

Yield Stability of Aromatic Upland Rice with High Yielding Ability in Indonesia

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Abstract : Aromatic rice variety, Mentikwangi, was crossed with high-yielding upland rice variety, Poso, and the pedigree was selected to obtain lines with high yielding and aromatic characters. The objectives of the research were to study the yield stability of aromatic upland genotypes across different locations and to select aromatic upland rice genotypes having wide adaptability, and or specific location adaptability. Yield stability of genotypes was estimated by using regression lines proposed by Finlay and Wilkinson. Some genotypes showed high yield stability and wide adaptability in different locations, and others showed good adaptability to a specific location. The lines having high yield stability and wide adaptability were G10 (405 g m⁻²), G19 (400 g m⁻²), G39 (418 g m⁻²), and G136 (411 g m⁻²), which may be considered as candidates of new aromatic upland rice cultivars. Situpatenggang had specific adaptability at the fertile locations; and Poso and G13 at the infertile locations. Genotype x location interactions for the yield and its components performance were observed.

Key words : Adaptability, Aromatic upland rice, Yield stability.

Rice is one of the most important food crops in the world and the second largest cereal crop. Rice is the staple food of nearly one-half of the world's population. It contributes over 20% of the total calorie intake of the human population (Chaudhary and Tran, 2001). In general, rice is boiled and eaten as a main dish; however, with the development of the processing industry and increased prosperity, it is processed to create a variety of rice products, as well as forming a constituent of a wide range of snack foods, baked products and beverages. Different kinds of preparation of rice demand different grain qualities; both physical and chemical. There are rice varieties which produce grain of a different kind in terms of physical appearance, chemical composition or aroma. A number of aromatic rice varieties are known in various countries. In India, Pakistan, Thailand, Bangladesh, Nepal, Iran, Afghanistan, Myanmar, and also Indonesia these rice varieties are the most prized.

There are many studies on aromatic rice in Asia. Breeding, production and future prospects of aromatic rice have been studied in China (Tang and Wang, 2001), India (Bentur and Krishnaiah, 2001; Modgal and Gupta, 2001; Rani and Krishnaiah, 2001; Singh et al., 2001), Cambodia (Sarom, 2001), Myanmar (Nwe et al., 2001), Pakistan (Mann and Ashraf, 2001), Thailand (Narula and Chaudhary, 2001) and Viet Nam (Nghia et al., 2001a, b).

In Indonesia, aromatic rice which have a perfumed, nutty flavour, aroma, and have a light, fluffy texture when cooked was already cultivated for a long time.

Farmers are usually growing local aromatic rice cultivars in an irrigated land, such as Pandanwangi, and Rojolele. However, the local cultivars are late maturity (more than 120 days) and sensitive to pest and disease. Several new aromatic rice cultivars were already released in recent years such as Bengawan Solo (1993), Sintanur (2001) and Batang Gadis (2002) which have high yielding, early maturing, and tolerant to pest and disease relatively.

Kato et al. (2006a) mentioned that developing of new water-saving rice production systems, besides enhancing and stabilizing of current rainfed rice production systems, was one of the major options for the increase of rice production using the limited water resource. Studies on the cultivar x environment interactions for yield of upland rice (Lafitte and Courtois, 2002), dry matter production of upland rice (Kato et al., 2006a), and grain yield of upland rice (Kato et al., 2006b) have been reported. However, information about aromatic rice specifically for cultivation in the upland is still limited. An upland aromatic rice cultivar, Situpatenggang, was already released in 2002.

In Indonesia, development of aromatic upland rice is of importance to improve upland rice quality and upland productivity. The upland area in Indonesia is around 11.6 million ha, and is not used for crop production optimally yet. The area for upland rice production is only 1.2 million ha, and it produces 2.6 million tons per year with productivity of 2.27 t ha⁻¹ (Central Bureau of Statistic, 2004).

Table 1. Plant height (cm) in each genotype at eight locations.

| Genotypes | Pwj | Bms | Kds | Tgl | Btg | Kbm | Crb | Bjn | Avg. |
|-----------|--------|--------|--------|--------|--------|--------|--------|--------|------|
| G9 | 121 de | 133 ce | 107 bd | 135 de | 116 bc | 143 eg | 111 cd | 109 de | 122 |
| G10 | 117 cd | 123 c | 112 bf | 125 cd | 95 ab | 136 de | 111 cd | 101 cd | 115 |
| G12 | 132 f | 127 cd | 116 df | 144 e | 105 b | 148 g | 125 ef | 121 f | 127 |
| G13 | 132 f | 133 de | 117 ef | 143 e | 111 bc | 146 fg | 116 de | 111 de | 126 |
| G19 | 113 bc | 111 b | 104 b | 122 bd | 83 ab | 127 bc | 103 bc | 95 bc | 107 |
| G34 | 108 b | 125 cd | 104 b | 125 cd | 99 ab | 136 de | 109 cd | 106 de | 114 |
| G35 | 136 f | 128 cd | 116 df | 125 cd | 100 ab | 156 h | 127 f | 109 de | 125 |
| G39 | 116 cd | 127 cd | 120 f | 126 d | 115 bc | 139 ef | 117 de | 112 e | 121 |
| G136 | 121 de | 138 e | 109 be | 108 b | 92 ab | 124 bc | 110 cd | 104 ce | 113 |
| Ps | 121 de | 128 cd | 114 cf | 133 de | 106 b | 146 fg | 121 ef | 121 f | 124 |
| Mw | 124 e | 127 cd | 106 bc | 121 bd | 139 c | 130 cd | 111 cd | 106 de | 121 |
| Slg | 85 a | 83 a | 79 a | 85 a | 67 a | 90 a | 81 a | 69 a | 80 |
| Stp | 111 bc | 104 b | 107 bd | 109 bc | 97 ab | 121 b | 97 b | 89 b | 104 |

