SHIFTING TRENDS OF BREAD WHEAT BREEDING IN ITALY ASSESSED
BY THE STUDY OF A TEMPORAL-BASED CORE COLLECTION

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INTRODUCTION

Germplasm collections represent valuable genetic resources for breeding programmes which aim to the synthesis of improved genotypes, better suited to the technological and nutritional needs of the market. One of the more recent ways to exploit the natural genetic diversity of germplasm collections is the so-called association analysis, or association mapping (AM), whose basic objective is to detect correlations between genotypes and phenotypes on the basis of linkage disequilibrium (LD). The sheer size of many germplasm collections often hinders their best exploitation; hence the need to identify core collections, i.e. representative samples of manageable size, where to perform the initial assessments, before re-exploring broader ranging materials. Given these assumptions, within the huge Triticum aestivum collection available at CRA-SCV, a sub-collection of 157 lines was identified and an association mapping project was started.

MATERIALS AND METHODS

A set of 157 bread wheat varieties representative of wheat breeding in Italy from the beginning of XX century up to date was assembled. The lines were classified into nine groups on the basis of their period of cultivation. Group 1 consists of local landraces, group 2 includes selections from local populations, group 3 comprises the first cultivars obtained by Nazareno Stampellp by crossing Italian and foreign germplasm. Each of the remaining groups consists of cultivars released in the following (consecutive) period of twenty years, and having at least one parent in the previous group. The lines were cropped (single rows 1.0 m long and 0.60 m apart) for two growing seasons (2010-11 and 2011-12) in two different locations in Italy; heading, growth habit, plant height, lodging and susceptibility to rusts (Puccinia spp), septoriose (Septoria), fusarium head blight (Fusarium spp), powdery mildew (Erysiphe graminis) were recorded. After harvest, the genotypes were characterized for spike shape, length, colour, density and awnedness, glumes hairiness, seed colour, size and vitreousness, according to the IBPGRB (1985) descriptors. The number of spikelets and seeds per spike, and the thousand-kernel weight (TKW) were also determined. The lines were subsequently ground to wholemeal with a 1-mm-sieve Cyclotec mill (Foss Tecator AB, Höganäs, Sweden). Protein content (PC) (N × 5.7, dry weight, AAC 39-10), and hardness (AAC 39-70 [AACC International, 2000]) were determined by a NIR System Model 6500 (FOSS NIRSystems, Laurel, MD). The SDS sedimentation volume was according to Preston et al. (1982). In parallel, DNA was extracted and analysed by the 90K wheat infinium array (Illumina). The phenotypic traits were analyzed by univariate (i.e., ANOVA) and multivariate (i.e., Correspondence analysis; CA) approaches. For CA the quantitative variables were converted to multiple categories and then binarised together with the qualitative ones (Burt table).

RESULTS AND DISCUSSION

The lines were clustered into nine groups, from group 1, including ancient populations, to group 9, including cultivars released from 2000 to 2006. Significant differences for all the parameters were observed (ANOVA not reported). A clear trend from old to new varieties was observed, leading towards earliness and reduction of plant size (Fig. 1). The n° spikelets/spike did not show extensive variation among groups, while an increase of the n° seeds/spike, along with kernel weight reduction, was observed going from group 1 to 9 (Fig. 2). For qualitative parameters, a strong increase of kernel hardness was observed starting from the cultivars released in the ‘80s (group 7; fig. 3A). The eldest lines had higher protein content than the recent ones (Fig. 3B); however, in the recent lines is evident a gradual increase of SDS sedimentation volume, a good indicator of gluten quality, with the highest values in groups 7, 8 and 9 (Fig. 3C). This reflects the breeding trend in the last thirty years: besides yield improvement, a strong selection for qualitative traits was pursued.

The first axis of multivariate CA (Fig. 4) mainly discriminated between ancient (groups 1-3, left side of figure 4A) and more recent groups. Being the CA an analysis where observations and variables are positioned in the same space, it is possible to select the categorized variables which follow the same trend observed for the groups. In particular Fig 4B shows how (from ancient to newer – i.e. from left to right):

- Plant height tends to decrease
- Thousand kernels weight tends to decrease
- Protein content tends to decrease
- Awnedness follows this trend: from very long awn to awned and awnless
- Kernel size tends to decrease

The statistical analysis for the definition of allele diversity, the phenomic analyses (i.e., coupling genotypes and phenotypes information) population structure and LD investigations are currently under way.

REFERENCES

International Board for Plant Genetic Resources (IBPGR); Commission of the European Communities (CEC) (1985). Revised descriptor list for wheat (Triticum spp.). IBPGR, IBPGR/OECD.

ACKNOWLEDGEMENTS

The research was partly sponsored by the Italian Ministry of Agriculture in the framework of the Project RGV-FAO [DM 13763, 24/06/11; DM 1129, 12/10/12].