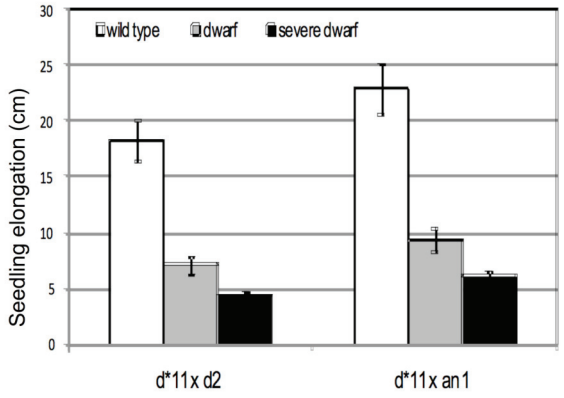

Figure 1. Stature of wild type, dwarf and severe dwarf seedlings in the selfed progeny of *d2/d*11* and *an1/d*11* double heterozygotes. Seedling elongation was determined at day ten after germination by measuring the distance between the scutellar node and the tip of the last leaf. Each value represents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

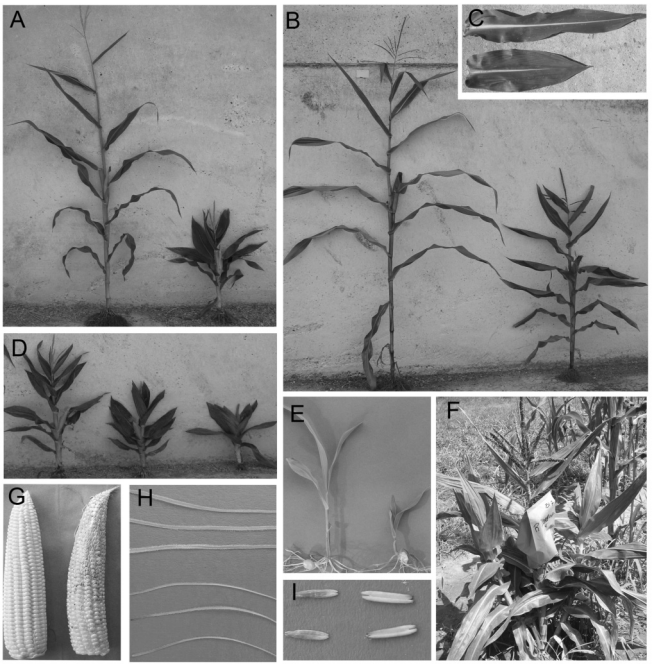

Figure 1. Phenotype of the new dwarf mutant: (A) wild type (left) and *D*-1023/+* mutant (right) whole plants at maturity in a W23 near-isogenic line; (B) wild type (left) and *D*-1023/+* mutant (right) whole plants at maturity in a W23 X B73 F1 hybrid genetic background; (C) leaves, wild type above 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).

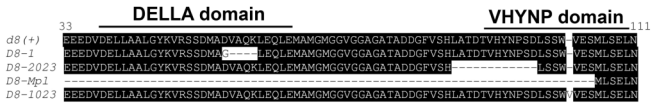

Figure 2. Partial alignment between the *d8* wild type allele and predicted proteins encoded by dominant mutant alleles. The wild type *d8* allele is compared with *D8-1*, *D8-2023*, *D8-Mpl* and *D8-1023* dominant mutant allele-encoded proteins with mutant N-terminals. Differences between wild type 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-

male spikelets in wild populations of teosinte occurs at a low frequency. Its significance can be questioned because, rather than being part of the natural variation in teosinte, it could just be a result of introgression from corn."

Recently the author has found these paired female spikelets in populations of teosinte race Chalco (Figure 1). Two types of "double kernel fruitcases", as the author has called them, were found: a) fruitcases with the two spikelets in parallel within the single cupule with an indurated outer glume covering each spikelet, as shown in the middle row of Figure 1; b) two spikelets grown in a different manner, one within the cupule covered by an indurated outer glume in the same way as the normal teosinte fruitcase with a single spikelet, and the second spikelet developing outside the cupule, due to elongation of the pedicel or rachilla, and covered by the floral bracts or glumes with a variously indurated outer glume. Frequently, the outer kernel becomes naked or almost so; the elongated rachilla is grown parallel to the rachis axis, therefore, this spikelet usually is positioned at the top of the fruitcase; and either one of the two spikelets can grow outward from the cupule. No case with the two kernels growing outside the cupule has been observed so far (see bottom row in Figure 1).

