



Stability analysis in wheat for grain protein

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Wheat is the second most important crop after rice both in terms of area and production in India. India produced a record 75.57 million tonnes of wheat from 28 million hectares with a productivity of 26.98 q/ha in the year 2000 [4]. There is growing concern to export wheat to have remunerative prices. This situation now calls for diversifying wheat breeding towards quality particularly bread and biscuit making. In this context grain protein content assumes significance as high protein is suitable for bread making and low protein content for biscuit-making [3]. Further, wheat is grown over a wide range of sowing time in India. Therefore, it was considered worthwhile to do stability analysis of grain protein content among 30 relatively new wheat lines by evaluating them over four dates of sowing.

The 30 wheat genotypes (Table 1) were evaluated in an experiment planted in four diverse environments, viz., rainfed, 24 October 2000 (E1), normal sown, 17 November 2000 (E2), late sown, 21 December 2000 (E3) and very late sown, 4 January 2001 (E4). The experiment was laid out in a randomized block design using four replications at Pantnagar. The experimental plot consisted of 4 rows of 2.5 m length. The planting distance was 23 × 10 cm. The protein content in grains was determined with the help of Kjeltack Auto 1030. Statistical analysis included Eberhart and Russell [2] and Perkins and Jinks [5].

Out of various stability analysis methods available, the Eberhart and Russell, and Perkins and Jinks methods have been commonly used. These are statistically related. The $1 + \beta$ stability parameter proposed by Perkins and Jinks [5] detects stable genotypes in a manner similar to that of Eberhart and Russell [2] and $1 + \beta$ equals to 'b' of Eberhart and Russell [2]. Therefore both these methods were used. The pooled ANOVA (Table 2) following Eberhart and Russell [2] and Perkins and Jinks [5] showed highly significant mean squares due to genotype, environment and G × E interaction.

The general mean was highest (12.4%) under very late sown condition followed by late sown condition (11.5%), normal sown condition (11.3%) and rainfed-early sown condition (9.6%). Later sowing often results in higher grain percent [1]. The high protein genotypes included UP 2575, UP 2576, UP 262, UP 2513 and UP 256 (11.6-13.1%). The low protein genotypes were UP 2113 and UP 2530 (10.0-10.4%). As per the classification given by Rao [6], the wheat varieties with more than 12.5% protein are considered suitable for bread-making, those with less than 10.0% protein are suitable for cookie/biscuit-making and those with 10.0-12.0% protein are suitable for *chapati* making. Role of protein content and not of protein composition in influencing bread/biscuit making quality of wheat has been shown by Belshaw *et al.* [7]. With this classification in mind UP 2575 (13.1% protein) and UP 2576 (12.5% protein) should be good genotypes for bread making. A few genotypes with protein percentage close to 10.0% viz., UP 2113 (10.2%) and UP 2530 (10.4%) could be considered suitable for biscuit-making.

Except UP 262 and UP 2539, all the genotypes had $b/1 + \beta$ values approaching to 1.0. UP 262 with b equalling 1.91 was found to be specifically adapted to favourable environment for protein content (Table 1). The stable genotypes for grain protein content ($s_d^2 = 0$) were UP 2338, UP 2382, UP 2425, UP 2528, UP 2530, UP 2562, UP 2574, PDW 215, Raj 3765 and Sonalika. Among these genotypes UP 2338, UP 2382, PDW 215, Raj 3765 and Sonalika are released and commercially established varieties and their stability with respect to protein over four dates of sowing adds additional strength to them.

References

1. Anderson W. K., Shackley B. J. and Sawkins D. 1998. Grain yield and quality : do these have to be a trade-off? *Euphytica*, 100: 183-188.

