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Research Article

Identification of high yielding finger millet RILs with wide/specific adaptation

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Abstract

Finger millet (*Elucine coracana* L. Gaertn), is one of the most important cereals in the sub-Saharan Africa and south Asia. Finger millet in India is grown in a wide range of agro-climatic zones which are highly variable resulting in complex genotype (G) × environment (E) interactions (I). Significant GEI challenge the breeders to identify genotypes suitable for a wide range of environments/specific environments. Twelve selected recombinant inbred lines (RILs) along with four checks were evaluated to characterize genotype × location interaction (GLI) and identify those that are widely/specifically adapted. The AMMI ANOVA showed significant mean squares due to genotype, location and GLI for days to 50 *per cent* flowering, plant height, finger length and grain yield plant^{-1}. Near perfect fit of interaction principal component (IPC)1 and IPC2 to the total GLI variation for most of the traits suggested a good approximation of the bi-plot with respect to the patterns of GLI and good predictability of RIL performance across four locations. The RILs such as RIL-3, RIL-104, RIL-143, RIL-183 and RIL-303 were found widely adapted. The RILs such as RIL-104, RIL-94, RIL-185 and RIL-302 were found specifically adapted to GKVK, Bengaluru and RIL-143 to Mandya for grain yield plant^{-1}.

Key words
Finger millet, adaptation, AMMI, bi-plot

Introduction

Finger millet (*Elucine coracana* L. Gaertn), a member of the Poaceae (Gramineae) family, is one of the most important cereals in the sub-Saharan Africa and south Asia. It is the third most widely cultivated millets after pearl millet (*Pennisetum glaucum*) and foxtail millet (*Setaria italica*) in the semi-arid tropical and subtropical regions of the world. Finger millet represents one of the crop components for food security of farmers inhabiting arid, infertile and marginal lands and as an ideal crop for famine reserves due to its long storability under ambient conditions. It has excellent nutritional value as its seeds contain 7 – 14% protein and is rich in calcium, iron, methionine, phosphorus, carbohydrate and other nutrients (Leung *et al.,* 1968).

Among the coarse cereals, finger millet accounts for 7 *per cent* area and 11 *per cent* of production in India. It is grown in an area of 1.19 million hectares in India with a production of 1.60 million tons and productivity of 1.3 t ha^{-1}. Development and deployment of high yielding widely adapted and/or highly stable varieties would contribute to sustainable finger millet production. Varieties exhibit fluctuating yields when grown in different environments or agro-climatic zones. This complicates demonstrating the superiority of a particular variety. Multi- environment yield trials are crucial to identify widely adaptable and/or highly stable high yielding cultivars and discover locations that best represent the target production environments (Yan *et al.,* 2000). Adaptability is the result of genotype, environment and genotype by environment interaction and generally falls into two classes: (1) the ability to perform at an acceptable level in a range of production environments, referred to as general adaptability, and (2) the ability to perform well only in desirable environments, known as specific adaptability (Farshadfar and Sutka, 2006).

Finger millet in India is grown in a wide range of agro-climatic zones which are highly variable resulting in complex genotype × environment interactions. The performance of advanced breeding lines should therefore be evaluated in multi-location trials to assess their yield performance and adaptability. The present investigation was carried out to evaluate selected RILs for their adaptability and performance of grain yield at four different locations of southern Karnataka.

Materials and methods

Experimental material: The material for the study comprised of 12 recombinant inbred lines (RILs) such as RIL-3, 94, 102, 104, 143, 152, 158, 183, 185, 281, 302 and 303 derived from PR 202 × GPU 48. PR 202 is a blast disease susceptible average yielding variety and GPU 48 is blast disease resistant high yielding released variety. The 12 RILs which have performed better than the better parent (GPU 48) for grain yield and component traits in F_5 generation were selected based on the evaluation of F_5 RILs during 2014 rainy season.

Layout of experiment: The seeds of 12 selected RILs along with four checks [PR 202 (a selection from Peddapuram local), GPU 48 (GPU 26 ×L 5), GPU 28 (Indaf 5 × IE 1012) and KMR 204 (GPU 26 × GE-1409)] were sown in randomized complete block design (RCBD) with two replications at four locations *viz.*, Gandhi Krishi Vignana Kendra (GKVK) Bengaluru, Agricultural Research Stations (ARS) Chintamani, Zonal Agricultural Research station (ZARS) Mandya and College of Agriculture Hassan, during 2015 rainy season. Each genotype was sown in two rows of 3m length with row-to-row spacing of 0.30m. Fifteen days after sowing, the seedlings were thinned and 25 plants were maintained per each entry. Recommended management practices were followed during the crop growth period to raise a healthy crop. The data on weather variables that prevailed in the four locations during crop growth period are presented in table 1.

