

AGRONOMIC AND QUALITY PERFORMANCE OF INTERNATIONAL WINTER WHEAT GENOTYPES GROWN IN KOSOVO

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SUMMARY

In the province of Kosovo there exists no local wheat breeding programme; cultivars grown were originally developed and registered in former Yugoslavia and other neighbouring countries. Within the general attempt to reconstruct the agriculture of Kosovo a three-year study was undertaken to establish winter wheat genotypes adapted to Kosovan growing conditions. Seventy-seven international winter wheat cultivars and/or breeding lines were tested for their agronomic and quality performance in 2000; forty-nine selected genotypes of the nursery were further tested in 2001 and 2002. The multivariate dataset included six yield- and twenty-two quality-related parameters which were subjected to principal component analysis and subsequently to cluster analysis. The 49 genotypes were differentiated into six groups. Two groups which included almost exclusively Central and Eastern European cultivars and breeding lines, respectively, turned out to be best adapted to the prevalent conditions. These genotypes revealed high agronomic and high quality performances, and could, therefore, serve as valuable wheat genetic resources for the buildup of a local winter wheat breeding programme in the future.

KEY WORDS: Floating check, multivariate analysis, *Triticum aestivum*, yield

INTRODUCTION

Wheat is the most important food crop in the world and it is the only material suited for the production of leavened bread and associated products. Approximately 80,000–100,000 ha winter wheat (*Triticum aestivum* L.) are planted annually in the Kosovo. Until now there exists no local breeding programme. Hence, the Kosovo does not possess wheat cultivars specifically adapted to its conditions. The predominant cultivars of the recent years are originating from Serbia and Montenegro ('Pobeda'), Croatia ('Lenta', 'Luna') and Austria ('Brutus', 'Justus'). The domestic wheat production with average yields of 2500–3000 kg ha⁻¹ does not guarantee the Kosovan self-supply; wheat for human consumption must be imported. There is an utmost need to establish a local breeding programme with the aim to create wheat cultivars specifically adapted to the prevalent growing conditions, and which could enable the Kosovo to improve both wheat production and quality. For this reason a set of international wheat cultivars and breeding lines were tested for their adaptation in a three-year study.

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MATERIALS AND METHODS

Seventy-seven winter wheat genotypes, in large parts genotypes from the Facultative and Winter Wheat Observation Nursery of the Turkey/CIMMYT/CARDA IWWIP, were grown in 15 m² plots in a randomized complete block design in 2000. Based on plot yield, thousand grain mass, protein content and micro-extensograph characteristics forty-nine genotypes were selected for further field trials. The 2001 and 2002 field trials were sown with a density of 600 kernels m⁻² and 5 m² plot size as row-column designs with three replications. All field trials were located in the Kosovo plain (Rrafshi i Kosovës), which lies 500-600 m above sea level, and is characterised by a longtime annual precipitation of 640 mm year⁻¹, and a longtime annual mean temperature of 10°C. Soil type was a vertisol. Fertilization followed the local standards: 60 N, 60 P and 60 K (kg ha⁻¹) before sowing and 60 N (kg ha⁻¹) in mid-March.

Protein content was determined by near-infrared transmittance spectroscopy (Infratec Food and Feed Analyzer 1255, Tecator AB, Höganäs, Sweden). Dough mixing characteristics were determined on 10 g flour samples (<250 µm particle size) using a Promylograph T3 apparatus (Max Egger, St. Blasen, Austria). Flour was mixed at 115 rpm with salted water (2% NaCl). In a first run flour water absorption required to produce a dough with a maximum consistency of 500 Promylograph units (PU) under the specified operating conditions was determined. In up to three following runs the recorded dough mixing parameters were: the length of the mixing curve, dough softening ratio (softening at curve rupture/curve length), and quality number (curve length from the start until the point where the decreasing curve falls below 450 PU). Doughs for micro-extension tests were mixed with the Promylograph until a peak consistency of 500 PU. Extension tests were performed using a texture analyser (Stable Micro System Ltd., Godalming, UK) equipped with the Kieffer dough and gluten extensibility rig (SMEWING 1995). Realisation of the extension test and analysis of the extension curves were described in detail by GRAUSGRUBER *et al.* (2002); recorded parameters were maximum resistance to extension, extensibility until maximum resistance, and the area under the curve until maximum resistance. SDS-PAGE of high molecular weight glutenin subunits (HMW-GS) was carried out according to the protocols of the Saatzucht Donau (Probstdorf, Austria) breeding company. Scores for HMW-GS composition were calculated according to PAYNE *et al.* (1984, 1987). SDS-sedimentation test was determined according to DICK & QUICK (1983) using 1 g whole-meal flour produced by a Cyclotec mill equipped with a 1 mm sieve.

