



### BACKGROUND

- · Lettuce is an important horticultural crop and its cultivation largely relies on hydroponic system which utilizes artificial light condition [1].
- Lettuce has a diploid genome (2n = 2x = 18) and its genome has been recently sequenced [2].
- · Heat shock factors (Hsfs) and Heat shock proteins (Hsps) are known to be involved in many environmental stresses in plants [3].
- In lettuce, Hsf and Hsp genes have not been identified and characterized.
- · For breeding lettuce cultivar suitable for hydroponic cultivation, it is important to identify Hsf and Hsp genes in lettuce, determine their chromosomal locations, and examine their responsivity to different light conditions.

### **METHODS**

### Identification and phylogenetic analysis

- · Using Hsf and Hsp protein sequences of A. thaliana, P. trichocarpa, and O. sativa. BLASTP search against lettuce genome database was conductive with E-value threshold of 1E-20
- Phylogenetic tree was constructed by Maximum Likelihood method and Le\_Gascuel\_2008 model [4] with 500 bootstrap replications.

#### Expression Analysis

· Control (CT), UV, and High light (HL) conditions were treated to lettuce cultivar "Codex" as uν



· gRT-PCR analysis was conducted to explore transcriptional changes by different light quality.

# Genome-wide Identification and Expression Analysis of Light-responsive Hsf and Hsp Genes in Lactuca sativa



Taehoon Kim<sup>1\*</sup>, Shafina Samraj<sup>1</sup>, Juan Jimenez<sup>1</sup>, Celina Gómez<sup>1</sup>, Tie Liu<sup>2</sup>, Kevin Begcy<sup>1</sup> 1Department of Environmental Horticulture. University of Florida 2Department of Horticultural Science. University of Florida \*email: taehoon.kim@ufl.edu

Type A

sHsp-Cl

sHsp-Cl

Cpn60

Cpn60c

	L. sativa	A. thaliana	P. trichocarpa	O. sativa
Hsf	32	21	28	25
sHsp	32	19	37	29
Hsp60	22	18	28	20
Hsp70	64	18	20	27
Hsp90	7	7	10	8
Hsp100	8	7	5	9

Table 1. Numbers of Hsf and Hsp genes in Lactuca sativa. Arabidopsis thaliana, Populus trichocarpa, and Oryza sativa.



Fig 2. Chromosomal distribution of lettuce Hsf and Hsp genes. Circles connected with lines indicate paralogous gene pairs originated from segmental duplications. Boxes represent tandemly duplicated genes.

Fig 3. Expression pattern of lettuce *Hsf* and *Hsp* genes under UV and HL conditions. Asterisks indicate statistical significance using Student's t-test (\* p<0.05, \*\* p<0.01, \*\*\* p<0.001). Same letter (a-e) represents genes in the same tandem duplicated gene cluster

### CONCLUSIONS

- Hsf and Hsp genes are identified in lettuce on a genome-wide scale
- The number of Hsp70 genes were tremendously increased in lettuce due to tandem duplication.
- · Most Hsf, sHsp, Hsp60, and Hsp70 genes are responsive to UV and HL
- This provides candidate genes for breeding a lettuce variety with better performance under hydroponic system.



UV/CT HL/CT

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Fig 1. Phylogenetic analysis of Hsf and Hsp genes in lettuce.



## RESULTS

- 32 Hsf, 32 sHsp, 22 Hsp60, 64 Hsp70, 7 Hsp90, 8 Hsp100 genes were identified in lettuce (Table 1).
- All genes were classified into different subfamilies based on the phylogenetic
- relationship with Arabidopsis homologs (Fig 1)
- The number of lettuce Hsp70 genes were considerably larger than those of A. thaliana, P. trichocarpa, and O. sativa. This resulted from intense tandem duplications of Hsp70 subfamily genes on chromosome 1, 8, and 9 (Fig 2).
- Most Hsf, sHsp, Hsp60, and Hsp70 genes were responsive to UV and HL, while the transcription level of Hsp90 and Hsp100 were not altered (Fig 3).

## REFERENCES

[1] Zhou et al. (2020). DOI: 10.3390/plants9111542 [2] Reves-Chin-Wo et al. (2017). DOI: 10.1038/ncomms14953 [3] Swindell, Huebner, & Weber (2007). DOI: 10.1186/1471-2164-8-125 [4] Le & Gascuel (2008), DOI: 10.1093/molbev/msn067