# Transcriptome profiling of cucumber lines characterized by dwarf plant architecture

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## Introduction

Plant architecture is significant agronomic trait closely linked to yield. The identification of genes controlling plant growth habit is a key objective in applied genetics, as this knowledge can be beneficial in modern plant breeding. In cucumber, efforts are being made to develop dwarf cultivars that would facilitate once-over mechanical harvest. This study aimed to characterize transcriptomes of cucumber lines exhibiting reduced plant growth habit.

## Material and methods

Transcriptome profiling was conducted for five cucumber lines (L502, L505, L507, L511, L512) characterized by altered plant growth habits. As a control cucumber line L500 (B10DH) characterized by normal growth was used (Fig. 1). Tissue samples were collected from 10-12 day-old plants at the 1-2 leaf stage, grown under controlled conditions. Three pooled samples, each consisting of six plants, were prepared for each line and used for RNA isolation. Library preparations were sequenced using the Illumina Novaseq platform and 150 bp paired-end reads were generated.

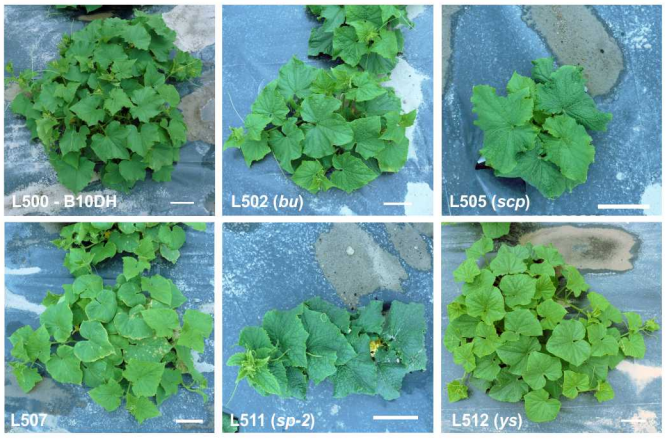


**Figure 1. Examples of plants representing inbred lines characterized by altered growth habits grown under field conditions. Scale bars, 10 cm.**

## Results

RNAseq analysis yielded high-quality sequence reads that were mapped to the reference genome 9930 v3 (Li et al. 2019) with an average of 93.9%. About 16.6K expressed genes were detected for each line (Tab. 1). Pearson correlation and Principal Component Analysis (PCA) demonstrated tight clustering of the biological replicates of each line and revealed that L505 characterized by dwarf plant architecture (Fig. 1) is the most distant from the control line L500 and other lines (Fig.2).

**Table 1. Summary of the RNA-seq and mapping of the reads for five cucumber inbred lines characterized by altered growth type and control line L500 (B10DH). Each sample represents pool of three biological replicates.**

| Line | Total raw reads (Mb) | Total lenght of clean reads (Gb) | Q30 | GC (%) | Total mapping ratio (%) | Uniquely mapping ratio (%) |
|---|---|---|---|---|---|---|
| L500 | 43.8 | 6.57 | 92.7 | 44.8 | 96.7 | 93.8 |
| L502 | 43.1 | 6.46 | 92.9 | 44.7 | 96.8 | 93.8 |
| L505 | 43.4 | 6.51 | 92.8 | 44.2 | 96.8 | 93.7 |
| L507 | 46.2 | 6.93 | 93.0 | 44.6 | 96.9 | 94.0 |
| L511 | 46.6 | 6.99 | 92.9 | 44.4 | 96.9 | 94.0 |
| L512 | 44.8 | 6.72 | 92.9 | 44.2 | 96.8 | 93.8 |

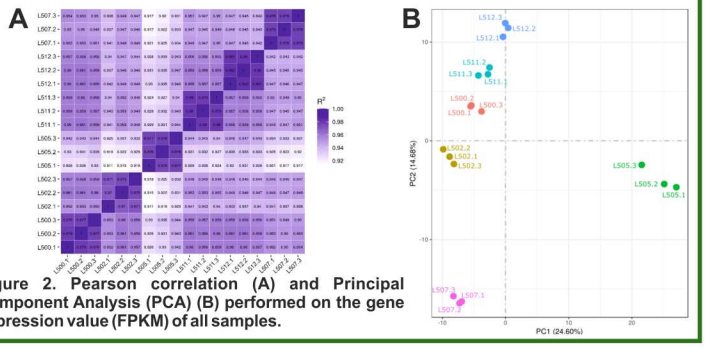


**Figure 2. Pearson correlation (A) and Principal Component Analysis (PCA) (B) performed on the gene expression value (FPKM) of all samples.**

## Results

Differentially expressed genes (DEGs) associated with altered growth type were preliminarily identified. Among the lines, L505 which carries the super compact (*scp*) gene (Niemirowicz et al. 1996) exhibited the most distinct transcriptomic profile (Fig. 3B). Approximately 1,300 DEGs were identified in this line as compared to B10DH, including 940 up-regulated and 353 down-regulated genes (Fig. 3A). The lowest number of DEGs was identified for L502 (483 DEGs), which possesses the bushy (*bu*) gene (Kubicki et al. 1986) and indicated the highest similarity to line B10DH (Fig. 3B). Transcriptome profiles of lines L511 carring the short petiole-2 (*sp-2*) gene (Rucińska et al. 1992) and L512 possesssing the yellow stem (*ys*) gene (Rucińska et al. 1991) showed the most similarity to each other (Fig. 3B). For these lines 566 and 614 DEGs were identified, respectively (Fig. 3A).

