

## Appendix 1.

### Calculation of TPI and protein consumed by *M. sexta* larvae.

In order to determine the amount of TPI and protein consumed by *M. sexta* larvae during the experiment, we estimated leaf TPI and protein values for days 1, 2, and 3 with daily leaf concentrations extrapolated from measurements at day 0 and day 4, and for days 5 - 10 with measurements at day 4 and day 11 for all rosette and stem leaf positions (Supplemental Figures 1-4). With these concentration values, the location of the larvae each day on the plant (Figs 1 and 3), and information from the literature about the average leaf area consumed by a *M. sexta* larvae during the first, second, and third instars [1], we calculated the amount of TPI and protein consumed (C) for larvae feeding on each genotype (Additional data file Fig. 5). These calculated values are products of the larvae's instar-specific feeding site, amount, and TPI and protein content of each leaf position consumed (Additional data file Tables 1a and b). Calculated values were obtained as follows: protein consumed = leaf protein content (mg/g) x larvae consumption (g) and for TPI consumed = leaf TPI content (nmol/g) x larvae consumption (g).

In order to determine the effect of larval movement on TPI and protein consumption, we simulated larval TPI and protein consumption on transformed ( $S_T$ ) and untransformed ( $S_{WT}$  and  $S_A$ ) genotypes by transposing either daily larval location data ( $S_{WT}$  and  $S_A$ ) or leaf TPI and protein content ( $S_T$ ) from untransformed (WT and A) to transformed (AS--, AS-, and S++) genotypes (Additional data file Tables 1a and b). For example, to calculate the  $S_T$  value in combination with WT either TPI or protein content and larvae location on AS-- genotype, we used the TPI and protein contents of the WT

and calculated the TPI and protein consumption using the larval location on AS-- plants

(Additional data file Table 1a).

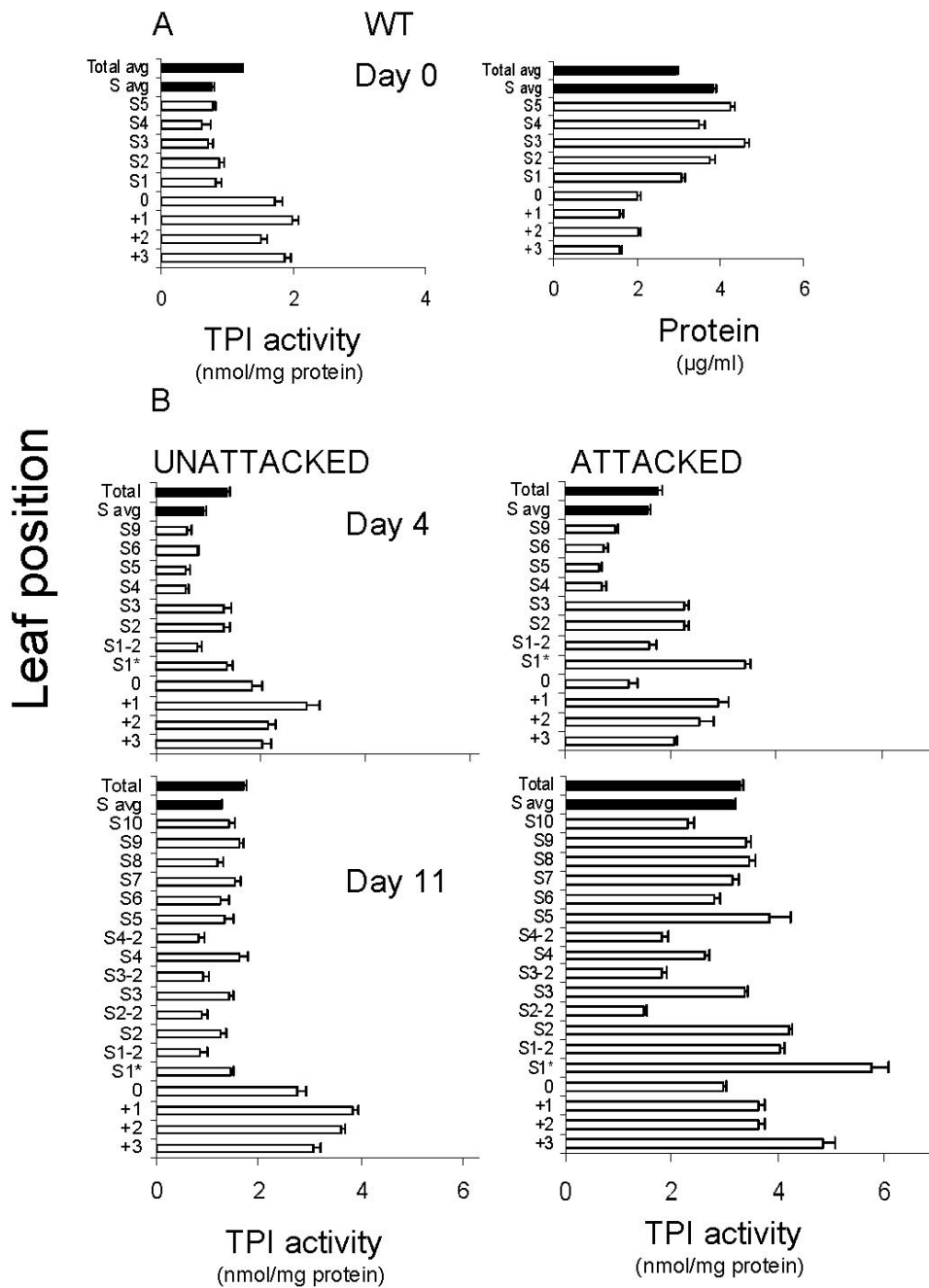
**Additional data file Table 1.** Combination of TPI and protein from different *N. attenuata* genotypes and larval location of different genotypes that have either calculated (C) or simulated (S) values. **a.** WT, AS-- and AS- genotypes. **b.** S++ and A genotypes. C values resulted from larval location and either TPI or protein from the same genotype.  $S_{WT}$  and  $S_A$  values resulted from transposing larval location data from untransformed (WT and A) to transformed (AS--, AS-, and S++) genotypes.  $S_T$  values resulted from transposing either TPI or protein contents from untransformed (WT and A) to transformed (AS--, AS- and S++) genotypes.

