

# Expression Analysis of the Tomato AAP Gene Family to N Supply in Cultivars with Contrasting Nitrogen Use Efficiency

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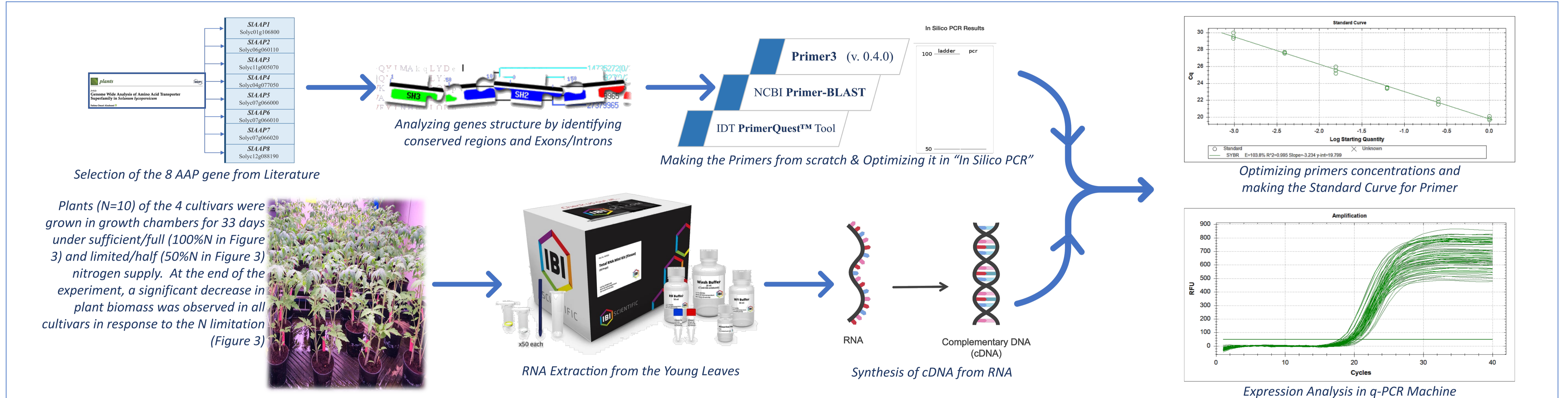
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## Introduction

Amino Acid Permeases (AAP) have a functional role in transporting amino acids across cellular membranes for distribution in the plant, being key targets among the physiological processes that determine yield and Nitrogen Use Efficiency (NUE). In order to gain insight into the molecular mechanisms involved in the amino acids partitioning in tomato (*Solanum lycopersicum* L.) and the responses to a limitation of N supply compatible with sustainable agriculture. We performed gene expression analyses in young leaves of 4 tomato cultivars with contrasting NUE at different N supply levels.

## Workflow



## Results

Table1: NUE contrasting cultivars used in the study

Genotype	Cultivar's Name	NUE
MM	Moneymaker	High
CV32	Cagón (De Canarias)	Low
CV70	Cuarenteno	High
CV82	Pequeño de Colgar	Low

