Genetic relationship and structure of Mediterranean durum wheat

Moragues M., Royo C., Sorrells M.E.

in

Molina-Cano J.L. (ed.), Christou P. (ed.), Graner A. (ed.), Hammer K. (ed.), Jouve N. (ed.), Keller B. (ed.), Lasa J.M. (ed.), Powell W. (ed.), Royo C. (ed.), Shewry P. (ed.), Stanca A.M. (ed.).
Cereal science and technology for feeding ten billion people: genomics era and beyond

Zaragoza : CIHEAM / IRTA
Options Méditerranéennes : Série A. Séminaires Méditerranéens; n. 81

2008
pages 71-73

To cite this article / Pour citer cet article

Moragues M., Royo C., Sorrells M.E. **Genetic relationship and structure of Mediterranean durum wheat.** In : Molina-Cano J.L. (ed.), Christou P. (ed.), Graner A. (ed.), Hammer K. (ed.), Jouve N. (ed.), Keller B. (ed.), Lasa J.M. (ed.), Powell W. (ed.), Royo C. (ed.), Shewry P. (ed.), Stanca A.M. (ed.). *Cereal science and technology for feeding ten billion people: genomics era and beyond.* Zaragoza : CIHEAM / IRTA, 2008. p. 71-73 (Options Méditerranéennes : Série A. Séminaires Méditerranéens; n. 81)

Genetic relationship and structure of Mediterranean durum wheat

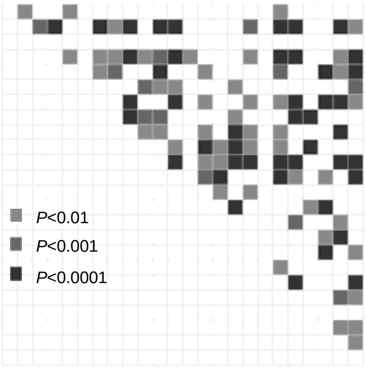
M. Moraguees*'[1], C. Royo and M.E. Sorrells***
*Department of Plant Breeding and Genetics, Cornell University,
240 Emerson Hall, Ithaca, New York 14953, USA
**Area de Conreus Extensius, Centre UdL-IRTA, Rovira Roure 191, 25198 Lleida, Spain.
[1]MEC/Fulbright Post-doctoral Scholar

SUMMARY – Twenty four unlinked SSR markers were used to genotype 192 durum wheat accessions from the Mediterranean region, consisting of 172 landraces and 20 modern widely grown varieties. Clustering and ordination methods provided a picture of the relationships between individuals, and the program Structure assigned genotypes to different groups using a Bayesian approach. Cluster analysis showed that the accessions tended to group according to their geographical origin. All accessions from Turkey, but one, grouped together. Modern Spanish and Italian cultivars clustered together excepting cultivar Simeto, which clustered with a group of Italian landraces. Population was structured in three clusters: one formed by landraces from the Middle East, Egypt and the Balcan Peninsula, another formed by landraces from the western Mediterranean countries and a third one consisting in all modern cultivars, excepting Simeto.

Genetic diversity plays a vital role in developing new cultivars. Genetic stocks conserved in genebanks, such as landraces are a valuable source of diversity. Landraces may have useful alleles for genes responsible for adaptation, but are difficult to use because they often contain several genotypes and it complicates the determination of the allele frequency for large sets of accessions. In this paper, we present an approach to determining the genetic relationships and structure between a set of 192 durum wheat accessions from the Mediterranean region.

Material and methods

Twenty four unlinked SSR markers (Fig. 1) were used to genotype 192 durum wheat accessions from the Mediterranean region, consisting of 172 landraces and 20 modern widely grown varieties. Diversity indices and LD parameter r^2 were calculated with the PowerMarker software (Liu and Muse, 2005). UPGMA cluster analysis based on Nei distance (Nei, 1972) was used to determine the genetic relationships between accessions and origins.