**TPI and protein from genotypes**

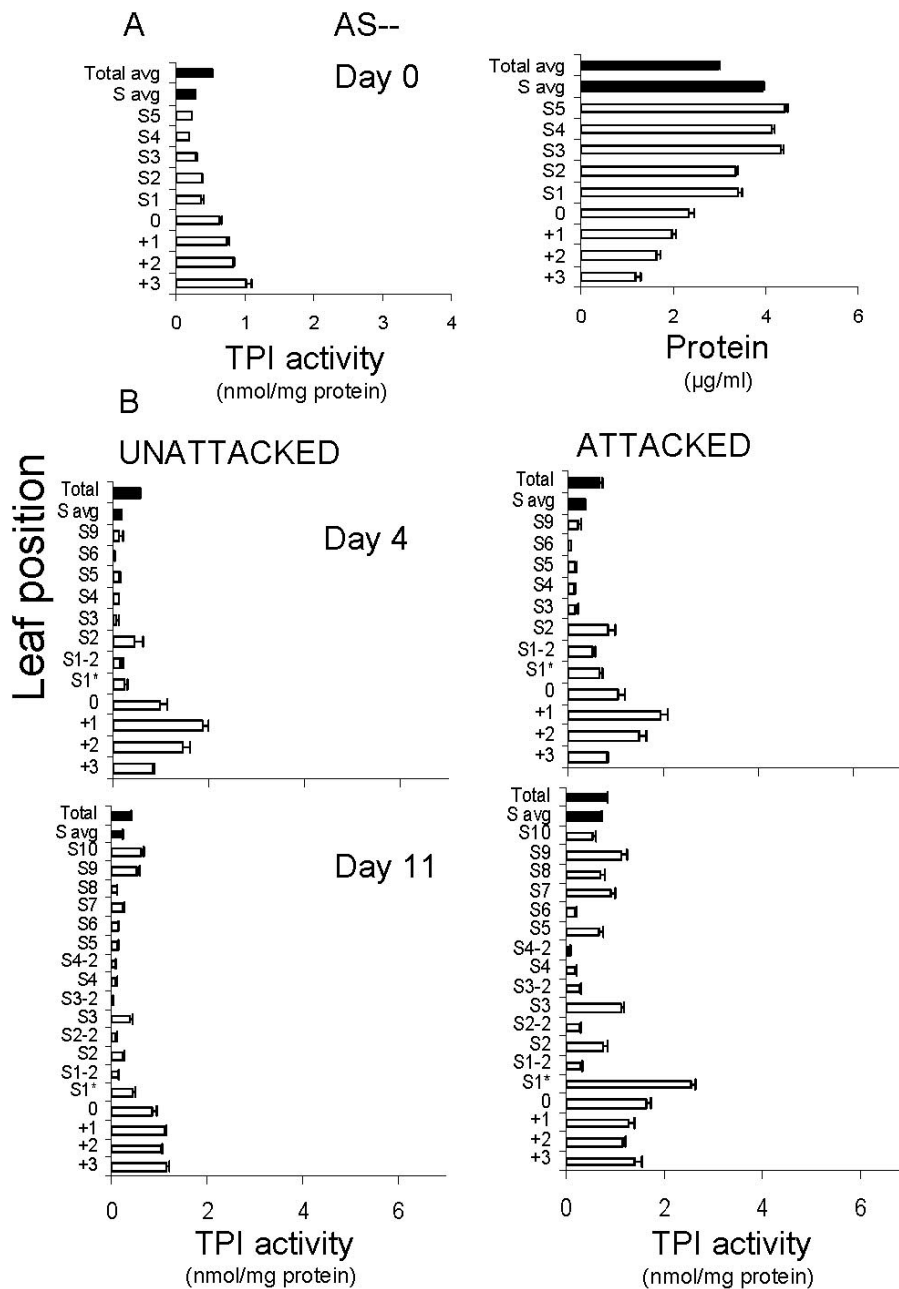
		<b>a</b>			<b>b</b>		
		WT	AS--	AS-	S++	A	
Larval location	WT	C	$S_{WT}$	$S_{WT}$	S++	C	$S_T$
	AS--	$S_T$	C		A	$S_A$	C
	AS-	$S_T$		C			

