0.0307 | 0.0135 | 0.0127 | 0.059 | -0.0103 | 0.0198 | 0.0028 | 0.0146 | 0.891** |
| PLen | 0.0511 | -0.098 | 0.2152 | 0.2206 | -0.051 | 0.2906 | 0.1938 | 0.174 | -0.1034 | -0.092 |
| FGP | 0.1736 | 0.1446 | 0.3246 | 0.3502 | 0.1514 | 0.3015 | 0.452 | 0.271 | -0.0984 | 0.846** |
| SPP | 0.0127 | 0.0403 | 0.2606 | 0.2786 | 0.0173 | 0.2174 | 0.2177 | 0.3632 | -0.0669 | 0.853** |
| TGWt | 0.0071 | 0.0364 | 0.0119 | 0.0104 | 0.0177 | -0.0254 | 0.0155 | 0.0131 | 0.0713 | -0.182 |

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Note: Diagonal values are direct effects, Residual effect = 0.1676, Significant at * $P < 0.05$; ** $P < 0.01$.

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191 DTF = Days to flowering, PHt = Plant Height, EffT = Effective tillers hill⁻¹, PSR =
 192 Panicle/Straw weight ratio, HI = Harvest Index, PLen = Panicle Length, FGP = Filled grain
 193 percent, SPP = Spikelet panicle⁻¹, TGWt = 1000 grains weight, YPP = Yield plant⁻¹

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4. CONCLUSION

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197 The agronomic performance of the rice genotypes showed **highly significant** differences
 198 among the genotypes **with** respect to all the traits. This indicates that the genotypes tested in
 199 this study contained adequate genetic variability for breeding purpose. Genetic variance was
 200 higher than environmental variance and heritability were higher than 80 % for all traits,
 201 ensuring the predominance of the genetic components among genotypes. **The slight**
 202 **differences between genotypic and phenotypic coefficients of variation (GCV and PCV) were**
 203 **found in almost all the characters. It is due to presence of sufficient amount of genetic**
 204 **variability in the genotypes which may facilitate selection of genotypes as breeding**
 205 **materials.** High heritability with high genetic advance for spikelet panicle⁻¹ and filled grain
 206 percent, their strong and positive correlation and the positive direct effect on yield plant⁻¹
 207 indicated that these are the **important** indicator characters and their manipulation through
 208 **selection can be done.** These characters can be utilized as selection criteria for further
 209 breeding programs related to high yielding rice varieties. **Genetic variability parameters**

210 pointed out that all the traits tested in this study could be considered as the important
211 parameters for ensuring of high yielding genotypes. In addition to this, regarding the results
212 of the correlation and path coefficient analysis, effective tillers hill⁻¹, panicle/straw ratio,
213 harvest index, filled grain percent and spikelet panicle⁻¹ are the major traits for the
214 improvement of high yield in rice and direct selection based on these traits among all the
215 tested genotypes would be powerful and practical for planning successful plant breeding
216 programme.

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219 **COMPETING INTERESTS**

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Authors have declared that no competing interests exist.

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346 **APPENDIX 1. List of local rice genotypes used for this study**

| No. | Germplasm | Source | No. | Germplasm | Source |
|-----|---------------|-----------------------|-----|---------------|----------------------|
| 1 | BaKauk | DaWai, YAU collection | 22 | LawThawGyi | DAR, Seed Bank |
| 2 | BayKyaung | DAR, Seed Bank | 23 | LetYoneGyi | DAR, Seed Bank |
| 3 | GaukRa | DAR, Seed Bank | 24 | LetYwesin | DAR, Seed Bank |
| 4 | KalarGyi | Mon, YAU collection | 25 | LopaZa | DAR, Seed Bank |
| 5 | KalarLay | DAR, Seed Bank | 26 | MaeKhalar-5 | DAR, Seed Bank |
| 6 | KuTaungMyoTun | DAR, Seed Bank | 27 | MaungPhaLo | DAR, Seed Bank |
| 7 | KhaingShweWar | Myeik, YAU collection | 28 | MuyinSaba | DAR, Seed Bank |
| 8 | KhaoHline | DAR, Seed Bank | 29 | PaDinThuMa | DAR, Seed Bank |
| 9 | KhaoLai | DAR, Seed Bank | 30 | PhoKawGyi | DAR, Seed Bank |
| 10 | KhaoLamil | DAR, Seed Bank | 31 | PyawtTun | YAU collection |
| 11 | KhaoLan | DAR, Seed Bank | 32 | SeinGyi | DAR, Seed Bank |
| 12 | KhaoLin | DAR, Seed Bank | 33 | ShweHinThar | DAR, Seed Bank |
| 13 | KhaoLiPaw | DAR, Seed Bank | 34 | ShweYinAye | Shan, YAU collection |
| 14 | KhaoMaPhut | DAR, Seed Bank | 35 | TaTaungPo | DAR, Seed Bank |
| 15 | KhaoNyoHon | DAR, Seed Bank | 36 | TaungAtBeSaba | DAR, Seed Bank |

| | | | | | |
|----|-----------------|----------------|----|---------------|-----------------------|
| 16 | KhaoPhaLin | DAR, Seed Bank | 37 | TaungHtakePan | Bago, YAU collection |
| 17 | KhaoPiPaung | DAR, Seed Bank | 38 | TaungYarSaba | DAR, Seed Bank |
| 18 | KhaoTan | DAR, Seed Bank | 39 | TinTayar | YAU collection |
| 19 | KhaowaA | DAR, Seed Bank | 40 | WetSiPhyu | DAR, Seed Bank |
| 20 | KunLone | DAR, Seed Bank | 41 | YarPyae | YAU collection |
| 21 | KyweChaeManaing | DAR, Seed Bank | 42 | YawShweWar | DaWai, YAU collection |

UNDER PEER REVIEW