Field trial data were analysed according to their experimental design. Adjustments for nearest neighbour effects were applied using techniques as described by VOLLMANN *et al.* (1996). Single years' genotypic means of agronomic and quality traits – in total 28 variables – were subjected to multivariate analyses to provide useful additional information and to show interrelationships among wheat genotypes. First a principal component analysis (PCA) was performed on the correlation matrix of agronomic and quality measurements. Hierarchical clustering was then carried out using Ward's minimum variance method, which minimises within-cluster sums of squares across all partitions. Genotypic scores (eigenvectors) of principal components with eigenvalues >1.0 were used for clustering. Subsequently, analysis of variance (ANOVA) was performed across clusters and years. Due to unequal cell sizes of the clusters a general linear model (GLM) was applied. All statistical analyses were carried out using SAS 8.2 and SPSS 8.0 software. Performances in regard to yield, protein content,

mixing quality number and extension curve area within the single years were expressed relatively to a floating check (the respective highest performance) as proposed by JENSEN (1976). Using this method it is possible to identify genotypes with an above average performance in all three test years and the most important traits.

RESULTS AND DISCUSSION

In all field trials a significant influence of spatial variation was detected. The analysis of variance including longitudinal nearest neighbour adjustments as covariates was the most efficient model in reducing the error mean square. VOLLMANN *et al.* (1996) also demonstrated that in experiments with long and narrow plots longitudinal neighbour adjustment models are superior to other models. Heterogeneity in field conditions and their effect on experimental results is a main problem in agricultural experiments, especially in large experiments. Numerous authors have proposed different statistical models to analyse spatial variation (for review see e.g. GLEESON 1997, KEMPTON 1997).

Eight principal components (PC) with an eigenvalue >1.0 were extracted by PCA; they together accounted for 81.3% of the total variance. PCA projects the information in the original inter-correlated variables onto a small number of new variables, which are linear combinations of the original variables. The combination of PCA and cluster analysis to describe multivariate variation of crop germplasm was applied successfully in recent years by e.g. CARTEA *et al.* (2002), GRANATI *et al.* (2003), and KAMARA *et al.* (2003). Based on the first 8 PC, six clusters were distinguished within the set of 49 genotypes (Figure 1). Cluster 1 and 2 comprised the genotypes with a generally better performance over all traits, while cluster 3 and 4 had medium performance, and cluster 5 and 6 included the truly wretched genotypes. Cluster 1 includes cultivars of Austrian origin and the well adapted standards 'Bezostaya 1' and 'Balkan'. This cluster is characterised by high values for protein and gluten content, extensograph extensibility and curve area, flour water absorption, mixing quality number and SDS sedimentation test. Cluster 2 includes mainly genotypes from other Central and Eastern European countries (Hungary, Romania, Czech Republic and Ukraine). This cluster had somewhat lower values than cluster 1 for all traits, apart from yield, extensograph resistance, and dough softening. Cluster 3 includes genotypes from the USA and from multinational breeding programmes. This cluster is characterised by somewhat lower values for most quality parameters compared to the first two clusters. Genotypes of cluster 4 exhibited high thousand grain mass, and relatively high values for yield, SDS sedimentation and HMW-GS score. Cluster 5 exhibited low values for all parameters. Although the geographic origin of genotypes of cluster 4 and 5 is almost the same, they obviously distinguished in their performance; cluster 5 was significantly inferior. Cluster 6 composed genotypes characterised by poor quality. The low quality of cluster 5 and 6 could be probably attributed to the presence of respectively 35% and 31.3% of genotypes carrying the 1BL.1RS wheat-rye chromosome translocation. As reviewed by LELLEY *et al.* (2004) the effect of this chromosome translocation is generally unfavourable for gluten and baking quality. The often reported positive effect on agronomic traits especially in dry condition was not confirmed by this study. The genotypes within groups created by cluster analysis have similar agronomic and quality properties. Remarkably of cluster 1 is, that it included 'Bezostaya 1', which is

known as a precious donor of both quality and adaptation genes, and six cultivars which derived from crosses including this cultivar in their pedigree, i.e. 'Agron', 'Balkan', 'Exklusiv', 'Exquisit', 'Josef', and 'Spartakus'.