## References

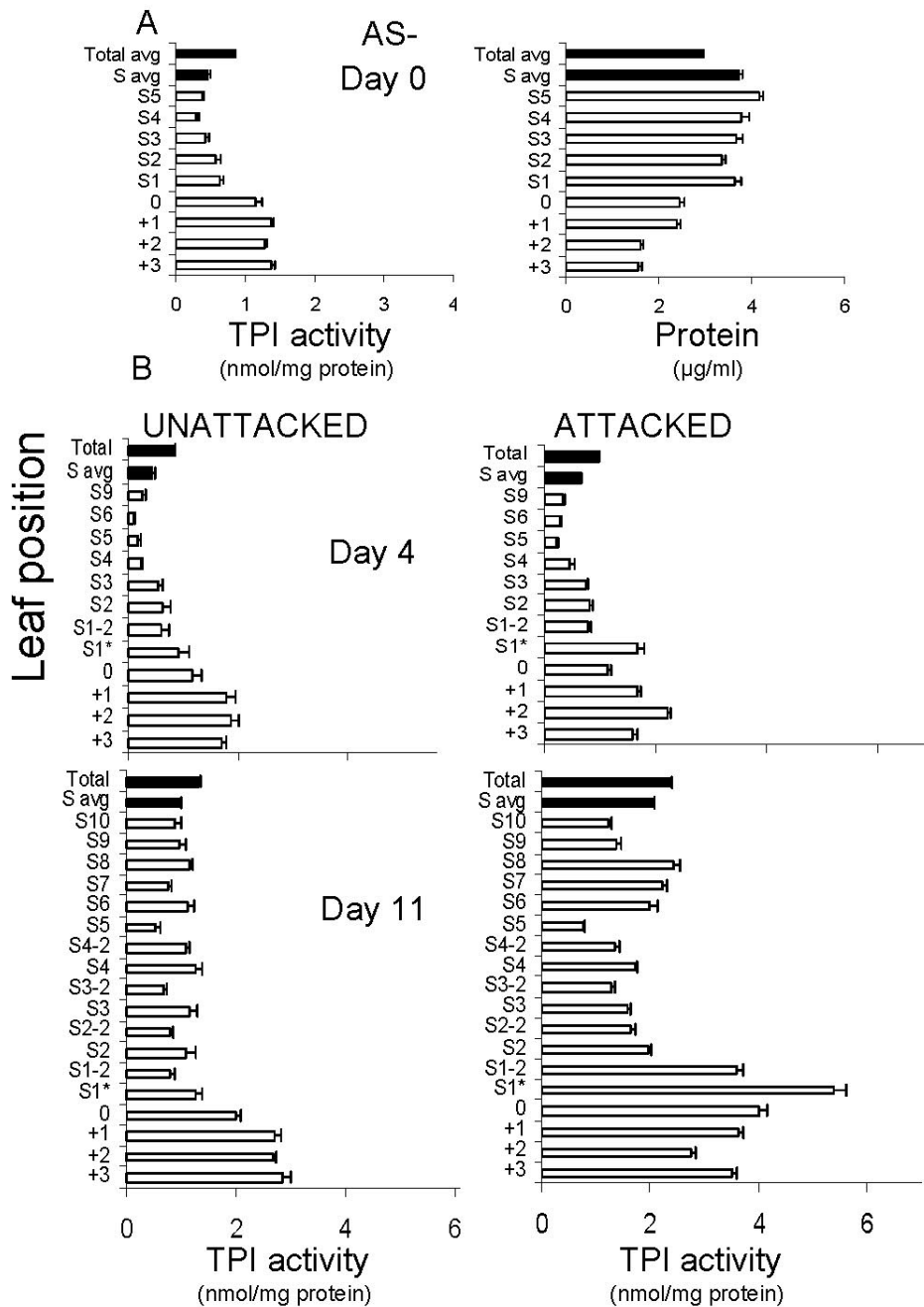
1. AH Madden, FS Chamberlin: **Biology of the tobacco horn-worm in the southern cigar-tobacco district.** *USDA Tech Bull* 1945, **986**:1-51.