Sampling of plants and data collection: Data were recorded on five randomly chosen plants in each genotype in both replications on days to 50 *per cent* flowering, (Days to 50 *per cent* flowering was recorded as days taken from sowing date to the stage when ears have emerged from 50 *per cent* of main tillers) plant height (cm) (The height of the main tiller was measured from the ground level to the tip of the ear at dough stage in centimeters), finger length (cm) (Finger length was measured as the length from base to tip of the longest finger of the ear borne on main tiller at dough stage and expressed in centimeters) and grain yield plant^{-1}(g) (Total grain yield of five plants were weighed and the mean value was computed and expressed as grain yield plant^{-1} in gram).

Pooled ANOVA: The quantitative trait means of each RIL and each check were used for pooled ANOVA.

Additive Main effects and Multiplicative Interaction (AMMI) Analysis: The traits means of 12 RILs and four checks were subjected to Additive Main effects and Multiplicative Interaction (AMMI) model (Gouch and Zobel, 1988) to detect and characterize the patterns of interaction of RILs with production environments of four locations. The additive main effects of genotypes and locations were fitted by univariate ANOVA followed by fitting genotype × location interaction (GLI) by principal component (PC) analysis based on the following model.

$$Y_{ij} = \mu + g_i + e_j + \sum_{k=1}^{n} \lambda_k \alpha_{ik} \gamma_{jk} + \varepsilon_{ij}$$

Where, $Y_{ij}$is the trait value of i^{th} genotype in the j^{th} location, μ is the experimental mean trait value, g_i and ej are the i^{th}genotype and j^{th} location mean deviation from experimental mean trait value, respectively. λ_k is the squre root of eigen value of the k^{th} PC axis, α_{ik} and γ_{jk} are the interaction PC scores for k^{th}PC of the i^{th} genotype and j^{th}location, respectively and ε_{ij} is the residual. The parameters of AMMI II model were estimated using least square principle implemented by GENSAT software, version 12.

Visual and objective criteria were used to interpret GLI patterns of RILs and their specific/wide adaptation. The visual criterion was based on Genotype + Genotype × Location (GGL) bi-plot (Yan *et al.*, 2000). Objective criterion was based on the estimates of AMMI stability value (ASV) (Purchase *et al.*, 2000) and stability index (SI) (Farshadfar, 2011).

GGL bi-plot criteria to interpret GLI and identify RILs with specific/wide adaptation: GGL bi-plot methodology which is a combination of AMMI bi-plot and GGL concepts (Yan *et al.* 2000) was used for visual interpretation of patterns of GLI. The GGL bi-plot is based on the following model.

$$Y_{ij} - \overline{Y_j} = \lambda_1 \alpha_{i1} \gamma_{j2} + \lambda_2 \alpha_{i2} \gamma_{j2} + \varepsilon_{ij}$$

Where, Y_{ij}= trait mean of j^{th} genotype in the j^{th} location; Y_j= trait mean of all the genotypes in the j^{th} location; λ_1 and λ_2 are the square root of eigen values of first and second IPCA axes, respectively; α_{i1} and α_{i2} are the scores of the first and second IPCA, respectively for the i^{th} genotype, γ_{i1} and γ_{i2} are the first and second IPCAs respectively for i^{th} location.

There are numerous ways to use a GGL bi-plot, but the polygon view of the bi-plot is most relevant. Genotype × location interaction principal component (PC) 1 (IPC 1) scores were plotted against their IPC 2 scores to visually identify RILs with specific/wide adaptation and similarity between RILs and locations. The RILs that are more similar to each other in terms of their trait expression are more close to each other in the GGL bi-plot than those that are less similar. The RILs placed near the origin of IPC1 *vs* IPC 2 bi-plot are regarded as better adaptable across locations than those located far from the origin (Crossa *et al.*, 1990). The RILs that are farther from bi-plot origin are connected with straight lines so that a polygon is formed with all other RILs contained within the polygon. A set of lines were drawn from the bi-plot origin perpendicular to each side of the polygon. The perpendicular lines to the polygon sides divide the polygon into sectors, each having its own winning genotype which is the vertex genotype for that sector (Yan *et al*., 2000). The areas between the two perpendicular axes cutting the polygon side are considered as mega environments. These mega environments in the present study are regarded as mega locations. The vertex genotype for each sector is the one which is the best performer for the environments falling within that sector and mega locations.