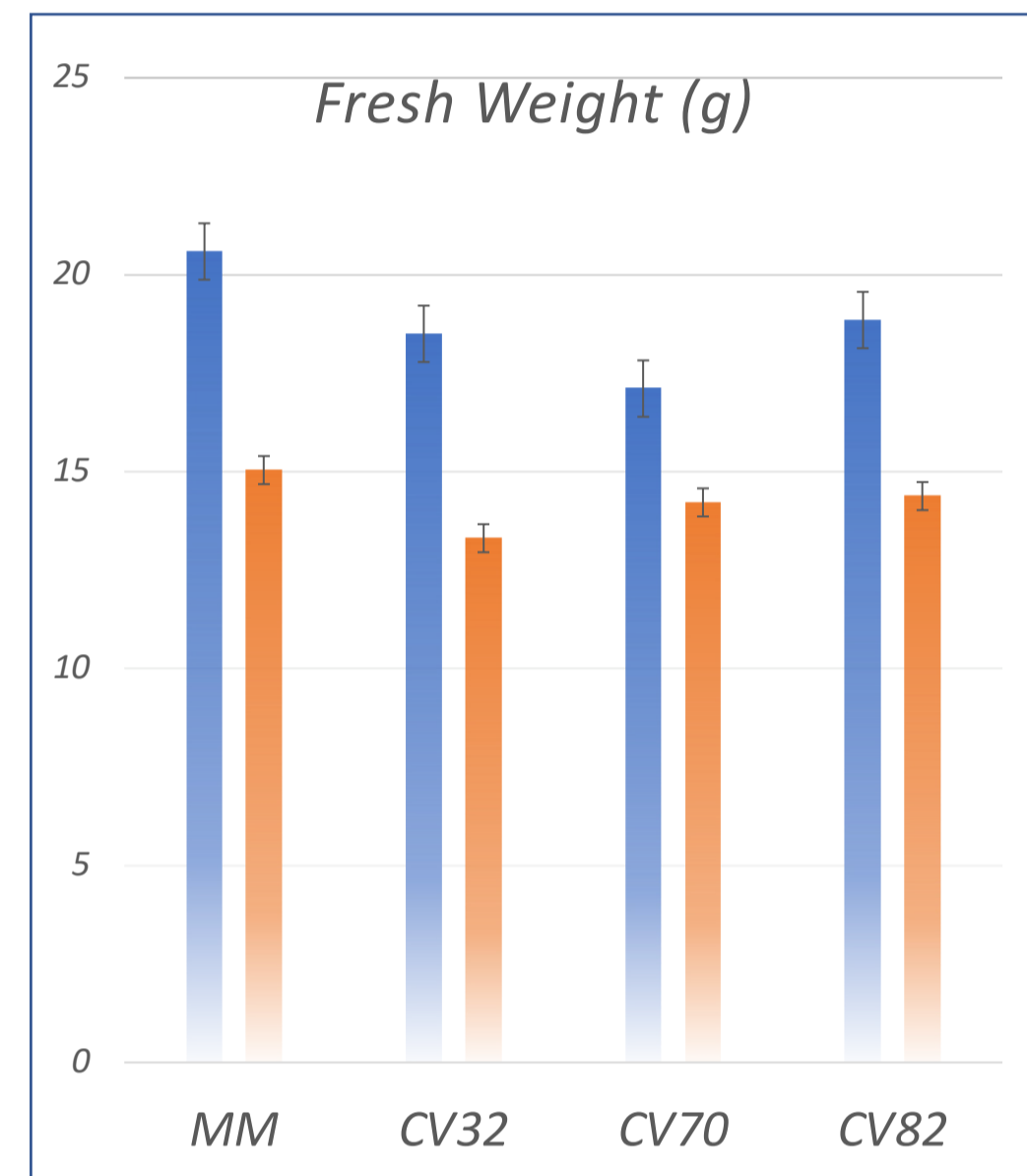


Figure 3: Total plant biomass (mean  $\pm$ SE) in response to the N supply.