Values with the same letter in a column do not differ significantly at $p=0.05$.

(Pwj, Bms, Kds, Tgl, Btg, Kbm, Crb, Bjn were Regency of Purworejo, Banyumas, Kudus, Tegal, Batang, Kebumen, Cirebon, Banjarnegara, respectively).

We have studied the development of the aromatic upland rice in Indonesia. It started with crossing upland rice tolerant to drought with lowland aromatic rice. Poso cultivar (high-yielding upland rice, tolerant to drought, Indica type) and Mentikwangi (low-land aromatic rice, Javanica type) has been conducted in 2001. Genetic studies and the maternal effect of aromatic character have been reported (Totok et al., 2005). The pedigree has been selected from the F2 to F5 generation for aromatic upland rice lines (Totok, 2004). In 2004, 50 selected lines of F5 were examined for their growth and yield performance. Among them, 25 lines were aromatic, and among those 25 aromatic lines, 19 lines were high yielding in terms of grain yield per plant. Preliminary yield trial was conducted for 19 lines, and 9 lines were selected as aromatic and high yielding upland lines (Totok and Utari, 2005).

It is necessary to examine the yield stability of the aromatic upland rice, and to obtain lines having high yield stability across different locations and/or having specific locational adaptability. The yield stability across different locations varies with the genotype (Fehr, 1987). Finlay and Wilkinson (1963) used regression analysis for estimating the stability. Relationship between the yield at each location and the location index was expressed to a straight line (regression line) for each genotype and for mean yield of all genotypes. Then, the regression lines for the yield of each genotype were compared with that for the mean yield of all genotypes over all locations to estimate the yield stability of each genotype.

Yield and yield components of a crop are influenced by genotype (G), environment (E), and their (GxE) interaction. Every factor of the environment has a potential to cause differential performance, associated

with GxE interaction (Fehr, 1987). GxE interaction was measured by the analysis of variance.

Materials and Methods

1. Materials

Nine rice lines obtained by crossing between Poso (Ps) cultivar (high yielding upland rice, tolerant to drought, Indica type) and Mentikwangi (Mw) cultivar (lowland aromatic rice, Javanica type) were used in this experiment. Four other rice cultivars, namely Ps and Mw (as parents), Silugonggo (Slg), and Situ Patenggang (Stp) were also used as reference genotypes. Slg and Stp were upland rice cultivars released in 2002 by Ministry of Agriculture, Indonesia. Thus, 13 genotypes in total were used in this field experiment.

2. Methods and design

The 13 genotypes were planted in the upland at eight different locations in Java, Indonesia in January 2006 and harvested in May 2006. The locations were Purworejo (Pwj), Banyumas (Bms), Kudus (Kds), Tegal (Tgl), Batang (Btg), Kebumen (Kbm), Cirebon (Crb) and Banjarnegara (Bjn). At each location, seeds of each genotype were sown directly in a 5×2.5 m plot in the rate of 3–4 seeds per hole. Seedlings were thinned to 2 seedlings per genotype. Planting distance was 25 cm between rows and between plants. No irrigation was applied. Water supply was depended on the rainfall. The experiment was a randomized complete block design with three replications. Fertilizer rate was $200 \text{ kg ha}^{-1} \text{ N}$, $100 \text{ kg ha}^{-1} \text{ P}_2\text{O}_5$ and $100 \text{ kg ha}^{-1} \text{ K}_2\text{O}$.

