The genus *Dasypyrum*—part 2. *Dasypyrum villosum*—a wild species used in wheat improvement

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**Abstract** *Dasypyrum villosum* (L.) P. Candargy is discussed as a species commonly used in wheat improvement. Chromosomal localization of the potentially useful traits and chromosomal position of some morphological and isozyme markers are shown. The investigations using molecular RAPD, AFLP, SSR, RFLP markers and in situ (GISH, FISH) hybridization experiments on *D. villosum* itself and in wide hybrids with *Triticum* are summarized. The article also presents the information about designation of *D. villosum* chromosomes and the current knowledge on the phenomenon of two-coloured *D. villosum* caryopses.

**Keywords** *Dasypyrum* (Haynaldia) · Markers · Useful traits · Triticeae

**Introduction**

*Dasypyrum villosum* (L.) P. Candargy (*Triticeae, Poaceae*) (synonym *Haynaldia villosa* (L.) Schur) is one of the two *Dasypyrum* species. This annual diploid grass, 2n = 2x = 14 (VV) is native to a northeastern part of the Mediterranean region and Caucasus area (De Pace and Qualset 1995; Frederiksen 1991). *D. villosum* is a vigorous ruderal plant growing on the harsh, moisture-stressed soils. In the past it was common in wheat fields but now it occurs predominantly in areas markedly disturbed by humans—along roads sides, on calcareous quarry dumps—and sparse populations can be observed near seashores, boundaries of pine woods and on the borders of uncultivated fields. It constitutes an important component of wild grass plant communities and is rarely found at altitudes higher than 1,000 m a.s.l. (De Pace and Qualset 1995). A peculiar characteristic of *D. villosum* is the presence of distinct tufts of the long hairs on the keel of the glume and apex of the lemma and of dark and light-colored kernels in the same spikelet (Frederiksen 1991; Sando 1935).

**Two-coloured caryopses in *Dasypyrum villosum***

*Dasypyrum villosum* produces caryopses with different morphologic features in the same spike and within the same spikelet: “clear” (yellow) and “dark” (brown)—the latter are shorter and thinner than the former. The inheritance of the seed color does not show any dominance effect, nor does it follow Mendelian segregations (Stefani...
Plants that develop from these two types of caryopses do not present significative morphologic differences at maturity and they produce ears with both “clear” and “dark” caryopses (Stefani and Onnis 1983).

On the other hand, these two types of caryopses differ in the protein composition of the endosperm with regard to glutelins and prolamin, both within and among different _D. villosum_ populations, as showed by Grilli et al. (1988) on the basis of a biochemical analysis.

In these two types of caryopses one can observe a different seed dormancy behavior (Paciolla et al. 1991) and a different energy and power of germination and viability during aging (Meletti and Onnis 1961; Stefani and Onnis 1983, 1984). “Clear” caryopses show shorter seed dormancy (Paciolla et al. 1991) and germinate slightly more rapidly than “dark” ones, but during aging the latter maintain a high germination capacity and viability in comparison with the former, showing germination ability until after 8 years of storage (Stefani et al. 1998). In seedlings from “clear” caryopses De Gara et al. (1991) observed a decrease of ascorbate peroxidase activity, a key enzyme involved in removing the hydrogen peroxide produced by cell metabolism during ageing processes and during some types of stresses, while the level of ascorbate peroxidase activity remains unchanged in seedlings from “dark” caryopses of the same age. This occurrence may be correlated with the onset of a biochemical pathway in the “clear” caryopses leading to morphological anomalies of seedlings, both in the roots and in the aerial portion, and to the loss of seed germination capacity (De Gara et al. 1991). In the “clear” caryopses Innocenti and Bitonti (1980) observed an increase of the histone/DNA ratio in 2c root meristematic nuclei during the storage period, while it remains almost constant in “dark” ones. The mitotic cycle duration in meristems of embryos germinated from the “clear” caryopses was longer than that of embryos germinated from “dark” ones (Innocenti and Bitonti 1983).

Cremonini et al. (1994) showed by C-banding a slightly variable chromosomal distribution of heterochromatin between brown and yellow caryopses. They also studied the nuclear DNA content in plants grown from the two types of caryopses and found 20–24% more of DNA in early prophase nuclei of seedlings from yellow caryopses than in early prophase nuclei of seedlings from brown caryopses. Frediani et al. (1994) using different investigation methods (dot-blot and in situ with a 396 bp _D. villosum_ repeat element as a probe) found a similar tendency, but the differences in the DNA content were smaller. They also showed an increase of genome size during germination, which was greatest in caryopses with the smallest genome. Redundancy modulations of subtelomeric and other repeated DNA sequences were proven to be involved in these genomic changes. A certain optimal redundancy level of these fluid domains was suggested to be a part of regulatory mechanisms acting during specific developmental steps in _D. villosum_ plants (Frediani et al. 1994). Recently, Obermayer and Greilhuber (unpublished data) negated size plasticity associated with caryopses color of _D. villosum_. They showed lack of significant differences of genome size between yellow and dark brown caryopses from 17 _D. villosum_ accessions (Greilhuber 2005).

Using a set of _Triticum aestivum–Haynaldia villosa_ addition lines and analysing chromosome morphology, homoeologous pairing and some biochemical markers, Sears (unpublished data) designed _H. villosa_ chromosomes as 1Ha–7Ha (Liu et al. 1995). De Pace et al. (1988a) confirmed this designation with the evidence of isozyme and rDNA analyses. Friebe et al. (1987), basing on the C-banding pattern, renamed the seven pairs of _H. villosa_ chromosomes as A–G, respectively, which corresponded to those 1Ha–7Ha of Sears. Zhong et al. (1996), basing on the sequential C-banding-GISH analysis, showed a general similarity with the results of Friebe et al. (1987).

Basing on karyotype and banding analysis of another set of disomic _T. aestivum–H. villosa_ addition lines, Liu et al. (1988) agreed partially with Sears and they used the symbols V1–V7 as