An objective criterion to identify RILs with specific/wide adaptation: To facilitate an objective method of identifying RILs with specific/wide adaptation across locations, the AMMI stability value (ASV) was estimated (Purchase *et al*., 2000).

$$ASV = \sqrt{\left[\frac{SS\ IPC1}{SS\ IPC\ 2}(IPC1\ score)\right]^2 + (IPC2\ score)^2}$$

Where, SS IPC1 and SS IPC2 are sum of squares attributable to first two IPC’s. Conceptually, ASV is the distance from zero in a two dimensional scattergram of IPCA 1 *vs* IPCA 2 scores (Purchase *et al*., 2000). Since the IPCA 1 scores generally contributes proportionately more than IPCA 2 scores to GLI, it is weighted by the proportional difference between IPCA 1 and IPCA 2 scores in order to compensate for the relative contribution of IPCA 1 and IPCA 2 scores to total genotype × location sum of squares. Higher magnitude of estimates of ASV indicates specific adaptation, while lower magnitude of ASV indicates wide adaptation (Purchase *et al*., 2000). To facilitate simultaneous selection of RILs for different quantitative traits and adaptability, stability index (SI) which incorporates both quantitative traits mean and stability in a single criterion (Farshadfar, 2011) was estimated as SI= RASV+ RY (*i.e.* ranks of RILs based on quantitative traits mean over locations added to ranks of genotypes based on ASV). The genotypes with low SI were regarded as those with high trait expression and wide adaptation.

Results and discussion

Genotypes very often differ in their responses to production environments represented by temporal (year-to-year) and spatial (location-to location) variation resulting in significant crossover genotype × year and genotype × location interactions (GLI) (Annicchirarico, 1992). From commercial crop production point of view, crop varieties should maintain consistent performance across years, referred to as stability and across locations referred to as adaptability (Lin and Binns, 1998). However, cross-over genotype × environment interaction (GEI) leads to inconsistent performance of best yielding genotypes across environments and challenge plant breeders and complicates variety recommendations (Annicchirarico, 1992). Nevertheless, GEI offer opportunities for selection of genotypes exhibiting favourable responses to only a few locations (exploitation of specific adaptation) or of genotypes with low frequency of poor yield across years in a location (exploitation of yield stability). However, it is widely acknowledged that only GLI could be exploited by selecting for specific adaptation or by growing specifically adapted genotypes (Annicchirarico, 1992). This is because, from a farmer’s point of view, location is a constant-not-variable factor and GLI effects are repeatable in time (Annicchirarico, 1992).

The stable genotypes which perform well under stress and low-input conditions are desirable under farmers’ conditions for sustainable finger millet production. It is therefore important to identify the causes of GEI in order to set up appropriate finger millet breeding objectives.

Detection of GEI: Non-significance of Bartlett’s test indicated homogeneity of error variance for each trait in the four locations and provided statistical justification for pooled analysis of variance. In pooled ANOVA, total variation was partitioned into sources attributable to genotypes, location, genotype × location and pooled error. Multilocation testing of 16 genotypes has shown not only significant genotypic effects but also significant effects of the location and GLI for all the productivity traits (Table 2). Bashir *et al.* (2014) reported that genotypic, environmental and G × L interaction effects were highly significant ($P < 0.01$) for grain yield. The significance of GLI indicates the differential performance of genotypes in the four locations (Table 2). This implies the necessity to examine patterns of adaptability of genotypes across locations. Several researchers have advocated numerous models and their associated parameters to assess the performance stability of genotypes (Eberhart and Rusell, 1966; Lin and Binns, 1988). However, no single stability model/parameter can adequately explain cultivar performance across environments.