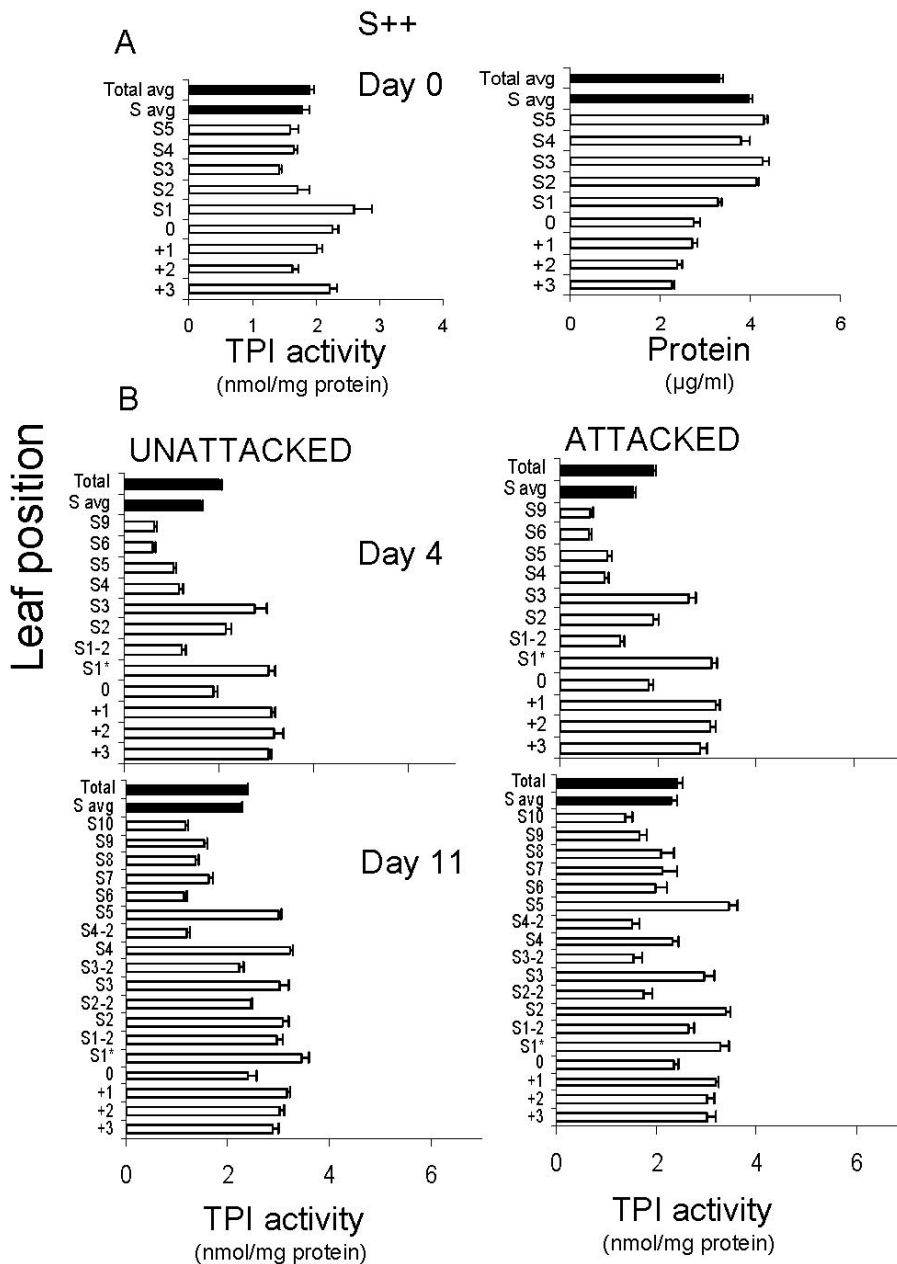
**Additional data file Figure 1. A.** TPI activity (mean  $\pm$  SEM) and protein content from different leaf positions of WT plants at the elongation stage before *M. sexta* larvae attack. **B.** TPI activity (mean  $\pm$  SEM) from different leaf positions of the WT plants at the elongation stage either unattacked or attacked by *M. sexta* larvae 4 and 11 d after neonates started to feed on the leaf at S1 position (\*). Solid bars show the average of TPI activity and protein content either of rosette and stem leaves (Total avg) or of stem leaves only (S avg). See Figure 1 for graphic depiction of leaf position.



