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ERRATUM

Erratum to: Intron-length polymorphism identifies a Y_2K_4 dehydrin variant linked to superior freezing tolerance in alfalfa

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We want to report slight modifications to the location of the introns described in the original version of the article. Changes result from variations in the determination of splicing sites. Apart from the addition or removal of amino acid residues in the region bordering the introns, the sequences remain unchanged. These changes do not affect the conclusions of the study and ensure concordance with sequence information deposited in GenBank. Corrected alignment of dehydrin sequences in Figs. 1 and 3 and adjusted intron length values (Table 3) are presented in the following pages. Nucleotide sequences are also corrected in Supplementary Figs. 1 and 2 available online. Accordingly, three statements in the Results section are amended as follows:

The second and third sentences of the second paragraph of the "Sequence analysis of the G2 group of Y_2K_4 dehydrins" subsection now read as:

Sequence analysis of cloned fragments revealed that the length of the open-reading frame of the G2 sequences varied from 858 bp to 921 bp (Fig. 3a). The shortest sequences were associated with the presence of a single nucleotide polymorphism at the expected exon–intron boundary, causing an upstream shift of the 5′ splicing site resulting in a slightly longer intron. Another group of smaller sequences (I_3-C and I_4) resulted from a deletion before the intron while their K-segments region was typical of the G2 group including the presence of the annealing site for primer 694r (Fig. 1).

Third sentence of the third paragraph in the same section now reads as:

Intron polymorphism arose mainly from length variation ranging from 189 up to 441 bp (Table 3).

The online version of the original article can be found under doi:10.1007/s00122-011-1735-0.

Electronic supplementary material The online version of this article (doi:10.1007/s00122-012-1805-y) contains supplementary material, which is available to authorized users.

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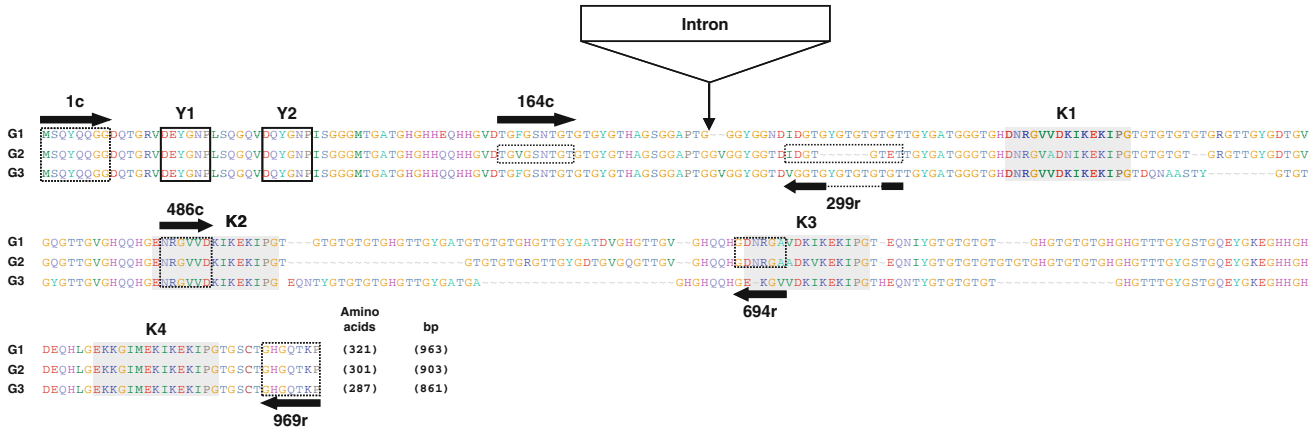

Fig. 1 Alignment of representative full-length coding sequences for the G1, G2 and G3 groups of size variants of Y_2K_4 dehydrins previously defined by Rémus-Borel et al. (2010) from partial sequences. These sequences are deposited in GenBank under the accession numbers JN226736 to JN226738. The location of a single intron is indicated. Conserved Y motifs are identified in *boxes with solid lines* while the K-segments are shown in *shaded areas*. Primers used for the amplification of internal regions of dehydrins are indicated. Nucleotide variations at annealing sites between the three groups of sequences are highlighted by *boxes with dotted lines*. The number of amino acids and nucleotides (bp) for the open reading frame is indicated at the end of the sequences