The Additive Main effect and Multiplicative Interaction Model (AMMI) can extract a large part of the GEI and is efficient in analyzing interaction patterns (Zobel *et al.*, 1988). Gauch (1992) also reported that AMMI model effectively capture a large portion of the genotype × environment interaction sum of squares clearly separating main and interaction effects and the model often provide an agronomically meaningful interpretation of the data.

AMMI ANOVA: The AMMI ANOVA showed significant mean squares due to genotype, location and GLI for days to 50 *per cent* flowering, plant height, finger length and grain yield plant^{-1} (Table 3). Genotype, location and GLI, respectively contributed 10.86%, 67.33% and 13.83% (for days to 50 *per cent* flowering), 4.88%, 87.23% and 5.60% (for plant height), 6.00%, 59.09% and 16.63% (for finger length) and10.73%, 65.17% and 14.42% (for grain yield plant^{-1}) of the trait variation. Fentie *et al*. (2014) reported main effects of E and G accounted for 59.64% and 9.61% respectively and G x E interaction accounted for 30.75% of the total variation for grain yield. Significant mean squares attributable to locations indicated differences in the influence of locations on the productivity of genotypes. The substantial contribution of GLI towards traits variation suggested differential responses of genotypes to locations. Significant GLI reduces responses to selection of superior genotypes. Hence, it is appropriate to assess yield stability under different production environment and identify genotypes with specific/wide adaptation. Further, the GLI was partitioned into two IPC axes by the Gollob's F-test (Gollob, 1968) which together explained ≥ 80% of the total GLI variance for all the traits indicating a good fit of AMMI model to the data.

GGL bi-plot: GGL bi-plot is useful in displaying 'which-won-where' pattern of the data that help to identify high-yielding and stable cultivars and discriminating representative test environments (Yan *et al.*, 2000). Only two IPC (IPC1 and IPC2) are retained in the model because such a model tends to be the best model for extracting patterns and rejecting noise from the data (Yan *et al.*, 2000). The partitioning of the G + GE sum of squares through GGE bi-plot showed that two significant IPCs explained >80% of G + GE sum of squares for most of the traits.

Positioning of RILs away from the origin on GGL bi-plot for days to 50 *per cent* flowering indicated that none of the RILs were widely adapted over all four locations (Fig 1). Hassan and Mandya locations were more or less similar for the expression of days to 50 *per cent* flowering. With respect to plant height none of the RILs were widely adapted. The RIL-152 showed specific adaptation to Bengaluru and Chinthamani locations. The RILs viz., RIL-302 and RIL-281 showed wider adaptation for finger length. With respect to grain yield plant^{-1}, the RIL-3 and RIL-281 showed near-origin position on GGL bi-plot suggesting their wider adaptation. Hassan and Chinthamani locations were similar for the expression of grain yield plant^{-1}. RIL-104 adapted specifically for Bengaluru location for grain yield plant^{-1}.

Near perfect fit of IPC1 and IPC2 to the total GLI variation for most of the traits (Fig 1) suggested a good approximation of the bi-plot regarding patterns of GLI and good predictability of RIL performance across four locations. GGL bi-plot provides an excellent means for visual interpretation of GLI patterns and identification of adaptable genotypes. However, it does not provide an objective means to identify genotypes with specific/ wide adaptation.

AMMI Stability Value (ASV): The ASV is the distance from the coordinate point to the origin in a two dimensional plot of IPCA1 scores against IPCA 2 scores in the AMMI model. ASV aids selection of relatively stable high yielding genotypes. An ideal genotype should have high mean grain yield and low magnitude of ASV. Based on these criteria, RILs with low ASV like RIL-302 and RIL-185 for days to 50 *per cent* flowering; RIL-183 and RIL-104 for plant height; RIL-143, RIL-302 and RIL-281 for finger length and RIL-158, RIL-102 and RIL-303 for grain yield plant^{-1} (Table 4) were identified as widely adaptable across four locations.

Stability Index (SI): Cotes *et al.* (2002) reported that breeding for stable mean yields has over shadowed the goal for increased yield. The SI is a useful parameter to identify stable genotypes based on both mean yield and stability. The RILs, RIL-3 and RIL-303 for days to 50 *per cent* flowering; RIL-104 and RIL-183 for plant height; RIL-143, RIL-281 and RIL-302 for finger length and RIL-158, RIL-102 and RIL-185 for grain yield plant^{-1} with lower SI value were considered as widely adapted.