Data for plant height (cm), the number of productive tillers per hill, panicle length (cm), the number of grains per panicles, 1000-grain weight (g),

Table 2. The number of productive tillers per hill in each genotype at eight locations.

| Genotypes | Pwj | Bms | Kds | Tgl | Btg | Kbm | Crb | Bjn | Avg. |
|-----------|---------|---------|---------|---------|---------|---------|---------|---------|------|
| G9 | 21.2 de | 18.5 a | 16.5 ac | 16.0 be | 21.9 cd | 19.1 bc | 18.1 bd | 15.1 bc | 18.3 |
| G10 | 23.3 e | 17.8 a | 22.6 de | 19.3 de | 15.8 ab | 20.3 c | 19.5 cd | 13.6 ac | 19.0 |
| G12 | 18.0 bc | 12.9 bd | 22.2 ce | 12.9 ab | 15.0 ab | 19.7 bc | 17.5 bd | 13.7 ac | 16.5 |
| G13 | 17.9 bc | 12.0 cd | 20.5 bd | 13.0 ab | 17.6 bc | 19.8 bc | 18.7 bd | 11.8 ac | 16.4 |
| G19 | 20.3 ce | 15.7 ac | 19.5 bd | 15.0 bd | 11.8 a | 21.2 c | 15.2 ab | 10.7 ac | 16.2 |
| G34 | 20.4 c | 15.2 ac | 12.3 a | 15.9 be | 13.3 ab | 20.4 c | 15.4 ab | 10.9 ac | 15.5 |
| G35 | 23.1 e | 14.3 ac | 16.3 ab | 13.9 bc | 12.0 a | 20.3 c | 20.7 de | 11.2 ac | 16.5 |
| G39 | 19.5 bd | 11.9 cd | 19.5 bd | 16.3 be | 21.9 d | 16.0 ab | 16.7 ac | 10.0 ab | 16.9 |
| G136 | 18.7 bd | 14.7 ac | 21.4 be | 15.3 bd | 11.7 a | 19.5 bc | 20.2 cd | 12.2 ac | 16.7 |
| Ps | 16.4 b | 13.9 ac | 20.3 bd | 18.0 ce | 14.4 ab | 18.3 ac | 15.5 ab | 13.4 ac | 16.3 |
| Mw | 19.7 cd | 15.9 ac | 20.8 be | 16.9 be | 17.7 bc | 22.0 c | 23.9 ef | 12.3 ac | 18.7 |
| Slg | 19.5 bd | 16.9 ab | 26.4 e | 20.3 e | 24.5 d | 22.2 c | 25.9 f | 16.9 c | 21.6 |
| Stp | 13.3 a | 89 d | 17.7 ad | 9.2 a | 11.4 a | 14.9 a | 13.1 a | 7.9 a | 12.1 |

Values with the same letter in a column do not differ significantly at $p=0.05$.
(For Pwj, Bms, Kds, Tgl, Btg, Kbm, Crb and Bjn see Table 1).

Table 3. Panicle length (cm) in each genotype at eight locations.

| Genotypes | Pwj | Bms | Kds | Tgl | Btg | Kbm | Crb | Bjn | Avg. |
|-----------|---------|---------|---------|---------|---------|---------|---------|---------|------|
| G9 | 23.2 d | 25.0 ac | 24.9 bc | 24.4 ac | 23.8 bc | 29.3 g | 24.9 ce | 22.3 bc | 24.7 |
| G10 | 23.6 d | 25.3 ab | 25.0 bc | 25.8 be | 23.2 bc | 27.8 df | 24.1 bd | 23.6 bd | 24.8 |
| G12 | 23.8 d | 24.3 ac | 24.7 bc | 26.3 ce | 28.0 d | 29.0 fg | 25.4 de | 24.6 bd | 25.8 |
| G13 | 23.8 d | 23.4 be | 25.7 bc | 27.1 de | 24.1 d | 28.4 fg | 23.2 ac | 24.2 bd | 25.0 |
| G19 | 21.8 b | 23.0 ce | 24.8 bc | 24.1 ac | 18.9 a | 26.7 cd | 22.8 ab | 23.0 bd | 23.1 |
| G34 | 22.0 bc | 22.6 e | 22.7 a | 24.8 ad | 23.7 bc | 26.2 bc | 23.4 ad | 23.5 bd | 23.6 |
| G35 | 25.5 e | 22.5 e | 25.1 bc | 27.5 e | 22.8 bc | 28.7 fg | 25.0 ce | 23.9 bd | 25.1 |
| G39 | 23.5 d | 24.9 ad | 26.3 c | 25.3 be | 22.2 bc | 28.2 eg | 26.2 e | 23.5 bd | 25.0 |
| G136 | 23.0 cd | 25.7 a | 23.9 ab | 25.1 be | 23.2 bc | 27.0 ce | 23.9 bd | 24.8 cd | 24.6 |
| Ps | 23.5 d | 24.1 ae | 26.1 c | 26.0 ce | 22.0 bc | 28.1 eg | 23.9 bd | 25.5 d | 24.9 |
| Mw | 21.6 b | 22.9 de | 24.1 ab | 25.0 be | 21.6 b | 27.2 ce | 23.2 ac | 22.7 bc | 23.6 |
| Slg | 19.9 a | 20.7 f | 22.3 a | 22.3 a | 17.7 a | 22.6 a | 21.7 a | 17.7 a | 20.6 |
| Stp | 21.2 b | 24.6 ad | 25.0 bc | 23.3 ab | 21.7 b | 25.4 b | 22.4 ab | 22.0 b | 23.2 |

Values with the same letter in a column do not differ significantly at $p=0.05$.
(For Pwj, Bms, Kds, Tgl, Btg, Kbm, Crb and Bjn see Table 1).

and grain weight (g) per hill were collected from 5 randomly chosen plants from each plot. Yield (g) was measured from 5 m² effective plots. Data were analyzed combined with variance. Means were separated by Duncan's Multiple Range Test (DMRT) when the variance analysis revealed significant differences (Steel and Torrie, 1980).