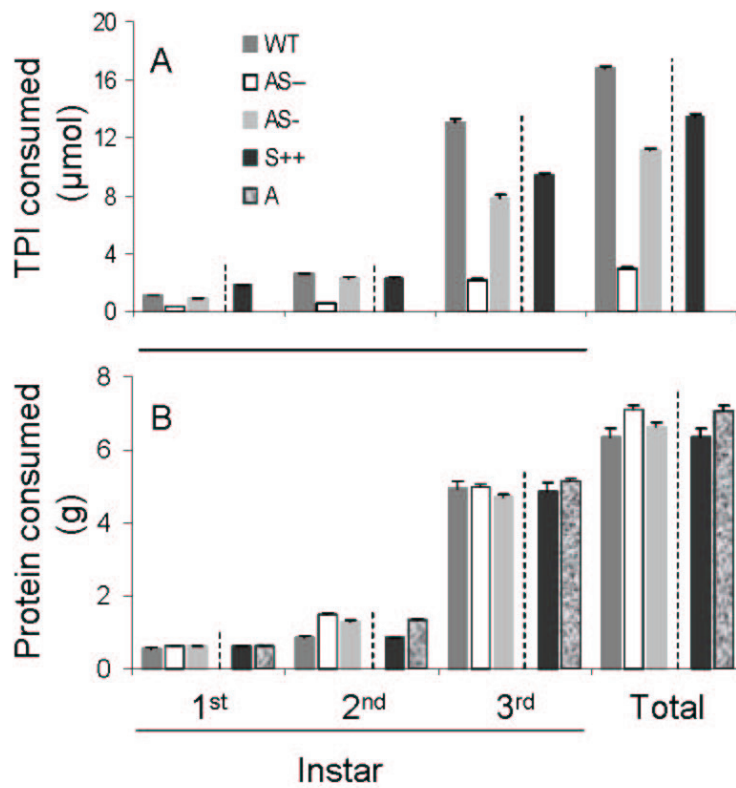
**Additional data file Figure 2. A.** TPI activity (mean  $\pm$  SEM) and protein content from different leaf positions of AS-- plants at the elongation stage before *M. sexta* larvae attack. **B.** TPI activity (mean  $\pm$  SEM) from different leaf positions of the AS-- plants at the elongation stage either unattacked or attacked by *M. sexta* larvae 4 and 11 d after neonates started to feed on the leaf at S1 position (\*). Solid bars show the average of TPI activity and protein content either of rosette and stem leaves (Total avg) or of stem leaves only (S avg). See Figure 1 for graphic depiction of leaf position.