Identification of specifically/ widely adapted accessions: The RILs such as RIL-3, RIL-104, RIL-143, RIL-183 and RIL-303 were found widely adapted as indicated by lower estimates of ASV and SI and higher trait mean values. The widely adapted RILs can be used in breeding programme and specifically adapted RILs can be used for region specific breeding. The RILs such as RIL-104, RIL-94, RIL-185 and RIL-302 were found specifically adapted to GKVK, Bengaluru and RIL-143 to Mandya for grain yield plant^{-1}.

Conclusion

The results indicate a significant effect of genotype, location and GLI with respect to yield *per se* traits. According to AMMI and GGL bi-plot methods, RIL-3, RIL-104, RIL-143, RIL-183 and RIL-303 were identified as widely adapted.

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Table 1. Meteorological data of four locations during crop growth period

Location	Latitude	Longitude	Rain fall (mm)	Min. Temp. (˚C)	Max. Temp. (˚C)	Soil Type	Agro-climatic zone
Bengaluru	12˚ 58'N	77˚35'E	591.00	18.04	27.58	Red soil	Zone 5
Mandya	12˚79'N	76˚96'E	713.00	22.20	28.50	Red clay	Zone 6
Chinthamani	13˚40'N	78˚07'E	817.50	18.62	29.09	Sandy loam	Zone 5
Hassan	13˚06'N	76˚10'E	806.00	17.69	28.17	Red loamy	Zone 6

Table 2. Pooled ANOVA of selected finger millet RILs evaluated over four locations for productivity traits

Sources of variation	Degrees of freedom	Mean sum of squares			
		Days to 50% flowering	Plant height (cm)	Finger length (cm)	Grain yield plant^{-1} (g)
Location (l)	03	351.18**	15353.77**	9.64**	490.98**
Genotypes (RILs + Checks) (g)	15	11.32**	171.63**	1.41**	16.17**
g × l	45	4.81**	65.75**	0.32**	7.24**
Pooled error (e)	60	1.91	18.65	0.18	3.20

** Significance @ P=0.05

Table 3. AMMI ANOVA of selected finger millet RILs for productivity traits

Source of variation	Degrees of freedom	Days to 50% flowering				Plant height (cm)				Finger length (cm)				Grain yield plant^{-1} (g)			
		MSS	F cal	P ≥ F	% variation	MSS	F cal	P ≥ F	% variation	MSS	F cal	P ≥ F	% variation	MSS	F cal	P ≥ F	% variation
Genotypes (RILs + Checks)	15	11.32	6.08	0.00	10.86	172.00	9.96	0.00	4.88	1.41	8.13	0.00	27.92	15	16.17	4.84	0.00
Locations	03	351.19	105.52	0.00	67.33	15354.00	352.58	0.00	87.23	9.65	37.22	0.00	38.10	03	490.98	107.09	0.00
G x L	45	4.81	2.58	0.00	13.83	66.00	3.82	0.00	5.60	0.32	1.83	0.01	18.88	45	7.24	2.17	0.00
IPCA 1	17	10.15	5.45	0.00	79.71	91.00	5.28	0.00	52.31	0.60	3.47	0.00	71.62	17	11.94	3.57	0.00
IPCA 2	15	2.20	1.18	0.31	15.25	61.00	3.56	0.00	31.13	0.20	1.14	0.34	20.85	15	6.66	1.99	0.03
Residual	13	0.84	0.45	0.94		38.00	2.19	0.02		0.08	0.48	0.93		13	1.76	0.53	0.90
Error	60	1.86	-	-		17.00	-	-		0.17	-	-		60	3.34	-	-

Table 4. Estimates of IPC scores and stability parameters to assess adaptability of selected finger millet RILs