Regression linear analysis proposed by Finlay and Wilkinson (1963) was used to analyze the yield stability of genotype, as follows.

$$Y_{ij} = \mu + g_i L_j + \sigma_{ij}$$

where:

Y_{ij} : yield mean of a genotype i at the j location,

μ : Population mean,

g_i : Regression coefficient of the i genotype,

L_j : Environmental index of the j location,

σ_{ij} : Regression deviation of the i genotype at the j location.

The genotype having the regression line above that for mean yield of all genotypes over all locations is considered to have high yield stability and capable of adapting to all the locations. Such genotype would increase the yield as the productivity of the location improves. The genotype having a regression line crossing that for the mean yield of all genotypes over all locations is considered to have adapted well to a specific location. The genotype having a regression

Table 4. The number of grains per panicle in each genotype at eight locations.

| Genotypes | Pwj | Bms | Kds | Tgl | Btg | Kbm | Crb | Bjn | Avg. |
|-----------|--------|---------|--------|--------|--------|--------|--------|--------|------|
| G9 | 114 a | 100 bd | 100 a | 104 a | 99 bc | 161 bd | 105 a | 82 b | 108 |
| G10 | 121 ab | 113 bd | 122 ac | 115 ab | 160 de | 149 bc | 120 ac | 84 b | 123 |
| G12 | 147 de | 127 b | 145 c | 152 cd | 201 e | 233 e | 149 cd | 119 cd | 159 |
| G13 | 141 ce | 116 bc | 137 bc | 146 c | 143 cd | 185 d | 148 cd | 103 bc | 140 |
| G19 | 135 be | 107 bd | 174 de | 136 bc | 80 a | 187 d | 132 ad | 114 cd | 133 |
| G34 | 130 ad | 116 bc | 115 ab | 140 bc | 157 cd | 165 bd | 135 ad | 122 cd | 134 |
| G35 | 140 ce | 112 bd | 115 ab | 128 ac | 117 bc | 139 ab | 126 ac | 112 cd | 124 |
| G39 | 149 ef | 124 b | 182 e | 137 bc | 107 bc | 243 ef | 184 e | 134 de | 158 |
| G136 | 127 ac | 111 bd | 137 bc | 141 bc | 111 bd | 175 cd | 138 bd | 125 cd | 133 |
| Ps | 141 ce | 123 b | 151 cd | 138 bc | 112 bc | 175 cd | 144 cd | 147 e | 141 |
| Mw | 122 ab | 91 cd | 124 ac | 130 ac | 136 bd | 164 bd | 126 ac | 104 bc | 125 |
| Slg | 121 ab | 83 d | 110 ab | 101 a | 73 a | 117 a | 111 ab | 56 a | 96 |
| Stp | 165 f | 184.9 a | 175 de | 176 d | 152 de | 265 f | 163 de | 115 cd | 175 |

Values with the same letter in a column do not differ significantly at $p=0.05$.
(For Pwj, Bms, Kds, Tgl, Btg, Kbm, Crb and Bjn see Table 1).

Table 5. One-thousand-grain weight (g) in each genotype at eight locations.

| Genotypes | Pwj | Bms | Kds | Tgl | Btg | Kbm | Crb | Bjn | Avg. |
|-----------|---------|---------|---------|---------|---------|---------|---------|---------|------|
| G9 | 25.4 bc | 27.1 bd | 20.9 ab | 23.2 ab | 24.4 d | 25.4 bc | 22.7 ab | 23.4 ab | 24.1 |
| G10 | 29.7 g | 29.1 a | 24.2 e | 29.2 e | 27.1 g | 27.7 d | 25.4 cd | 29.2 ef | 27.7 |
| G12 | 27.6 e | 26.8 bd | 20.3 a | 25.9 be | 26.0 g | 26.3 bd | 22.3 a | 26.5 cd | 25.2 |
| G13 | 29.9 g | 27.7 ac | 23.7 de | 27.2 ce | 26.7 g | 27.6 d | 24.4 bd | 29.6 f | 27.1 |
| G19 | 26.9 d | 26.9 bd | 21.2 ab | 28.6 de | 19.2 a | 25.4 bc | 24.0 ad | 23.6 ab | 24.5 |
| G34 | 25.5 bc | 25.8 ce | 20.0 a | 22.7 ab | 25.9 fg | 25.1 b | 23.8 ad | 23.2 ab | 24.0 |
| G35 | 25.6 c | 26.9 bd | 21.5 ac | 23.2 ab | 24.3 d | 23.3 a | 23.8 ad | 21.6 a | 23.8 |
| G39 | 27.4 de | 25.2 de | 21.3 ab | 24.9 bd | 24.9 ef | 25.7 bc | 23.5 ac | 24.9 bc | 24.7 |
| G136 | 24.9 b | 24.8 e | 20.6 ab | 19.7 a | 22.3 b | 26.8 cd | 22.8 ab | 24.7 bc | 23.3 |
| Ps | 28.3 f | 26.9 bd | 22.2 bd | 24.0 bc | 24.8 de | 26.0 bd | 24.3 bd | 25.1 bc | 25.2 |
| Mw | 28.2 f | 27.9 ab | 23.1 ce | 25.3 be | 22.8 bc | 26.3 bd | 25.2 cd | 27.2 de | 25.8 |
| Slg | 23.0 a | 21.1 f | 19.7 a | 21.9 ab | 22.1 b | 23.5 a | 22.9 ab | 23.3 ab | 22.2 |
| Stp | 27.3 de | 24.7 e | 20.9 ab | 23.6 ac | 23.6 cd | 25.6 bc | 25.6 d | 23.9 b | 24.4 |

