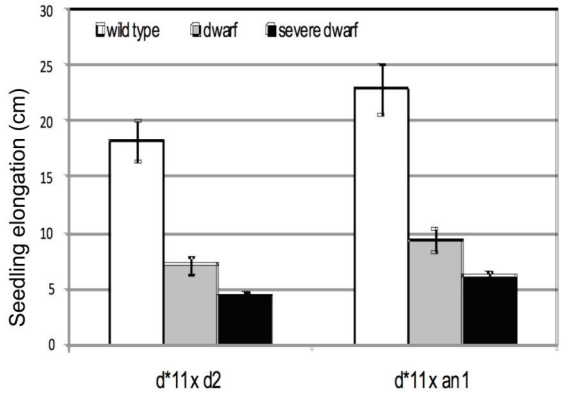

Figure 1. Stature of wild type, dwarf and severe dwarf seedlings in the selfed progeny of *d2/d*11* and *an1/d*11* double heterozygotes. Seedling elongation was determined at day ten after germination by measuring the distance between the scutellar node and the tip of the last leaf. Each value represents the mean (± std. dev) of three independent experiments.

These results seem to suggest that *d11** and *d2* or *an1* affect different biological pathways, both of which contribute independently to seedling elongation. It remains to be explained how *d11** shows non-complementation with *d1* and *d5,* two genes located on different chromosomes and controlling separate steps in GA biosynthesis.

Characterization of a dominant mutation of the *Dwarf8* gene

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We have isolated and characterized a new spontaneous dominant dwarf mutation that at maturity shows delayed flowering and reduced stature, ranging from 60-70% in a W23 NIL (Fig. 1A) to a 40-45% in a W23 X B73 F1 hybrid (Fig. 1B), caused by a reduced internode length. This mutant also shows thick broad leaves, that are 25-30% larger than wild type (Fig. 1C), a strong gene dosage effect on phenotype and a less severe phenotype in comparison with the *D8-1* dominant mutant, as shown in Fig. 1D. The dwarf phenotype is also easily detectable in the first stage of plant growth (Fig. 1E) and at maturity shows a tendency to produce tillers (Fig. 1F). In addition, the dwarf mutant is altered in its floral development. In fact, stamens are present in the terminal flowers of the ears (andromonoecious ear); however, they are sterile (Fig. 1G). The dimensions of the silks and anthers in the inflorescence are bigger by about 40% and 17%, respectively, compared to the wild type (Fig. 1H, I). The genetic analysis performed to understand the inheritance of this dwarf mutation demonstrated a monogenic dominant inheritance of this trait, and the map position was established on the long arm of chromosome 1. The results obtained from this analysis showed that *D*-1023* maps where *D8-ref* was located, and thus the mutation was renamed *D8-1023*.

The novel mutant allele was cloned and the alignment with *d8*(+) wild type alleles present in the database has shown a molecular lesion: an insertion of 3bp within the VHYNP domain, located in the 5' of the gene near the DELLA domain, which is responsible for the GA response (Fig. 2). This finding represents the first evidence of a dominant dwarfing mutation that does not involve the DELLA domain but is in the not yet well-characterized VHYNP domain, which is involved in protein degradation. We have found a new and interesting phenotype and we suggest a possible future modification of the VHYNP domain of the *D8* gene to modulate plant growth and to shorten excessively tall germplasm, with the aim of improving crop production.

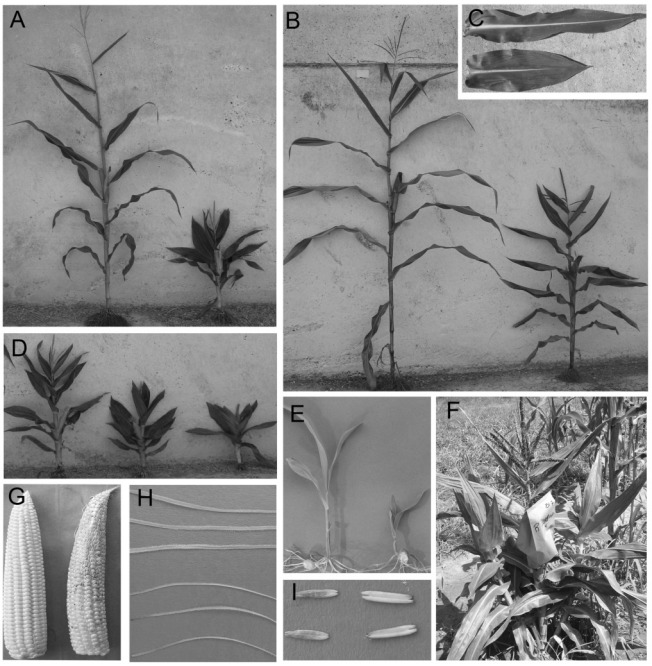

Figure 1. Phenotype of the new dwarf mutant: (A) wild type (left) and *D*-1023/+* mutant (right) whole plants at maturity in a W23 near-isogenic line; (B) wild type (left) and *D*-1023/+* mutant (right) whole plants at maturity in a W23 X B73 F1 hybrid genetic background; (C) leaves, wild type above and mutant below in a W23 near isogenic line; (D) from left to right *D*-1023/+*, *D*-1023/D*-1023*, *D8-1/+* whole plants in a W23 genetic background; (E) wild type seedling (left) and dwarf (right); (F) dwarf tillering growth habit in a B73 near isogenic line; (G) wild type ear (left) and dwarf anthered ear (right); (H) mutant silks (above) and wild type silks (below); (I) wild type anthers (left) and mutant anthers (right).

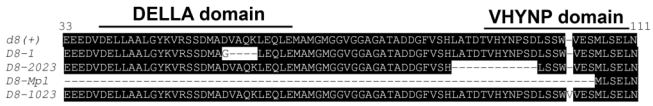

Figure 2. Partial alignment between the *d8* wild type allele and predicted proteins encoded by dominant mutant alleles. The wild type *d8* allele is compared with *D8-1*, *D8-2023*, *D8-Mpl* and *D8-1023* dominant mutant allele-encoded proteins with mutant N-terminals. Differences between wild type and mutant sequences (deletions, insertions and substitutions) are highlighted in white, and the previously identified highly conserved DELLA and VHYNP domains are shown.

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Double kernel fruitcases found in teosinte populations

--Kato Y., TA

Teosinte fruitcases traditionally are known to have only one developed spikelet each because the second one is suppressed during the ontogeny of the female inflorescence. According to Galinat (Corn and Corn Improvement, G. F. Sprague (ed.), pp. 1-47, 1988) the primary step for evolving teosinte to maize was the reactivation of the second spikelet to form the necessary link between these two plant taxa and he states that "The pairing of fe-