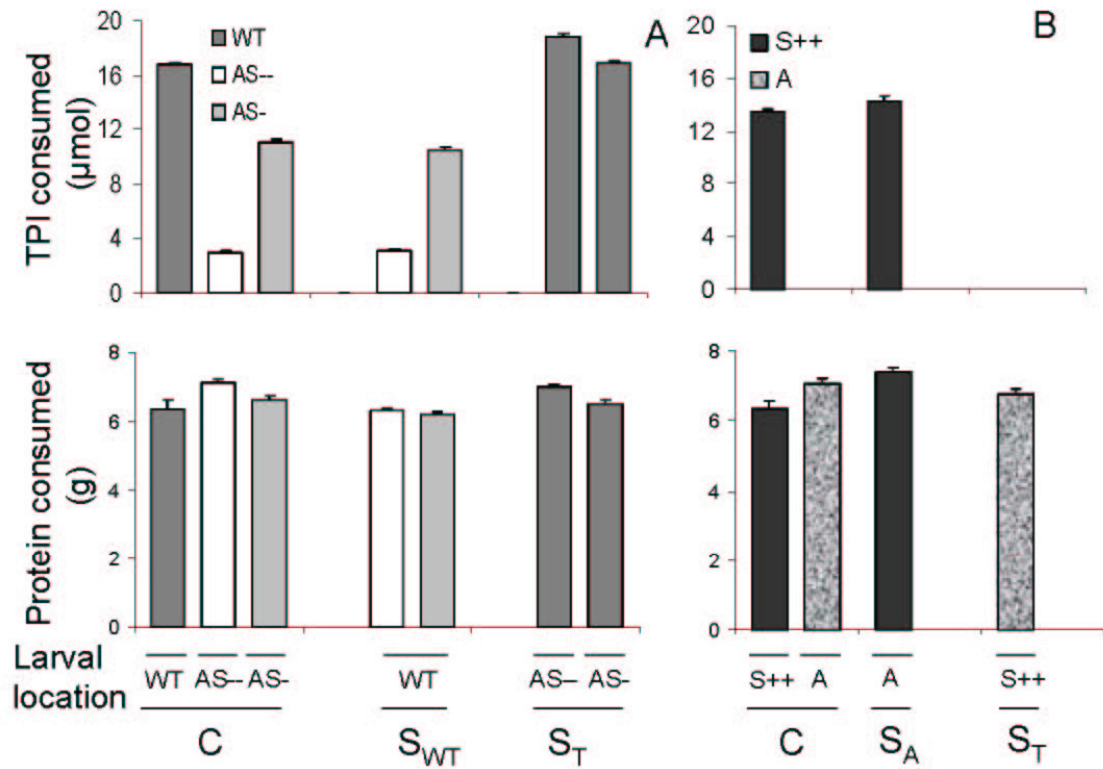
**Additional data file Figure 3. A.** TPI activity (mean  $\pm$  SEM) and protein content from different leaf positions of AS- plants at the elongation stage before *M. sexta* larvae attack. **B.** TPI activity (mean  $\pm$  SEM) from different leaf positions of the AS- plants at the elongation stage either unattacked or attacked by *M. sexta* larvae 4 and 11 d after neonates started to feed on the leaf at S1 position (\*). Solid bars show the average of TPI activity and protein content either of rosette and stem leaves (Total avg) or of stem leaves only (S avg). See Figure 1 for graphic depiction of leaf position.



**Additional data file Figure 4. A.** TPI activity (mean  $\pm$  SEM) and protein content from different leaf positions of S++ plants at the elongation stage before *M. sexta* larvae attack. **B.** TPI activity (mean  $\pm$  SEM) from different leaf positions of the S++ plants at the elongation stage either unattacked or attacked by *M. sexta* larvae 4 and 11 d after neonates started to feed on the leaf at S1 position (\*). Solid bars show the average of TPI activity and protein content either of rosette and stem leaves (Total avg) or of stem leaves only (S avg). See Figure 1 for graphic depiction of leaf position.



**Additional data file Figure 5.** Calculated TPI and protein consumed by *M. sexta* larvae fed on WT, AS<sup>-</sup>, AS<sup>-</sup>, S<sup>++</sup>, and A genotypes during the first, second and third instars. These calculated values are products of larvae's instar-specific feeding site, amount, and TPI and protein content of each leaf position consumed and are extrapolated from measurements from days 0 and 11.



**Additional data file Figure 6.** Calculated (C) and simulated (S) TPI and protein consumed by *M. sexta* larvae. **A.** Genotypes and larval location of WT, AS<sup>-</sup>, and AS<sup>-</sup>. **B.** Genotypes and larval location of S<sup>++</sup> and A. C values resulted from larval location and either TPI or protein from the same genotype. S<sub>WT</sub> and S<sub>A</sub> values resulted from transposing larval location data from untransformed (WT and A) to transformed (AS<sup>-</sup>,



AS-, and S++) genotypes.  $S_T$  values resulted from transposing either TPI or protein contents from untransformed (WT and A) to transformed (AS--, AS- and S++) genotypes (Supplemental Tables 1a and b).