Values with the same letter in a column do not differ significantly at $p=0.05$.
(For Pwj, Bms, Kds, Tgl, Btg, Kbm, Crb and Bjn see Table 1).

line below that for the mean yield of all genotypes over all locations is considered to have low yield adaptability across locations (Finlay and Wilkinson, 1963).

Results and Discussion

All of the nine upland rice lines and four reference cultivars sown at eight different locations grew well. Plants headed between 59 and 92 days after planting (DAP). The grains were harvested between 94 and 115 DAP.

Analysis of variance showed a significant effect of location, genotype and their interaction on yield and all yield components (data not shown). Table 1 shows the plant height of each genotype at each location.

Plant height varied significantly with the genotype of each location. The lowest plant was Slg in Batang (67 cm) and the highest was G35 in Kebumen (156 cm). They also had the lowest and the highest mean values as the average at all locations.

Tables 2~7 show the number of productive tillers per hill, panicle length, the number of grains per panicle, 1,000-grain weight, grain weight per hill, and yield, respectively, of each genotype at each location. These values significantly varied with the genotype at each location in plant height, indicating the genetic variability. This is because the genotypes used in this study originated from F_2 population of Mw x Ps crossing.

Table 6. Grain weight per hill (g) in each genotype at eight locations.

| Genotypes | Pwj | Bms | Kds | Tgl | Btg | Kbm | Crb | Bjn | Avg. |
|-----------|---------|---------|---------|---------|------|---------|---------|---------|------|
| G9 | 24.9 a | 22.7 ab | 17.1 a | 17.2 a | 30.8 | 25.2 a | 23.9 ab | 18.2 ac | 22.5 |
| G10 | 25.3 a | 21.1 ab | 34.0 bc | 27.5 ab | 42.3 | 27.7 ab | 23.7 ab | 16.9 ac | 27.3 |
| G12 | 29.9 bc | 14.0 bc | 27.7 ac | 18.1 ab | 37.9 | 26.6 ab | 23.1 a | 23.6 ac | 25.1 |
| G13 | 30.8 ce | 19.2 ab | 32.4 bc | 21.7 ab | 26.7 | 25.2 a | 26.0 ab | 18.0 ac | 25.0 |
| G19 | 33.2 df | 23.4 ab | 32.4 bc | 27.4 ab | 12.9 | 36.4 d | 26.2 ab | 17.8 ac | 26.2 |
| G34 | 26.3 ab | 22.7 ab | 19.1 a | 27.3 ab | 16.3 | 27.4 ab | 25.6 ab | 18.7 ac | 22.9 |
| G35 | 27.7 ac | 25.8 a | 18.3 a | 19.2 ab | 20.8 | 25.0 a | 24.4 ab | 13.4 a | 21.8 |
| G39 | 31.6 ce | 20.9 ab | 37.9 c | 23.7 ab | 30.4 | 36.0 d | 33.2 c | 20.3 ac | 29.3 |
| G136 | 35.9 f | 18.9 ab | 36.3 c | 18.9 ab | 31.9 | 33.5 bd | 26.4 ab | 26.6 bc | 28.6 |
| Ps | 29.8 be | 26.5 a | 38.1 c | 29.0 b | 22.1 | 27.3 ab | 24.3 ab | 29.6 c | 28.3 |
| Mw | 28.7 ac | 22.8 ab | 31.3 bc | 28.0 ab | 32.9 | 28.2 ac | 29.5 bc | 20.9 ac | 27.8 |
| Slg | 29.0 ad | 18.9 c | 22.8 ab | 22.1 ab | 11.7 | 27.2 ab | 25.3 ab | 14.0 ab | 20.1 |
| Stp | 33.5 ef | 20.8 ab | 27.7 ac | 16.9 a | 30.2 | 34.5 cd | 28.0 ac | 10.8 a | 25.3 |

Values with the same letter in a column do not differ significantly at $p=0.05$.
(For Pwj, Bms, Kds, Tgl, Btg, Kbm, Crb and Bjn see Table 1).