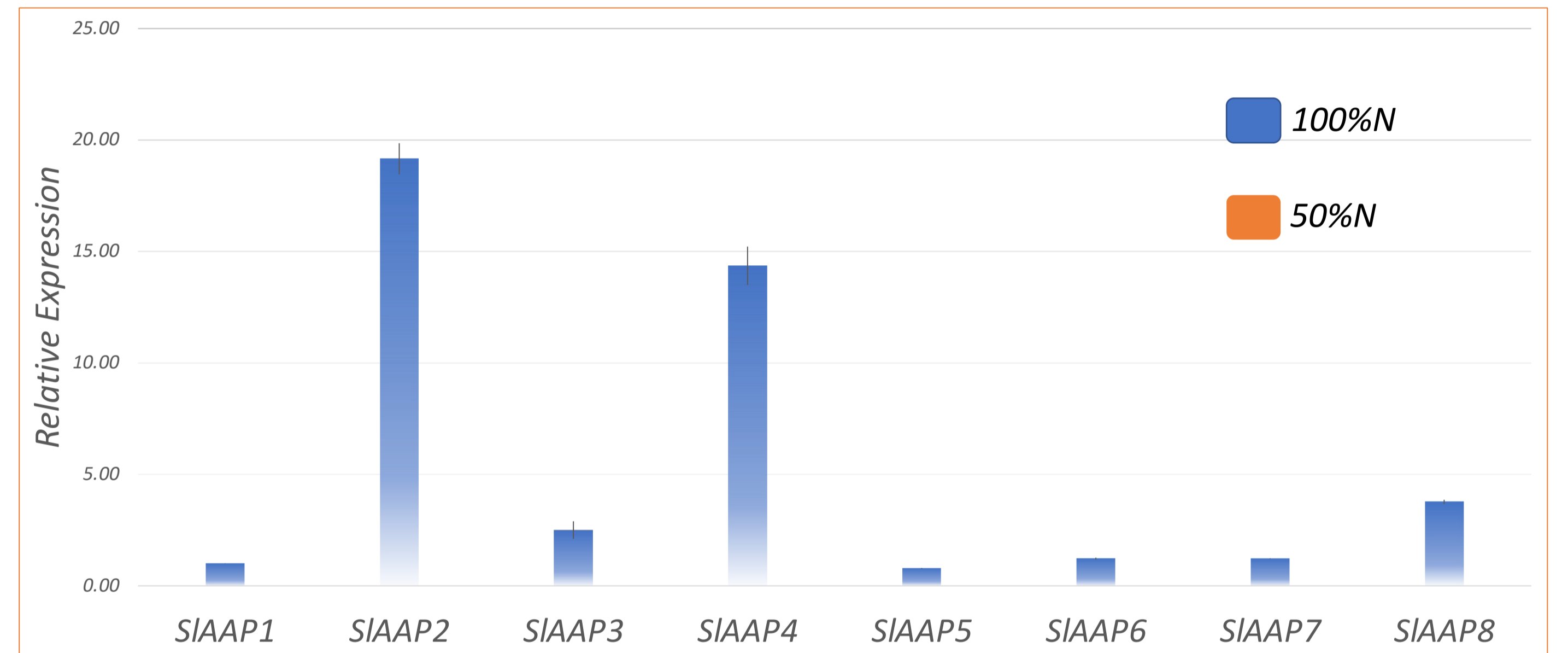


Figure 4: Relative expression levels (mean  $\pm$ SE) of the 8 studied AAPs in the reference cultivar Moneymaker under sufficient/full N supply.