Identity of test RILs	Days to 50% flowering								Plant height (cm)							
	Mean	Rank	IPCA 1	IPCA 2	ASV	Rank	SI	Rank	Mean	Rank	IPCA 1	IPCA 2	ASV	Rank	SI	Rank
03																
94	59.62	12	0.79	0.63	4.21	10	22	12.5	87.27	10	0.69	-0.13	1.09	5	15	7
102	59.50	14	-1.26	-0.37	6.56	15	29	15.5	89.16	6	-1.69	0.13	2.86	13	19	11
104	61.12	4	0.91	0.48	4.80	12	16	7.5	89.89	5	0.21	-1.01	0.94	3	8	2
143	60.25	7	-0.31	0.40	1.76	5	12	4.5	93.93	3	1.07	-0.45	1.67	10	13	5
152	60.25	8	-0.88	0.09	4.62	11	19	10.5	94.25	2	2.69	-0.18	4.50	16	18	10
158	60.88	5	1.23	-0.37	6.40	14	19	10.5	88.41	7	0.40	-2.32	1.37	7	14	6
183	60.25	9	-0.42	-0.25	2.12	8	17	9	87.40	9	0.21	0.57	0.84	2	11	4
185	59.62	13	-0.21	0.55	1.32	3	16	7.5	81.56	15	-2.16	-1.23	3.46	14	29	16
281	60.12	10	-1.26	0.14	6.61	16	26	14	86.26	11	0.11	2.37	1.55	9	20	12
302	59.75	11	0.28	-0.89	1.14	2	13	6	82.08	14	1.07	2.06	2.31	11	25	13
303	60.75	6	-0.38	-0.36	1.92	6	12	4.5	87.89	8	0.62	0.80	1.37	8	16	8.5
Parents																
PR 202	62.88	1	0.18	-0.78	0.28	1	2	1	94.50	1	-0.08	0.08	0.30	1	2	1
GPU 48	58.38	16	1.16	0.10	6.09	13	29	15.5	82.50	13	-2.55	0.83	4.39	15	28	14
Checks																
GPU 28	62.25	2	-0.46	0.67	2.56	9	11	3	92.05	4	0.92	-0.85	1.24	6	10	3
KMR 204	59.00	15	0.41	-0.57	2.00	7	22	12.5	80.27	16	-1.50	0.29	2.59	12	28	15
SEm±	0.72								2.48							
CD @ P=0.05	1.42								2.92							

Table 4. Cont.,

Genotypes	Finger length (cm)								Grain yield plant^{-1} (g)							
	Mean	Rank	IPCA 1	IPCA 2	ASV	Rank	SI	Rank	Mean	Rank	IPCA 1	IPCA 2	ASV	Rank	SI	Rank
03	4.97	14	-0.28	-0.20	0.86	6	20	12.5	14.65	13	-0.01	-1.22	1.10	6	19	10.5
94	5.61	8	0.23	0.09	0.84	5	13	4	15.33	8	0.66	0.43	1.50	10	18	9
102	5.31	12	-0.24	0.06	0.88	7	19	11	15.47	6	0.44	-0.23	0.74	2	8	2.5
104	5.63	7	0.52	-0.69	1.59	13	20	12.5	15.35	7	1.12	-1.01	2.03	12	19	10.5
143	6.50	1	0.00	0.08	0.28	1	2	1	15.07	11	-0.29	-1.19	0.92	4	15	7
152	5.89	2	-0.57	-0.31	1.89	14	16	8	13.15	15	0.36	0.92	1.20	7	22	13
158	5.74	5	0.29	0.30	1.14	12	17	9	15.55	5	0.11	0.06	0.33	1	6	1
183	5.78	4	-0.27	0.25	1.06	10	14	5	15.63	4	0.50	0.44	1.21	8	12	4.5
185	4.81	16	-0.78	-0.15	2.66	16	32	16	15.82	3	0.47	0.01	0.95	5	8	2.5
281	5.50	9	0.09	0.04	0.38	3	12	2.5	14.68	12	0.34	1.25	1.32	9	21	12
302	5.49	10	-0.04	0.10	0.35	2	12	2.5	15.08	10	1.02	-0.19	2.02	16	26	14
303	4.97	15	0.35	-0.29	1.09	11	26	15	15.12	9	0.22	0.41	0.78	3	12	4.5
Parents																
PR 202	5.23	13	-0.27	0.00	0.93	8	21	14	11.26	16	-1.23	0.24	2.54	15	31	16
GPU 48	5.73	6	0.25	0.12	0.93	9	15	6.5	17.47	1	-1.63	-0.12	3.28	16	17	8
Checks																
GPU 28	5.84	3	0.65	0.03	2.24	15	18	10	17.04	2	-0.88	0.07	1.82	11	13	6
KMR 204	5.35	11	0.07	0.56	0.79	4	15	6.5	14.21	14	-1.17	0.12	2.41	13	27	15
SEm±	0.21								0.77							
CD @ P=0.05	0.41								1.53							