Table 7. Yield (g m^{-2}) in each genotype at eight locations.

| Genotypes | Pwj | Bms | Kds | Tgl | Btg | Kbm | Crb | Bjn | Avg. |
|-----------|----------|----------|----------|----------|----------|----------|----------|----------|-------|
| G9 | 375.4 a | 324.0 bd | 113.4 a | 197.4 a | 493.2 ef | 372.0 ab | 401.8 ac | 109.0 ac | 325.4 |
| G10 | 381.4 a | 344.8 bd | 190.0 cd | 440.0 de | 666.6 g | 434.8 bd | 379.0 ab | 101.2 ac | 405.2 |
| G12 | 466.6 bc | 401.8 cd | 156.6 ac | 245.4 ab | 606.6 fg | 360.0 ab | 370.2 a | 141.6 ac | 372.4 |
| G13 | 492.6 cf | 293.0 bc | 230.0 de | 296.6 ad | 426.6 de | 317.6 a | 416.4 ab | 108.0 ac | 353.4 |
| G19 | 524.0 fg | 400.2 cd | 186.6 cd | 463.0 e | 206.6 ab | 575.2 f | 445.6 bc | 107.0 ac | 400.2 |
| G34 | 426.0 b | 326.6 bd | 106.6 a | 401.0 ce | 260.0 ac | 467.2 cd | 436.2 ac | 112.0 ac | 346.2 |
| G35 | 431.4 bc | 366.4 bd | 126.6 ab | 253.2 ac | 333.2 bd | 315.8 a | 389.8 ac | 80.2 a | 316.6 |
| G39 | 479.4 de | 281.8 b | 273.4 e | 387.0 be | 486.6 ef | 486.4 de | 531.6 d | 121.6 ac | 418.0 |
| G136 | 546.6 g | 308.6 bd | 243.4 e | 284.0 ac | 510.0 ef | 560.4 f | 421.8 ac | 159.6 bc | 410.6 |
| Ps | 494.0 ef | 275.6 b | 180.0 bd | 389.8 be | 353.2 cd | 418.4 bd | 389.4 ac | 177.6 c | 357.2 |
| Mw | 442.6 bd | 407.0 d | 183.4 cd | 356.4 be | 526.6 ef | 393.6 bc | 458.0 c | 125.2 ac | 395.4 |
| Slg | 470.6 ce | 148.8 a | 233.4 de | 293.8 ac | 186.6 a | 396.6 bc | 404.2 ac | 84.2 ab | 304.8 |
| Stp | 535.4 fg | 349.6 bd | 186.6 cd | 258.6 ac | 483.2 e | 549.0 ef | 448.6 bc | 65.0 a | 401.6 |

Values with the same letter in a column do not differ significantly at $p=0.05$.
(For Pwj, Bms, Kds, Tgl, Btg, Kbm, Crb and Bjn see Table 1).

The results indicated that each line responded differently to the location conditions, showing that the genotype's ranking differed with the sowing location. Different responses of upland rice cultivars to water conditions have been reported (Kato et al., 2006b). These results suggested that yield and yield components were influenced by genotype x location interaction as shown in our experiment. Lafitte and Courtois (2002) also reported that the anthesis date, leaf fresh weight, root pressure, leaf area and rooting depth of upland rice were changed by cultivar x environmental interaction,

The number of productive tillers per hill significantly varied with the genotype at each location.

The number of productive tillers per hill was lowest in Stp (8 tillers) at Bjn and highest in Slg at Kds (26 tillers). It was not different among G10, G12, G136 and Mw at Kds. Stp and Slg had the smallest and the largest number of productive tillers per hill, 12 and 22 tillers, respectively, on the average.

Panicle length was significantly different among genotypes at each location. Slg at Bjn had the shortest panicle (18 cm), which was not different from that at Btg. G9 at Kbm had the longest panicle (29 cm), which was not different from that of G12, G13, G35, G39 and Ps. Slg had the shortest panicle as the average at all locations, 21 cm. On the other hand, G12 had the longest panicle as the average at all locations (26 cm).

The number of grains per panicle was significantly different among genotypes at each location. The lowest number of grains per panicle was observed in Slg at Bjn and the highest in Stp at Kbm (265), which was not different from that in G39. Slg and Stp had the smallest (96) and largest (175) mean number of grains per panicle as the average at all locations.

The 1,000-grain weight was significantly different among genotypes at each location. Slg at Kds had the lightest 1,000-grain weight (20 g) and G13 at Pwj the heaviest (30 g), which was not different from that in G10. Slg and G10 also had the lightest and the heaviest mean 1,000-grain weight as the average at all locations, 22 and 28 g, respectively. Lafitte and Courtois (2002) reported that the mean 1,000-grain weight of 48 upland rice cultivars grown under nine different environments varied from 16.4 to 24.7 g. However, Fukushima et al. (2006) showed that the yearly variation of 1,000-grain weight was from 20.3 to 22.5 g in Akisayaka and from 22.0 to 22.9 g in Yumehikari.