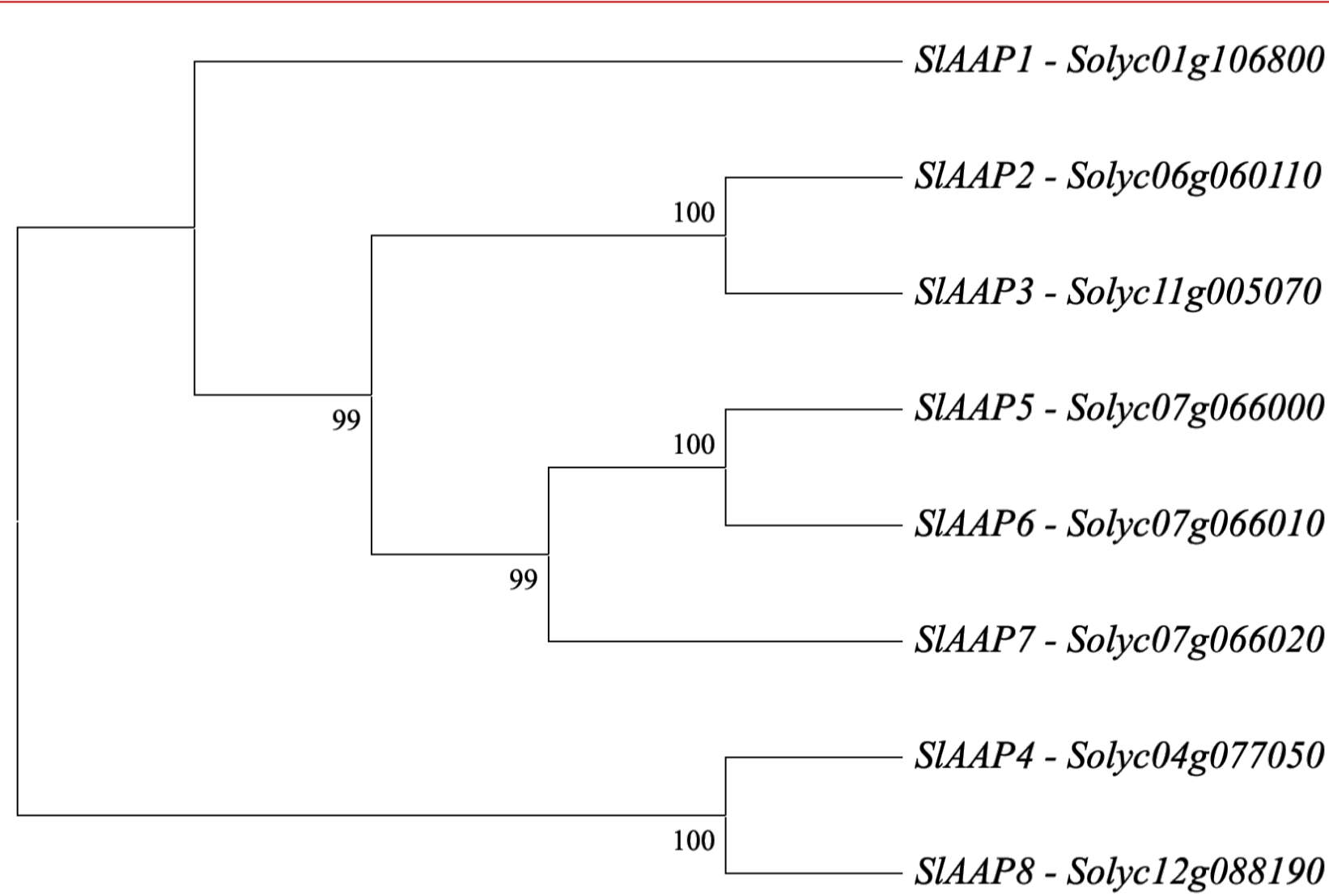


Figure 1: Phylogenetic tree of cDNA sequences of the SIAAPs by Maximum Likelihood Method. The bootstrap consensus tree inferred from 500 replicates is taken to represent the evolutionary history of the SIAAPs analyzed.

Among the AAP gene family, *SIAAP2* & *SIAAP3* showing to be closely related to each other similarly *SIAAP5* with *SIAAP6* and *SIAAP4* with *SIAAP8*.