Table 3 Number of intronic variant sequences in positive (D+) or negative (D−) genotypes

Intron variant		Frequency in		Length (bp)	Genotypes
		D+	D−		
I_1	A	16		211	1^+, 6^+, 22^+, 41^+
	B	1		211	6^+
	C	1		211	6^+
	D	1		211	41^+
I_2	A	1		215	41^+
	B		1	215	40^-
	C		5	215	40^-
	D		1	215	40^-
	E		1	189	9^-
I_3	A		1	268	10^-
	B		2	268	10^-, 11^-
	C		1	218	9^-
I_4	A		3	440	9^-
	B		1	439	9^-
	C		1	438	9^-
	D		1	439	9^-
I_5	A		1	439	11^-
	B		1	441	11^-
	C		1	440	11^-
	D		1	440	11^-

The length of the intron and the presence in genotypes positive (+) or negative (−) for the dehydrin RFLP is indicated

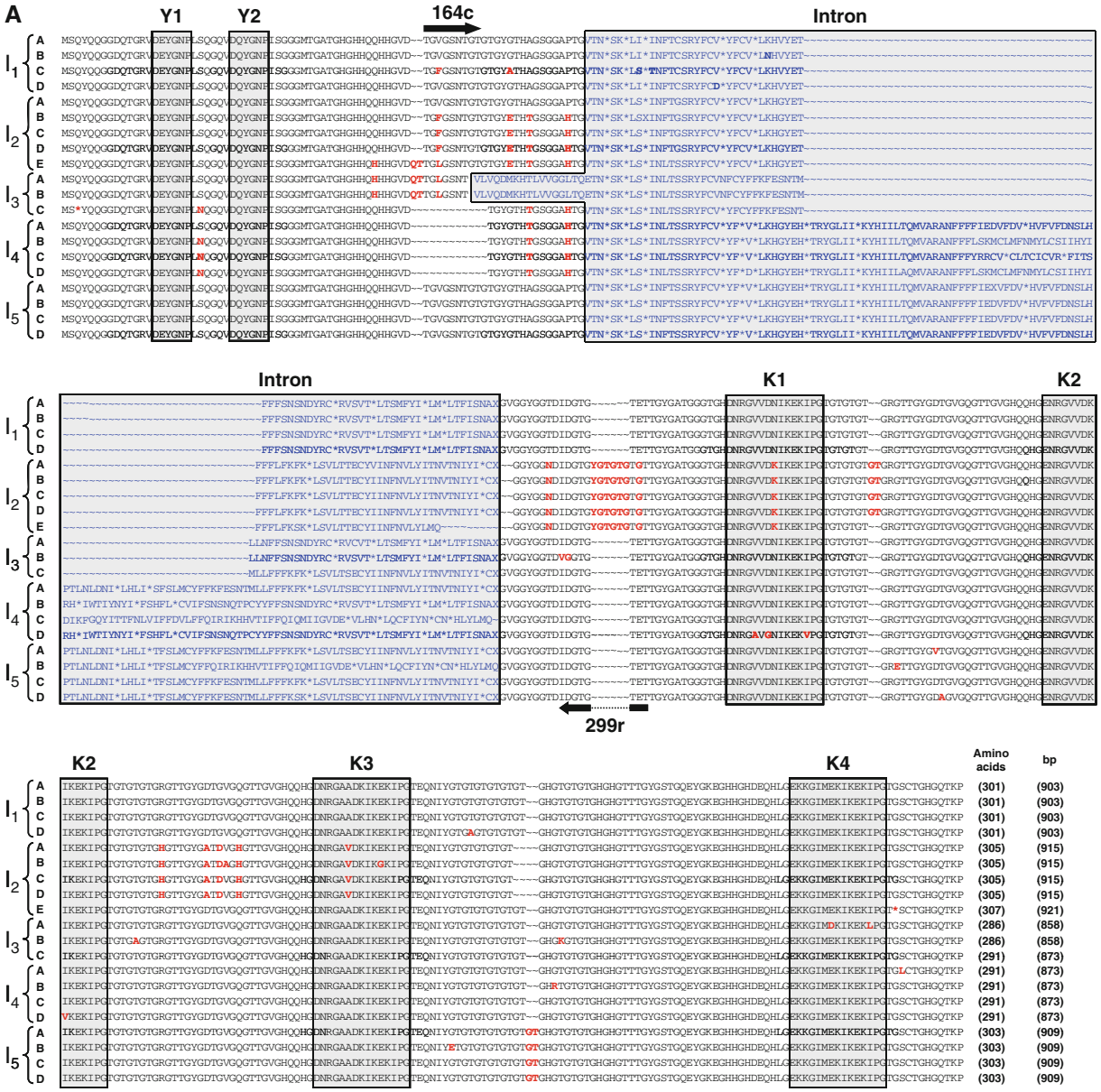

Fig. 3 **a** Full-length alignment of exonic and intronic sequences of the G2 group of Y_2K_4 dehydrins amplified with the 1c and 969r primer pair. The Y- and K-segments and the intron are indicated in *shadowed boxes*. Introns were translated into notional peptides for ease of comparison. Five groups (I_1–I_5) were defined by the presence of InDels and sequence variations in the intron