Table 1. Stability analysis for grain protein content in wheat

Genotypes	Protein percentage				Pedigree
	X	b	s_d^2	1+ β	
UP 262	11.9	1.91*	1.36*	1.91*	S 308/Bajio 66
UP 2113 ¹⁰	10.2	1.13	0.96*	1.13	UP 346/WG 377
UP 2338	10.9	0.84	0.16	0.84	UP 368/VL421//UP262
UP 2382	11.4	1.15	0.13	1.15	CPAN 2004/HD2204
UP 2425	11.0	0.76	0.31	0.76	HD 2320/UP 2263
UP 2506	11.2	1.79	2.16*	1.79	PBW154/HUW 381
UP 2513	11.8	0.81	0.57*	0.81	SEL III SO/HP 1659//CPAN 3050
UP 2526	10.7	0.57	2.97*	0.57	HD 2009/SKA//HD2329
UP 2528	11.5	0.30	0.11	0.30	F8IAPAR#980(SEL)
UP 25301	10.4	0.87	0.19	0.87	DL 802-1 /RAJ 3077
UP 2539	11.4	0.13*	3.58*	0.13*	UP 2338/WH 576
UP 2559	11.0	0.83	0.41*	0.83	SKAUZ/RABE
UP 2562	11.6	0.97	0.02	0.97	CMH77.308/3/MJI/GLA N/ /TRT/4/PEG//MRL/BUC
UP 2567	10.7	1.06	2.33*	1.06	SM-4/HSN 24E/CPAN 2099
UP 2569	10.0	0.86	6.09*	0.86	SM4-HSN 24E/CPAN 2099
UP 2574	10.6	1.25	6.04	1.25	UP 1176/WH 543
UP 2575 ²	13.1	0.47	2.61*	0.47	CPAN 1990/UP 2334
UP 2576 ²	12.9	0.61	7.70*	0.61	CPAN 1990/UP 2334
UP 2577	11.3	0.81	0.81*	0.81	HDR 77/UP2367
UP 2579	10.8	0.44	0.46*	0.44	UP 2370/PBW//RD 180
PBW 175	11.2	1.16	1.25*	1.16	HD 2160/WG1205
PDW 215	10.6	0.65	0.06	0.65	DWL 503 1 / DWL 5002
PBW 299	10.6	0.99	0.70*	0.99	BB/KAL/WL711//PBW6 5
PBW 343	11.3	1.91	0.67*	1.91	ND/VG7944//KAL//BB/ 3/YACO'S/4/VEE#5'S
PBW 373	10.8	0.82	1.02*	0.82	ND/VG/944//KALBB/3/ YACO 'S'/4/VEE#5'S
Raj 3077	11.6	1.20	1.94*	1.20	HD 2267/RAJ 1482
Raj 3765	10.9	1.29	0.26	1.29	HD 2402/VL 639
C 306	10.5	1.04	2.04*	1.04	REGENT 1974/3*CHZ//2*C 591/3 /PI9/C 281
Sonalika	11.1	0.89	0.19*	0.89	II 54.388/AN/3/ YT54/N10B//LR
WH 896	11.0	1.32	3.19	1.32	SIN'S'/ WH 852

*b value significantly different from $b = 1.0$; $s_d^2 > 0$ ($p = 0.05$); *1 + β value significantly different from $1 + \beta = 1.0$ ($p = 0.05$); 1. Genotypes suitable for biscuit making; 2. Genotypes suitable for bread making

Table 2. Pooled analysis of variance for grain protein content (%) in wheat

Eberhart and Russell 1966			Perkins and Jinks 1968 model		
Sources of variation	Degrees of freedom	Mean squares	Sources of variation	Degrees of freedom	Mean squares
Genotype (G)	29	1.84**	Genotype (G)	29	1.84**
Environment (E)	3	41.06**	Environment (E)/Joint regression	3	41.06**
G × E	87	0.72**	G × E	87	0.72**
E + G × E	90	2.07	Heterogeneity between regressions	29	0.64
E (linear)	1	123.18**	Remainder	58	0.76
G × E (linear)	29	0.64**	Pooled error	348	0.53
Pooled deviation	60	0.74**			
Pooled error	348	0.52			

**Significant at 0.01 P

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