						Frequency of	
Marker	**Chr.**	**Distance**	**Bin**	**Allele No**	**PIC**	**Two alleles**	**Three alleles**
Xbarc158	1A	114	1AL1-0.17-0.61	4	0.29	0.01	0
Xbarc263	1A	27	1AS3-0.86-1.00	6	0.57	0.08	0.01
Xbarc080	1B	86	1BL3-0.83-1.00	5	0.27	0.08	0
Xwmc453	2A	41		18	0.91	0.25	0.02
Xwmc175	2B	87	2BL4-0.50-0.89	16	0.83	0.1	0
Xwmc25	2B	25		10	0.66	0.05	0
Xcfa2134	3A	51		22	0.92	0.06	0
Xgwm155	3A	118	C-3AL3-0.42	12	0.85	0.14	0.01
Xgwm566	3B	60	C-3BS1-0.33	11	0.78	0.15	0
Xwmc420	4A	7		9	0.6	0.03	0
XBarc1045	4B	0	C-4BS4-0.37	6	0.55	0.09	0
Xgwm156	5A	72	C-5AL12-0.35/5AL12-0.35-0.57	11	0.86	0.24	0.02
Xgwm205	5A	32	5AS3-0.75-0.98	8	0.38	0.07	0
Xwmc150b	5A	55		10	0.84	0.04	0
XBarc1032	5B	35	5BL1-0.55-0.75	6	0.25	0.05	0.01
XBarc140	5B	127	5BL1-0.55-0.75	5	0.51	0.09	0.05
XBarc003	6A	0	6AS1-0.35-1.00	10	0.5	0.16	0.01
XBarc107	6A	20	C-6AL4-0.90*	10	0.78	0.06	0
Xwmc580	6A	91		16	0.88	0.04	0
XBarc354	6B	131		18	0.92	0.03	0
Xwmc486	6B	3		7	0.68	0.01	0
Xwmc494	6B	0		11	0.82	0.03	0
XBarc151	7A	89		15	0.89	0.06	0
Xgwm282	7A	100	7AL16-0.86-0.90	12	0.81	0.1	0.01
Mean				11	0.68	0.08	0

Fig. 1. *p*-values of LD across 24 unlinked SSR for the 192 durum wheat accessions and description and summary statistics of these SSR.

Structure (Pritchard *et al.,* 2000) was used to infer the genetic structure of the population and determine the optimum number of subpopulations (K) and the probability of each individual to belong to each group.

Results and discussion

The average frequency of multiple alleles for all loci was 0.08 when two alleles were detected, but close to 0 for detecting 3 alleles (Fig. 1). We were not able to estimate the within accession allele frequency because we bulked the

DNA from 10 plants. In this first step, we ignored the presence of the third allele, which was designated as the weakest band, and thus, was the lowest frequency allele in the accession or possibly a PCR artifact. The subsequent analyses were performed considering multiple alleles as genotype data with unkown gametic phase.