Figure 1. Normal and double kernel fruit cases of teosinte from the region of Chalco-Amecameca, State of Mexico-

The parallel orientation of the elongated pedicel of the external kernel in double kernel fruitcases in relation to the rachis axis, seems to indicate that they are not a consequence of introgression from maize into teosinte because the rachilla elongation in maize is perpendicular to the rachis axis. Besides, as Galinat (Univ. Massachusetts, Agric. Expt. Sta. Amherst, Bull. No. 585, 1970) states, "In a hybrid between modern maize and teosinte, the rachilla is shortened and the paired spikelets inclined and partially embedded within the cupule." However, because the present report is based on preliminary observations, the maize introgression hypothesis cannot be discarded completely yet until more detailed studies are made on these paired spikelet female fruitcases from teosinte race Chalco populations. In any event, the evolutionary significance of these findings is that the teosinte populations of 8,000 to 10,000 years ago probably produced the natural variation, which included the paired spikelet female fruitcases with naked kernels among other variants, before man of that time, upon observing this variation was motivated to start domestication of maize from teosinte. This evolutionary process intermediate between teosinte and maize is what Galinat (1988) called the "primary step" toward the origin of maize by means of "a reactivation of the second female spikelet".

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Molecular characterization of selected maize landraces in India using Simple Sequence Repeat (SSR) markers

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Intensive efforts have been initiated in the last few years on phenotypic as well as molecular characterization of the maize landraces in India. Significant variability in plant, ear, and tassel characteristics of maize landraces has been observed in Northeastern and Northwestern highlands of India with relatively less varietal diversity for those collected from the plains (Prasanna and Sharma, Indian J. Plant Genet Resources 18:155-168, 2005).

In the present study, a set of 48 Indian maize landraces was selected for SSR genotyping. These landraces are all important for breeding purposes, since they are mostly early maturing, with excellent yield characters and adaptability, along with biotic and abiotic stress tolerance. The selected germplasm represents diverse agro-ecological zones of India, spanning both NEH (29 landraces) and other regions (19 landraces). Thirty were obtained from the National Gene Bank at the National Bureau of Plant Genetic Resources (NBPGR), New Delhi, and 18 were collected by the Maize Genetics Unit, IARI, from Sikkim state in the NEH region in November 2005 (Table 1). SSR analysis employed fluorescent-dye labeled SSR primers (CIMMYT Applied Biotechnology Center's Manual of Laboratory Procedures (http://www.cimyt.org/ABC/Protocols/manual ABC.html) (Fig. 1).

Table 1. List of accessions selected for molecular characterization.

S.No.	Accession	State (India)*	S.No.	Accession	State (India)*
1	IML112	HP	25	IML429	Rajasthan
2	IML115	J&K	26	IML436	Rajasthan
3	IML132	Uttarakhand	27	IML452	MP
4	IML181	HP	28	IML454	MP
5	IML196	Manipur	29	IML479	MP
6	IML203	Nagaland	30	IML550	Sikkim
7	IML210	AP	31	IML558	Sikkim
8	IML215	Ar.P	32	IML560	Sikkim
9	IML232	Ar.P	33	IML565	Sikkim
10	IML235	Ar.P.	34	IML567	Sikkim
11	IML255	Meghalaya	35	IML587	Sikkim
12	IML267	Sikkim	36	IML588	Sikkim
13	IML282	Ar.P.	37	IML589	Sikkim
14	IML290	Jharkhand	38	IML590	Sikkim
15	IML293	Bihar	39	IML592	Sikkim
16	IML295	Jharkhand	40	IML594	Sikkim
17	IML297	WB	41	IML595	Sikkim
18	IML298	Meghalaya	42	IML602	Sikkim
19	IML321	Bihar	43	IML608	Sikkim
20	IML415	MP	44	IML610	Sikkim
21	IML420	Rajasthan	45	IML615	Sikkim
22	IML423	Bihar	46	IML616	Sikkim
23	IML427	Rajasthan	47	IML618	Sikkim
24	IML428	Rajasthan	48	IML637	Mizoram

*HP: Himachal Pradesh; J&K: Jammu and Kashmir; AP: Andhra Pradesh; Ar.P.: Arunachal Pradesh; WB: West Bengal; MP: Madhya Pradesh.