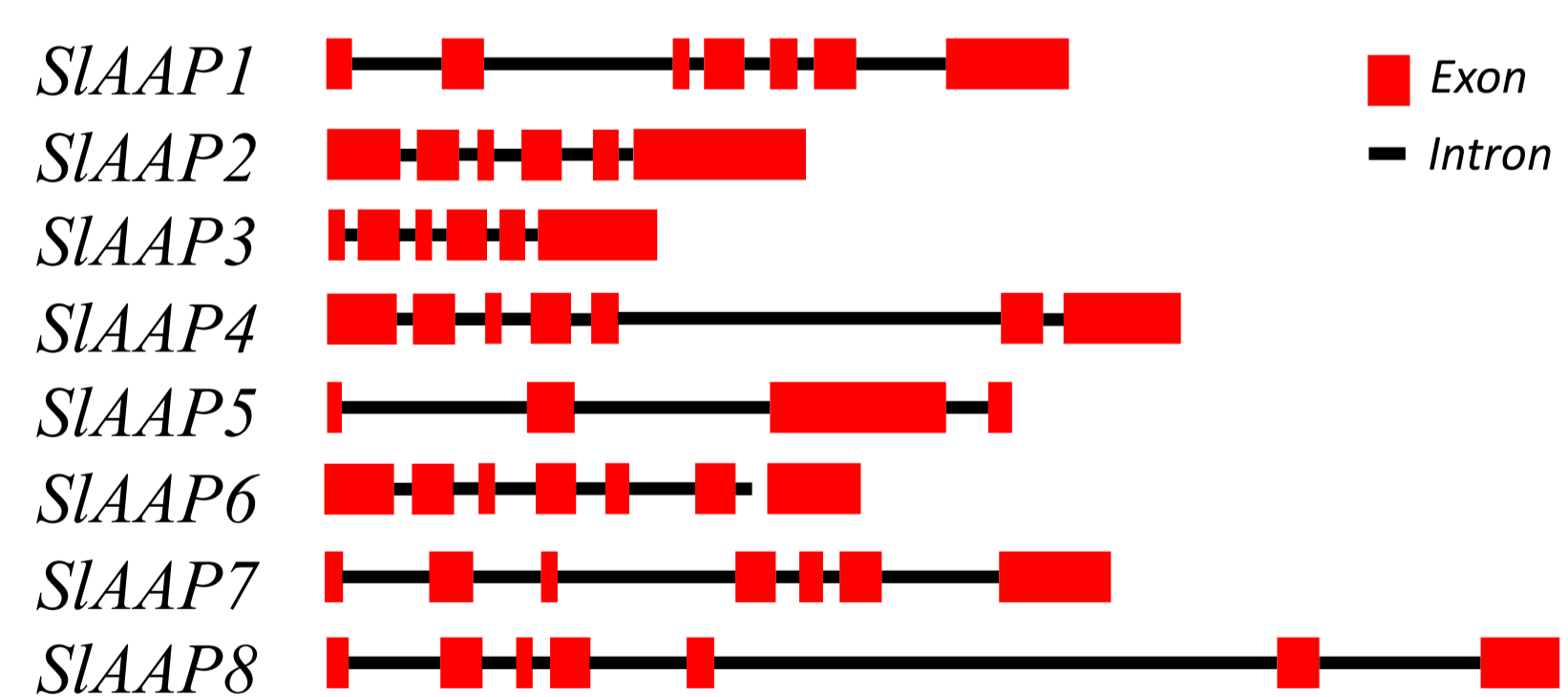


Figure 2: Exons-Introns structures of the identified AAP genes.