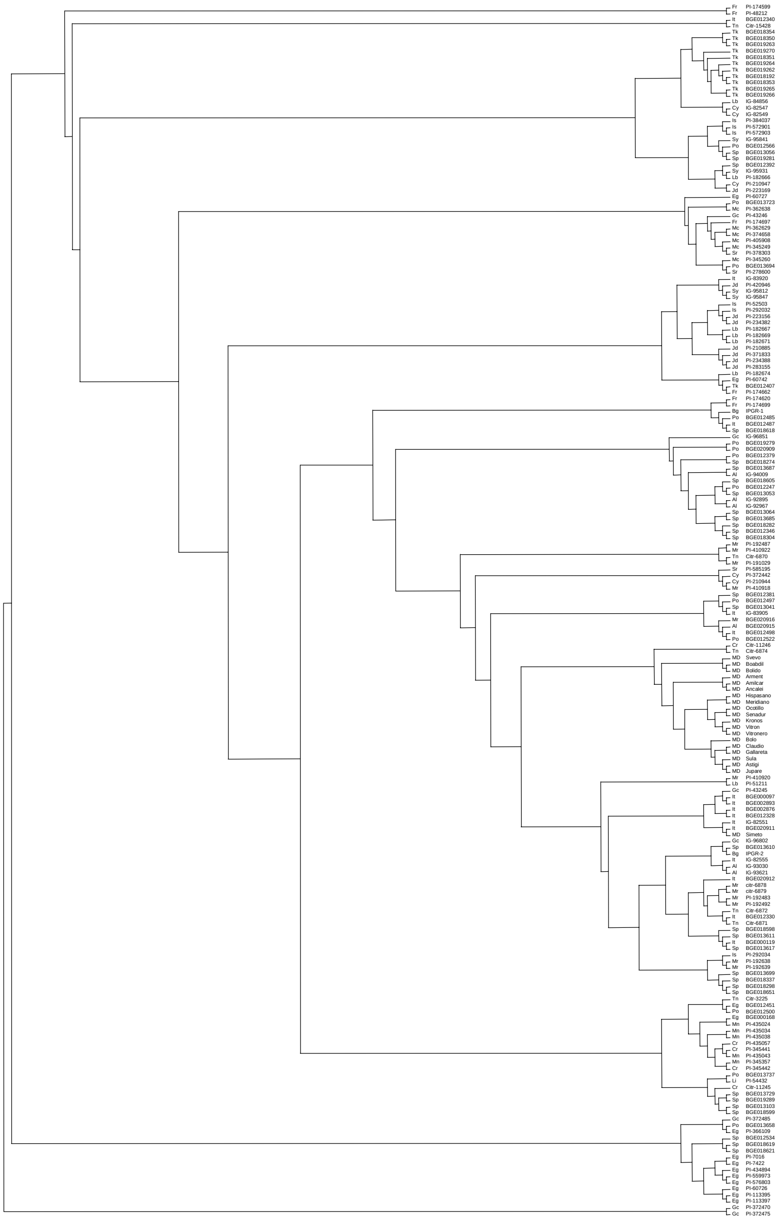


Fig. 2. Cluster analysis of the durum wheat accessions based in the allelic composition for 24 unlinked SSR.

Cluster analysis (Fig. 2) showed that the accessions tended to group according to their geographical origin. All accessions from Turkey, but one, grouped together. Modern cultivars, originating in Spain and Italy clustered together. They also showed a low average number of alleles and PIC values (3.7 and 0.38, respectively). The exception would be Simeto, which clustered with a group of Italian landraces.

The model-based clustering method was tested for K from 2 to 5. Only when 2 subpopulations were considered, were all accessions classified in one or the other at a $p>0.5$, and only 8 landraces from different origins were not classified in any of the three groups when K=3. Two of the three groups represented different geographical regions, i.e. one was mainly formed by landraces from the Middle East, Egypt and the Balcan Peninsula, while the other was formed by landraces from the western Mediterranean countries. The modern cultivars, excepting Simeto, were classified in the third group jointly with Turkish landraces. This result did not agree with the results of the distance-based cluster analysis (Fig. 2).

The LD parameter r^2 was significant for 39 % of the pairwise estimates (276) and varied from 0.002 to 0.074, with a median of 0.009. These values are lower of those found in elite wheat accessions (Breseghello and Sorrells, 2006), as was expected for a set of landraces.

References

Breseghello, F. and Sorrells, M.E. (2006). *Genetics,* 172: 1165-1177.
Liu, K. and Muse, S.V. (2005). *Bioinformatics,* 21: 2128-2129.
Nei, M. (1972). *American Naturalist,* 106: 283-292.
Pritchard, J.K., Stephens, M. and Donnelly, P. (2000). *Genetics,* 155: 945-959.