As determined by SDS-PAGE 75.5% of the investigated genotypes were homogenous in their HMW-GS composition; 18.4% exhibited the 1BL.1RS chromosome translocation. Altogether 19 combinations of HMW-GS were observed. The most frequent compositions were 2*/7+9/5+10 (21.5%), 2*/7+8/5+10 (12.3%), 2*/7/5+10 and 1/7+8/5+10 (9.2%). GRÖGER *et al.* (1997) demonstrated a clear positive relationship of subunits 2*/7+9/5+10 to most quality tests in Austrian grown wheats. Scoring schemes for the single HMW-GS alleles were devised by various authors (PAYNE *et al.* 1987, POGNA *et al.* 1987, CERNY *et al.* 1992). Today, wheat breeders concentrate in their selection on HMW-GS which provide high score values. This narrows the number of allelic variants controlling glutenin subunits (MORGOUNOV *et al.* 1993). That was also indicated in the present study: the favourable alleles 7+9, 7+8, and 5+10 in any combination had a high portion of the investigated material (60%). However, only a part of the genotypes carrying favourable HMW-GS alleles revealed also satisfying results in the dough mixing and extension tests. The selection for technological quality using e.g. only protein content and electrophoresis as selection criteria is for sure not target-oriented, since a great part of baking quality is also influenced by low-molecular weight glutenins, gliadins and/or the quality of the starch. In regard to baking quality it is advisable to select the progenies of crosses using a wide range of tests, e.g. indirect quality traits, rheological and baking tests in order to select truly the genotypes with the best technological quality.

ANOVA revealed significant genotype (i.e. cluster), year and genotype by year interaction (G×Y) effects for all traits except for thousand grain mass and wet gluten content. Significant G×Y resulted from the different abilities of genotypes to adapt to environmental conditions. In 2001 all clusters exhibited higher yields with the exception of clusters 3 and 6 which show more or less same yield levels in all three years; genotypes of these two cluster seem to be more adapted to drought. The higher yields in 2001 can be attributed to the favourable distribution of rainfall in April and May. Besides for yield a strong influence of the year was also observed for protein content, dough extensibility and flour water absorption. Highest protein contents were observed in all three years for genotypes of cluster 1. A significant G×Y was observed for the extensograph parameters, while the mixing parameters were influenced strongly by genotypic effects and only less by the year and/or interaction.

For parameters with a significant interaction term in the ANOVA, comparisons of means were carried out within each single year. Highest yields were realised in all three years by clusters 1 and 2, followed by cluster 4. Cluster 1 and 2 had also the highest protein content, followed by cluster 5. For almost all extensograph parameters as well as for mixing characters cluster 1 and 2 performed best. The generally superior performance of cluster 1 for both agronomic and quality traits rely on the genetic background of the genotypes. All Austrian cultivars included in this study were selected for growing in the eastern part of Austria, which is characterised by hot and dry summers, and low rainfalls, conditions similar to the growing situation in Kosovo. Hence, it is not wondering that Austrian cultivars were equal and/or even superior in their overall performance to well known and adapted, but older standards like 'Balkan' and 'Bezostaya 1'.