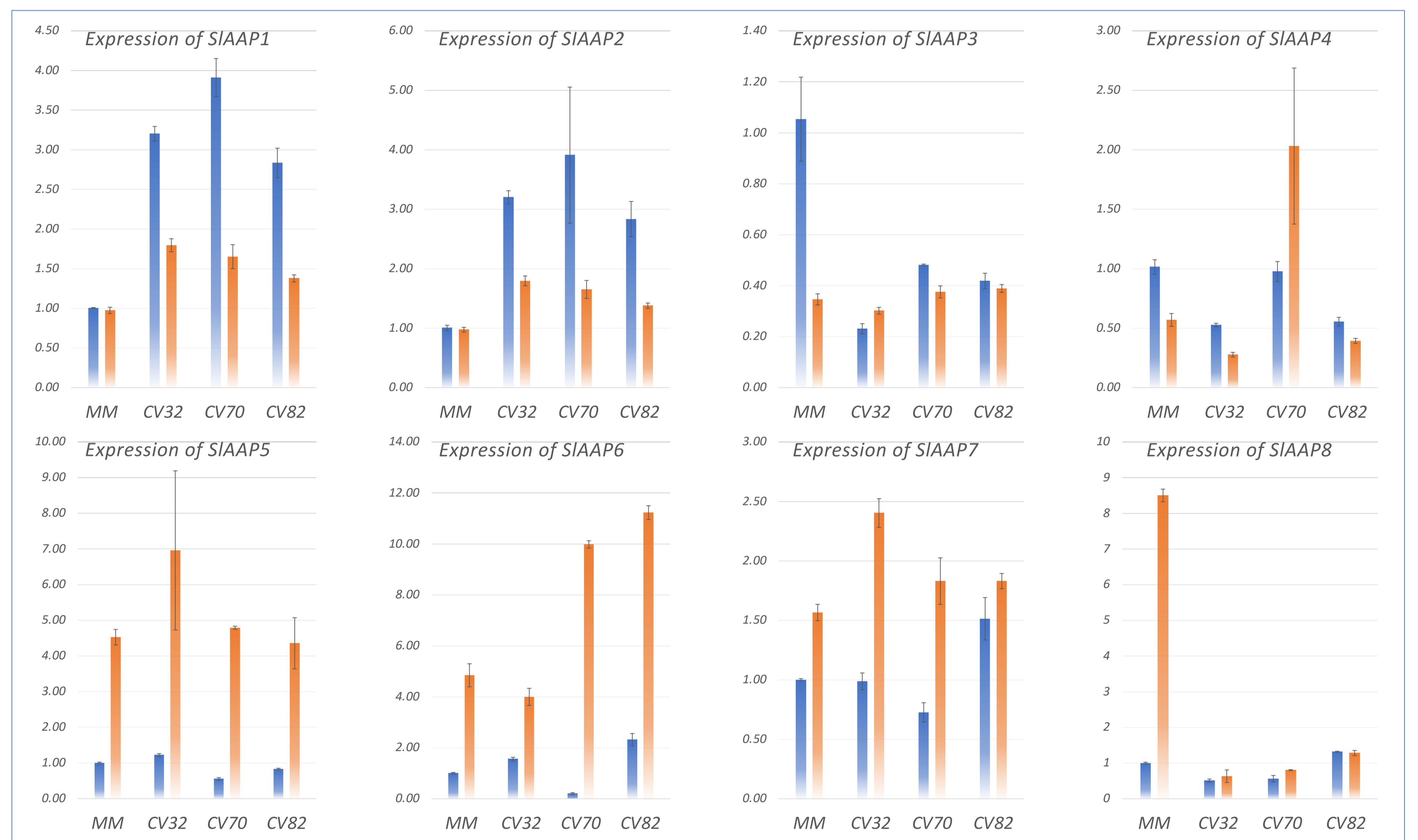


Figure 5: AAPs relative expression levels (mean  $\pm$ SE) among cultivars (MM, CV32, CV70 and CV82) under sufficient/full (100%N) and limiting/half (50%N) N supply.

## Conclusion

This study shows the AAP gene family's expression profile in young leaves with contrasting NUE tomato cultivars (Table 1) under different N supply levels. Among the 8 AAP genes, *SIAAP2* and *SIAAP4* showed the highest expression levels, suggesting that these permeases might be responsible for the amino acid loading into the phloem in sources. A high variability among cultivars was observed in the expression of each AAP gene under sufficient/full N (100%N) supply condition (Figure 4). Furthermore, high variability was also observed under limiting/half N (50%N) supply condition. Furthermore, a consistent induction of the expression of *SIAAP5*, *SIAAP6*, and *SIAAP7* genes was observed at limiting/half N (50%N) supply (Figure 5).

## Future Goals

- Expression analysis in the tomato cultivars during the reproductive development stage to identify the permeases involved in amino acid phloem loading in mature leaves and unloading in fruits. These results would allow the identification of the permeases involved in N partitioning for yield and fruit quality.
- Identifying the genes and QTLs involved in N transport to the tomato fruit to speed up the crop breeding for NUE in a 'low N inputs' agriculture.