



FIGURE 7 Phenotypic analysis of maize *s5hMu* mutant plants grown in the field. a) Representative picture of WT siblings and *s5h Mu* maize mutants at 70 days after germination (DAG). b) *s5h Mu* and WT sibling plant height at different DAGs. Plant height was measured in 10 plants from each genotype, from 70 to 90 DAGs. Results represent the average of 10 different plants \pm S.E from one experiment. At each DAG, asterisks over the bar indicate significant differences between genotypes (Student's t-test, $p < 0.05$). c) Number of senescent leaves per plant in WT and *s5hMu* maize lines analyzed from 70 to 90 DAGs. Results represent the average of 10 different plants \pm S.E from one experiment. Different letters indicate statistically significant differences applying one-way ANOVA ($P < 0.05$). d) Expression analysis of maize senescence marker genes. Relative expression levels of *SAG12*, *SWEET1b*, *MIR3* and *STP2* analyzed by qRT-PCR in leaf #11 from *s5hMu* mutants and WT siblings. Each reaction was normalized using the cycle threshold values corresponding to the *ACTIN1* and *MEP* mRNAs. Data are represented as the means \pm S.E of 3 biological replicates from three different experiments. e and f) Chlorophyll a (e) and b (f) content in leaf #11 from *s5hMu* mutants and WT siblings. Results represent the average of 4 biological replicates \pm S.E from one experiment. Asterisks indicate significant differences between genotypes (Student's t-test, $p < 0.05$).