Grain weight per hill was significantly different among genotypes at each location. Slg at Btg had the lightest (12 g) and G13 at Pwj the heaviest (31 g) grains. Slg and G10 had the lightest and the heaviest grain weight per hill as the average at all locations, 22 and 28 g, respectively.

Yield (g m^{-2}) at each location was significantly different among genotypes. The yield was lowest in Stp at Bjn (65.0 g m^{-2}) and highest in G10 at Btg (666.6 g m^{-2}) which was not different from that in G12 at Bjn. Slg and G39 were genotypes having the lowest and the highest yield as the average at all locations, 304.8 and 418.0 g m^{-2} , respectively (Table 7).

The lines having higher mean values of yield components than the reference cultivars had a higher yield than the reference cultivars. For instance, G10 had larger number of tillers per hill than Ps, Mw and Stp; longer panicle than Mw, Slg and Stp; heavier 1,000-grain weight than any other cultivar, resulting in high average yield (405 g m^{-2}). G19 had a larger grain number per panicle than either Mw or Slg, heavier 1,000-grain weight than either Stp or Slg, heavier grain weight per hill than any other cultivar, resulting in a high average yield (400 g m^{-2}). G39 had a larger number of tillers per hill than Ps and Stp, longer panicles than any other cultivar, higher grain number per panicle than Ps, Mw and Slg, heavier 1,000-grain weight than Stp and Slg; and heavier grain weight per hill than any other cultivar, resulting in a high average yield (418 g m^{-2}). G136 had a larger number of tillers per hill than either Ps or Stp; longer panicle than Mw, Slg and Stp; a larger number of grains perpanicle than either Mw or Slg; and heavier grain weight per hill than any other cultivar, resulting in high average yield (411 g m^{-2}). Thus, G10, G19, G39 and G136 had higher yield components than the others. On the other hand, Fukushima et al. (2006) indicated that a larger

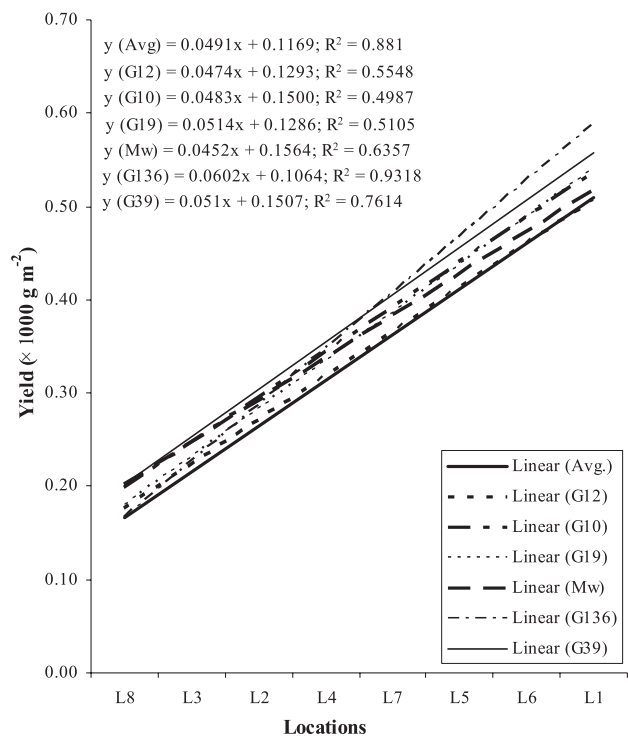


Fig. 1 Regression lines for genotypes above that for the mean yield (g m^{-2}) of all genotypes at different locations. (L1–L8 were: Pwj, Bms, Kds, Tgl, Btg, Kbm, Crb and Bjn, respectively).

number of spikelets per unit area and having sink and source abilities during the late ripening stage were the two characters required for high yielding ability of Akisayaka rice cultivar. Our results confirmed the high yield component on the average contributed to high yielding ability.

Table 7 shows that yield of G39 was higher than or not significantly different from that of at least 3 reference cultivars at all locations. Yields of G136 and G19 were higher than those of 3 reference cultivars at all locations, except for G136 at Tgl and G19 at Btg. However, the yield of G10 was higher than that of reference cultivars, at 5 locations; Kbm, Btg, Tgl, Kds and Bms. Our study suggested that G10, G19, G39 and G136 are aromatic rice lines having high yielding ability across different locations. The yield of G10, G19, G39, and G136 are 405 g m^{-2} , 400 g m^{-2} , 418 g m^{-2} , and 411 g m^{-2} , respectively.