and their flanking regions. Variations in amino acids in the exons are indicated in *bold letters*. The orientation and anchoring sites of primers 164c and 299r are indicated with *black arrows*. The number of amino acids and nucleotides (bp) for the open reading frame is indicated in *brackets* at the end of each sequence. A representative sequence from each group was deposited in GenBank under accession numbers JN226739 to JN226743. **b** Full-length alignment of coding sequences of variant A of the intron group I_1. The Y- and K-segments are indicated in *shadowed boxes* and the location of the intron is shown. The orientation and anchoring sites of primers 164c and 299r are indicated with *black arrows*. Variations in amino acids are indicated in *bold letters*. Identification of D+ genotypes in which sequences were found is provided in the *left margin*. The number of observed sequences in D+ genotypes is indicated at the end of each peptide sequence

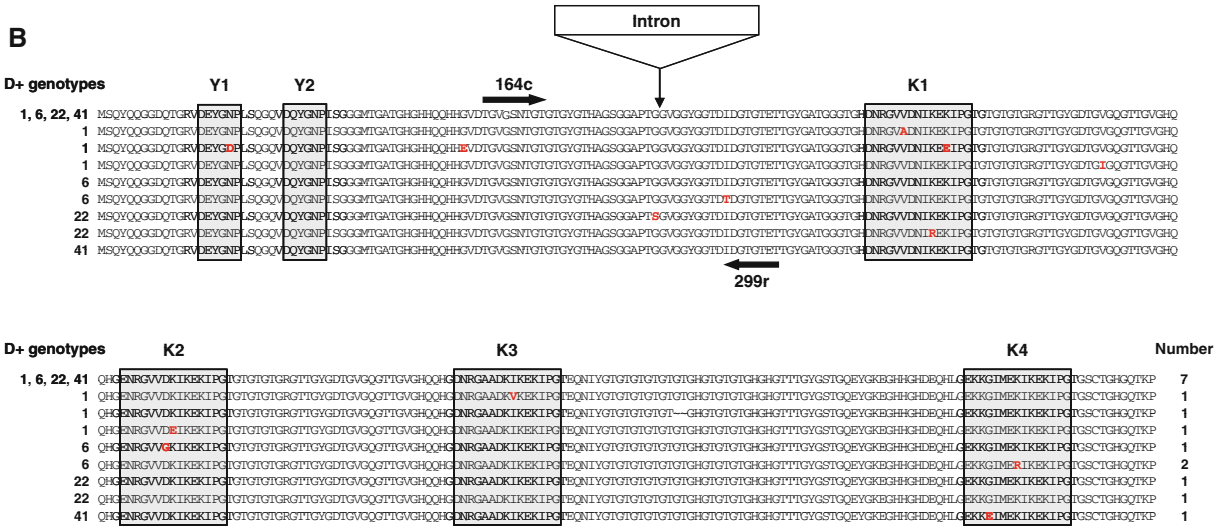

Fig. 3 continued