## SL203

연사 3

# The Molecular Basis of Two Spontaneous Mutants at the *Brittle-2* Locus of Maize

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To elucidate the molecular basis of spontaneous mutations in maize, two spontaneous mutants were analyzed; one(bt2-7503) produces the increased size of transcript while the other (bt2-C) produces a transcript of wild type size but the steady-state level of transcript is significantly increased. The cDNAs were cloned and sequenced. The sequnce of the mRNA 5′ end was obtained by direct RNA sequencing. The sequence data of bt2-C revealed three single-base substitutions in the coding region, resulting in three amino acids alterations. mRNA sequence of bt2-7503 revealed two unspliced introns (123bp and 314bp) between nucleotide #720 and #721 and between #900 and #901 of the wild type cDNA. The sequence of those introns was obtained by sequencing PCR amplified fragments from bt2-7503 genomic DNA and mRNA. Both genomic and mRNA sequences were identical and revealed that the nucleotide sequence of those introns was imported from a non-allelic gene(termed as Bt2-like). In the 5′ of the 314bp intron, both sequences were composed of two sequence populations; Bt2-like intron sequence and duplicated sequence originating from the exonic sequence from nucleotide #901 to #939 within Bt2