The genotype having the regression line above that for the mean yield of all genotypes over all locations is estimated to have high yield stability. Our study showed that G10, G12, G19, G39, G136 and Mw had regression lines above that for the mean yield of all genotypes over all locations. It shows that these genotypes may have high stability and good adaptability across 8 locations (Fig. 1).

The genotype having the regression line crossing that for the mean yield of all genotypes is estimated

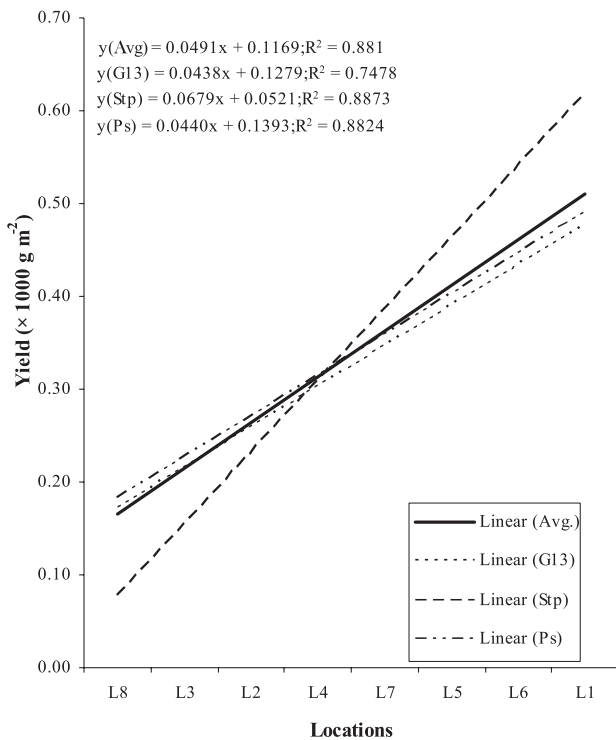


Fig. 2. Regression lines for genotypes above that for the mean yield (g m^{-2}) of all genotypes at different locations. (For L1 - L8 see Fig. 1).

to have specific adaptability. In this study, Stp is considered to have specific adaptability to the fertile (high productive) locations, whereas Ps and G13 have specific adaptability to the infertile (low productive) location (Fig. 2).

The regression lines crossing each other revealed the genotype x location interaction. The locational difference in yield of the genotype relative to that of other genotypes shows the locational change of the ranking of the genotype.

The genotype having the regression line below that for the mean yield of all genotypes over all locations is estimated to have low yield stability. G9, G34, G35 and Slg are considered to have low stability (Fig. 3).

Based on the high yielding (Table 7), high yield components (Tables 2~6) and high yield stability (Fig. 1), G136, G39, G19 and G10 are considered as prospective aromatic upland rice lines having high yielding ability, high yield stability and wide adaptability.

In conclusion, yield stability across different locations varied with the genotype. Some genotypes had high yield stability and wide adaptability to all locations, and some others had high adaptability to specific location. The lines having high yield stability and wide adaptability were G10 (405 g m^{-2}), G19 (400 g m^{-2}), G39 (418 g m^{-2}), and G136 (411 g m^{-2}), which are considered as candidates for new aromatic upland rice cultivars. The genotypes having specific adaptability

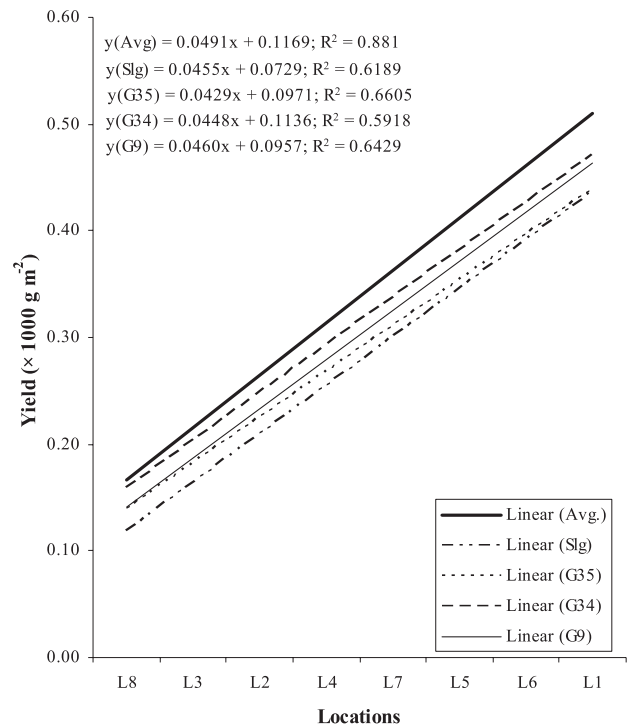


Fig. 3. Regression lines for genotypes below that for the mean yield (g m^{-2}) of all genotypes at different locations. (For L1 - L8 see Fig. 1).

were Stp at the fertile locations, and Ps and G13 at the infertile locations. Genotype x location interaction for the yield and its components were observed. Yield components contributing to higher yielding ability was confirmed.

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