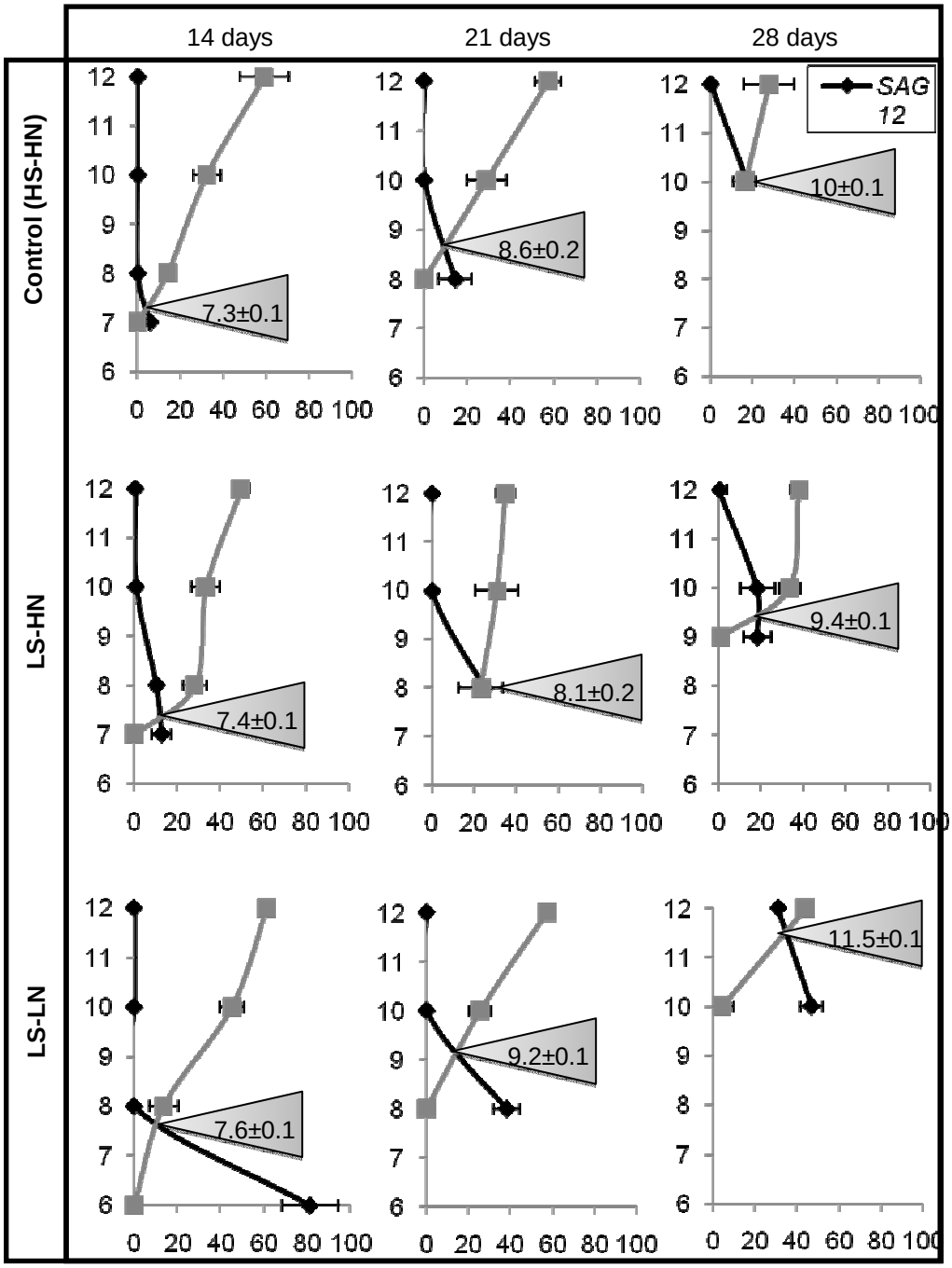
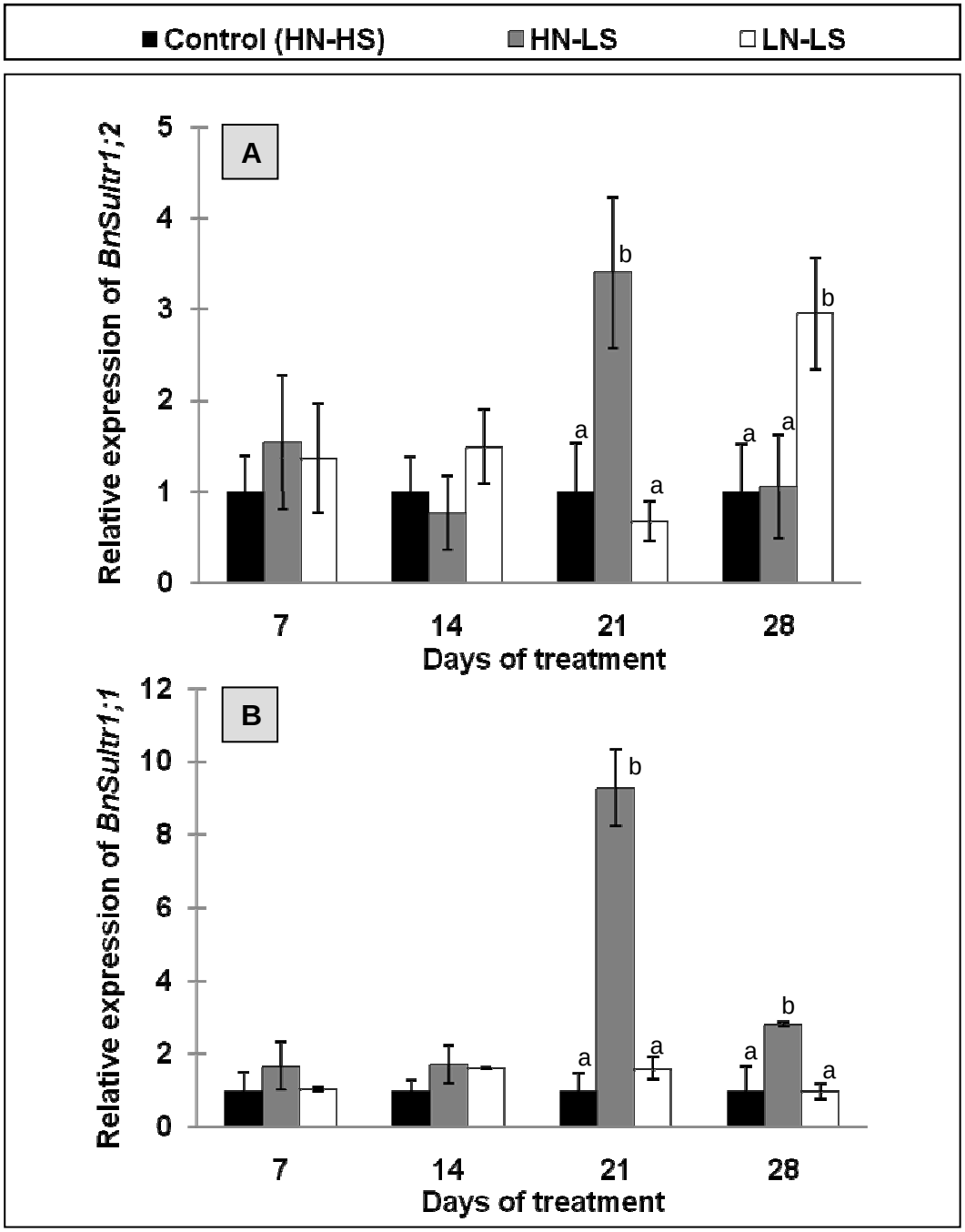