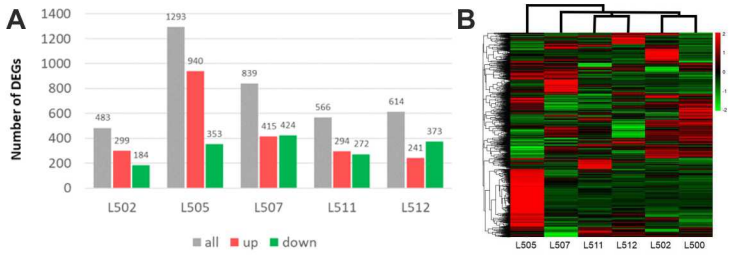


**Fig. 3. Summary (A) and heatmap (B) of DEGs identified for five inbred lines characterized by altered growth type in comparison to control line L500 - B10DH. Red and green colors represent up- and down-regulated genes, respectively.**

Regarding Gene Ontology, in terms of molecular function the majority of DEGs were associated with heme and tetrapyrrole binding, as well as transferase and oxidoreductase activities (Fig. 4A). KEGG analysis revealed the highest number of DEGs were linked to phenylpropanoid biosynthesis, MAPK signaling pathway, plant hormone signal transduction, as well as phenylalanine, alpha-linoleic, and linoleic metabolisms in most lines (Fig. 4 B).

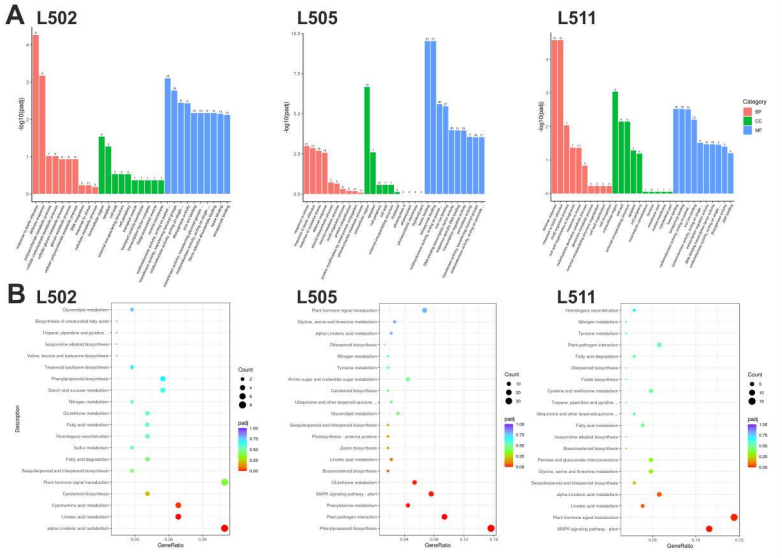


**Fig. 4. Gene Ontology (GO) classification (A) and KEGG pathway enrichment analysis (B) of DEGs identified for selected lines L502, L505 and L511. BP - biological process, CC - cellural component, MF - molecular function.**

## Summary

DEGs associated with altered growth habits were preliminarily identified for five lines differing in plant architecture (L502, L505, L507, L511, L512).

Line L505 characterized by dwarf growth type exhibited the most different transcriptomic profile from others.

**This study provides a transcriptomic framework for further identification of novel genes conditioning plant growth architecture in cucumber.**

The study received supported from a research program of the Polish Ministry of Agriculture and Rural Development titled "Basic research for biological progress in crop production 2021-2027" task 33 "Identification of selected genes associated with the growth type of cucumber plants (*Cucumis sativus* L.)".

**References**

1. Kubicki B. et al. Induced mutations in the cucumber (*Cucumis sativus* L.) IV. A mutant of the bush type of growth, Genet Pol, 1986, 27, 273-286
2. Li Q. et al. A chromosome-scale genome assembly of cucumber (*Cucumis sativus* L.), Gigascience, 2019, 8, giz072
3. Niemirowicz-Szczytt K. et al. An induced mutation in cucumber: super compact. Cucurbit Genet Coop Rep, 1996, 19, 1-3
4. Rucińska M. et al. A cucumber (*Cucumis sativus* L.) mutant with yellow stem and leaf petioles. Cucurbit Genet Coop Rep, 1991, 14, 8-9
5. Rucińska M. et al. A cucumber induced mutations. II. A second short petiole mutant. Cucurbit Genet Coop Rep, 1992, 15, 33-34