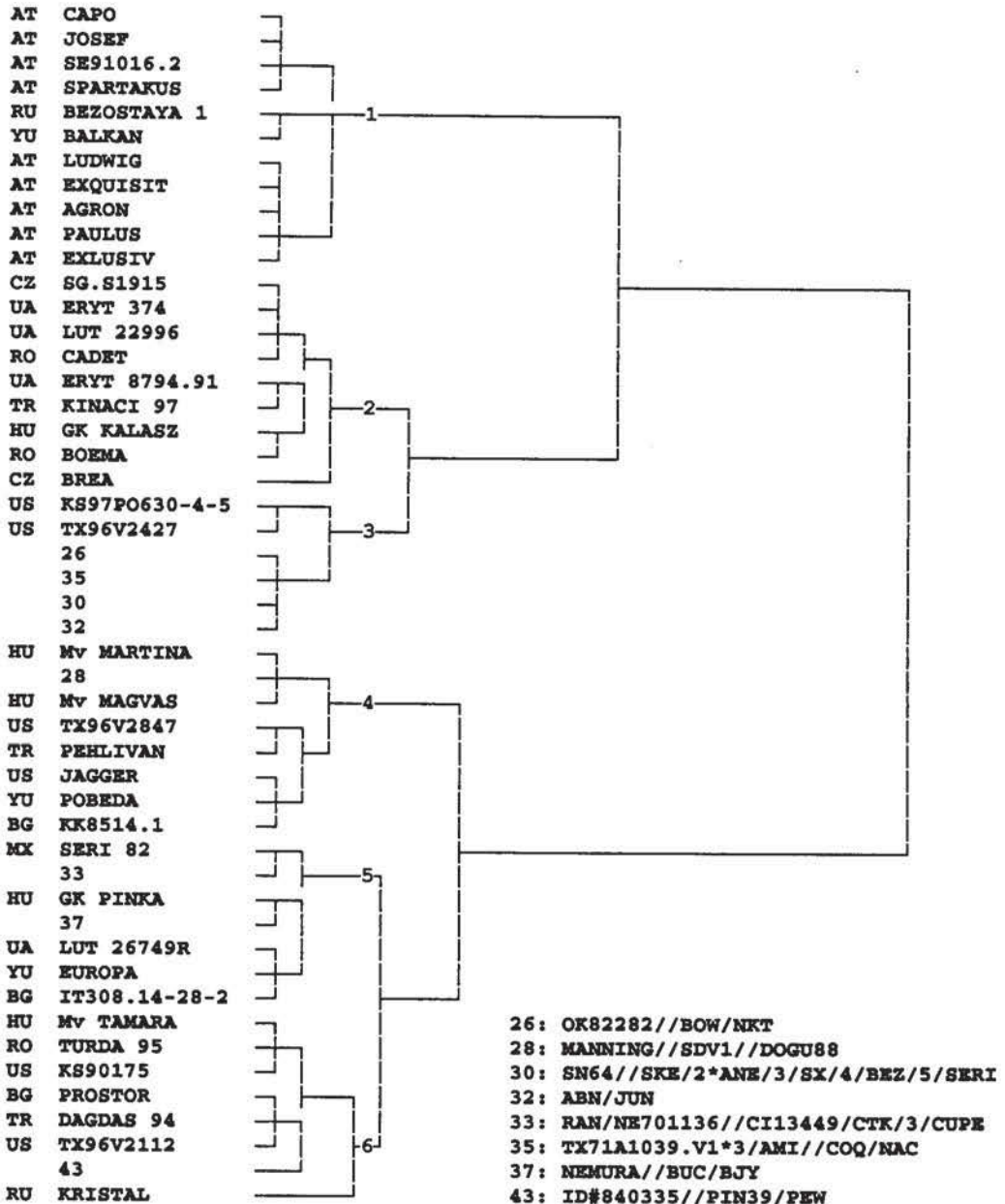


Figure 1. Dendrogram based on genotypic scores of eight principal components. The origin of genotypes is indicated by the ISO3166 country code as prefix. Pedigrees of CIMMYT breeding lines are indicated bottom-right of the dendrogram.

Table 1. Performance of selected genotypes considering four important traits (Data are presented only for the years 2001 and 2002; performances above the mean performance are printed in bold; highest performances are underlined).