Supplemental data #1: Results of RT–PCR analysis of *SAG12* and *Cab* gene expressions in leaves from control (HS-HN), LS-HN and LS-LN plants of oilseed rape, expressed as a percentage of the maximum of both transcripts obtained in overall leaf rank studied. The intersection points, obtained at each date, are indicated by the grey arrows. They refer to the theoretical nodal position of the last leaf rank subjected to senescence (*i.e.* displaying *SAG12* up-regulation and *Cab* down-regulation, concomitantly, in leaf blade), used to determine the progression of senescence (see Fig. 2).



Supplemental data #2: Results of RT–PCR analysis of *BnSultr1;1* and *BnSultr1;2* gene expressions in lateral roots from control (HN-HS), HN-LS and LN-LS plants of oilseed rape. The results of expression are relative to the result obtained in control plants (HN-HS) at each date of harvest. Q-PCR amplifications were performed by using *BnSultr1;1* forward primer: 5'- AGATATTGCGATCGGACCAG -3' and reverse primer: 5'- GAAAACGCCAGCAAAGAAAG -3', and *BnSultr1;2* forward primer: 5'- GGTGTAGTCGCTGGAATGGT -3' and reverse primer: 5'- AACGGAGTGAGGAAGAGCAA -3'. As indicated for *BnSultr4;1* PCR analysis, *EF1-a* gene (Accession no: DQ312264), was used as an internal control gene. Details otherwise as for Fig. 3. As previously reported by Parmar *et al.* (2007), these data indicated that *BnSultr1;1* and *BnSultr1;2* gene expressions were significantly increased (since 21 days) in response to limitation of S supply (LS-HN).

Supplemental data #2 ; Dubousset *et al*., 2009