Genotype	YLD-01 ¹	YLD-02	PROT-01	PROT-02	A-01	A-02	MQN-01	MQN-02
SPARTAKUS	761.8	663.6	13.8	14.7	828.8	1549.0	4.0	2.9
CAPO	972.6	633.9	14.6	14.2	742.6	1553.7	3.1	3.3
LUDWIG	890.4	634.6	14.6	14.1	879.1	1238.3	2.9	3.1
ERYT 374	852.4	603.4	13.0	13.9	1273.0	899.6	3.3	2.7
EXQUISIT	809.2	622.7	14.2	15.7	962.7	1241.4	2.8	2.4
JOSEF	794.5	744.0	13.5	14.5	673.6	1333.1	3.1	3.5
GK KALASZ	951.5	641.3	13.4	14.3	1326.0	613.7	3.9	3.3
BREA	979.9	731.4	12.1	15.6	1083.3	1073.6	2.0	2.7
EXKLUSIV	754.4	507.4	16.0	16.1	1223.9	1432.5	3.0	3.5
SG.S1915	1048.4	561.0	14.4	14.6	852.6	748.9	3.0	2.5
BEZOSTAYA 1	700.7	459.0	14.6	15.6	920.2	1013.0	2.8	3.0
JAGGER	767.1	618.3	13.1	13.4	669.6	1095.4	3.2	2.1
POBEDA	805.0	555.0	12.6	14.0	680.2	1159.1	2.4	2.2
BOEMA	636.4	521.5	12.5	13.3	730.6	877.8	3.0	3.0
BALKAN	529.0	546.8	14.8	14.5	519.8	1160.6	2.4	2.4
GK PINKA	787.1	613.8	12.6	12.7	795.6	672.8	2.8	1.5
EUROPA	846.1	584.8	11.7	14.0	578.1	680.5	2.1	2.4
KRISTAL	1053.7	572.1	11.2	13.7	318.2	1381.2	1.7	1.5
IT308.14-28-2	811.3	671.8	13.2	14.5	415.0	531.4	1.9	1.6
Mv MAGVAS	606.9	657.0	11.1	13.1	810.2	1016.1	2.0	2.7
KINACI 97	754.4	475.4	12.9	13.1	1139.0	576.4	3.3	2.0
SERI 82	632.2	485.8	13.2	13.1	853.9	167.8	2.4	2.3
Mean performance	743.0	564.5	13.0	13.9	721.2	848.2	2.7	2.4

¹ YLD, yield (g m⁻²); PROT, protein content (%); A, micro-extensograph curve area (g×mm); MQN, Promylograph mixing quality number (min); 01, 2001; 02, 2002

In Table 1 the performances relative to a floating check representing the respective highest performance are presented for selected genotypes. It is obvious that genotypes with an above average performance in all or almost all traits by year combinations are located only in cluster 1 and 2. Besides the excellent performing cultivars ('Spartakus', 'Capo', 'Ludwig', 'Eryt 374', 'Exquisit', 'GK Kalasz') a few other cultivars/breeding lines have to be mentioned for their remarkable performances: 'Bezostaya 1' showed excellent performances regarding protein content, and acceptable performances regarding the dough mixing and extension tests, however, failed to outperform the yield mean performance; 'Pobeda' showed generally unstable performances across the years, and revealed below average mixing characters; 'GK Pinka' showed above average yield in all years, however, was unstable in regard to dough extension and mixing, and failed in regard to protein content; 'IT308.14-28-2' on the other side revealed above average performance for yield and protein content, however, was a very poor performer in the dough extension and mixing tests.

CONCLUSION

Based on the triannual analysis, it can be concluded that principal components analysis combined with cluster analysis is an efficient method for the evaluation of a wide range of traits together. In the investigated material six clusters were differentiated based on their genetic background and geographical origin. The most favourable HMW-GS compositions 2*/7+9/5+10 and 2*/7+8/5+10 were identified in clusters 1 and 2. These two clusters were also characterised by a superior performance in all investigated quality traits. Clusters 5 and 6 which had a higher proportion of 1BL.1RS translocation chromosomes did not show satisfying quality properties. ANOVA indicated significant G×Y for most traits. The effect of the year was especially great for yield and protein content, while for a range of quality characteristics the genotypic main effect was substantial. All the above mentioned arguments lead to the conclusion that clusters 1 and 2 which include Austrian cultivars and cultivars of Central and Eastern European countries, are best suited to the Kosovan conditions and can serve as valuable wheat genetic resources for the buildup of a local Kosovan winter wheat breeding programme in the future.

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