



# The epper Genome

Presented by:  
**Afnan Khaled**

Introduction to genomics (485)  
Spring 2019/2020



# Outline

- Genome papers
- Fun facts
- General information about the genome
- Sequencing strategy
- Sequencing method
- Assembly
- Genome outcome
- Questions



# Genome Papers

ARTICLES

nature  
genetics

OPEN

## Genome sequence of the hot pepper provides insights into the evolution of pungency in *Capsicum* species

Seungill Kim<sup>1,2,8</sup>, Minkyu Park<sup>1,2,28</sup>, Seon-In Yeom<sup>1,2,28</sup>, Yong-Min Kim<sup>1,2,28</sup>, Je Min Lee<sup>1,2,28</sup>, Hyun-Ah Lee<sup>1,28</sup>, Eunyoung Seo<sup>1,28</sup>, Jaeyoung Choi<sup>3</sup>, Kyeongchae Cheong<sup>3</sup>, Ki-Tae Kim<sup>3</sup>, Kyongyong Jung<sup>3</sup>, Gir-Won Lee<sup>4</sup>, Sang-Keun Oh<sup>1,2</sup>, Chungyun Bae<sup>1</sup>, Saet-Byul Kim<sup>1</sup>, Hye-Young Lee<sup>1</sup>, Shin-Young Kim<sup>1</sup>, Myung-Shin Kim<sup>1</sup>, Byoung-Cheorl Kang<sup>1,2,5</sup>, Yeong Deuk Jo<sup>1</sup>, Hee-Bum Yang<sup>1</sup>, Hee-Jin Jeong<sup>1</sup>, Won-Hee Kang<sup>1</sup>, Jin-Kyung Kwon<sup>5</sup>, Chanseok Shin<sup>3</sup>, Jae Yun Lim<sup>3</sup>, June Hyun Park<sup>3</sup>, Jin Hoe Huh<sup>1</sup>, June-Sik Kim<sup>1</sup>, Byung-Dong Kim<sup>1</sup>, Oded Cohen<sup>6</sup>, Ilan Paran<sup>6</sup>, Mi Chung Suh<sup>7</sup>, Saet Buyl Lee<sup>7</sup>, Yeon-Ki Kim<sup>8</sup>, Younhee Shin<sup>9</sup>, Seung-Jae Noh<sup>9</sup>, Junhyung Park<sup>9</sup>, Young Sam Seo<sup>10</sup>, Suk-Yoon Kwon<sup>11</sup>, Hyun A Kim<sup>11</sup>, Jeong Mee Park<sup>11</sup>, Hyun-Jin Kim<sup>11</sup>, Sang-Bong Choi<sup>12</sup>, Paul W Bosland<sup>13,14</sup>, Gregory Reeves<sup>13</sup>, Sung-Hwan Jo<sup>15</sup>, Bong-Woo Lee<sup>15</sup>, Hyung-Taeg Cho<sup>16</sup>, Hee-Seung Choi<sup>16</sup>, Min-Soo Lee<sup>16</sup>, Yeisoo Yu<sup>17</sup>, Yang Do Choi<sup>3</sup>, Beom-Seok Park<sup>18</sup>, Allen van Deynze<sup>19</sup>, Hamid Ashrafi<sup>19</sup>, Theresa Hill<sup>19</sup>, Woo Taek Kim<sup>20</sup>, Hyun-Sook Pai<sup>20</sup>, Hee Kyung Ahn<sup>20</sup>, Inhwa Yeam<sup>21</sup>, James J Giovannoni<sup>22,23</sup>, Jocelyn K C Rose<sup>24</sup>, Iben Sørensen<sup>24</sup>, Sang-Jik Lee<sup>25</sup>, Ryan W Kim<sup>26</sup>, Ik-Young Choi<sup>27</sup>, Beom-Soon Choi<sup>27</sup>, Jong-Sung Lim<sup>27</sup>, Yong-Hwan Lee<sup>3</sup> & Doil Choi<sup>1,2</sup>

## Whole-genome sequencing of cultivated and wild peppers provides insights into *Capsicum* domestication and specialization








Cheng Qin<sup>a,b,c,1</sup>, Changshui Yu<sup>b,1</sup>, Yaou Shen<sup>a,1</sup>, Xiaodong Fang<sup>d,e,1</sup>, Lang Chen<sup>b,1</sup>, Jiumeng Min<sup>d,1</sup>, Jiaowen Cheng<sup>c</sup>, Shancen Zhao<sup>d</sup>, Meng Xu<sup>d</sup>, Yong Luo<sup>b</sup>, Yulan Yang<sup>d</sup>, Zhiming Wu<sup>f</sup>, Likai Mao<sup>d</sup>, Haiyang Wu<sup>d</sup>, Changying Ling-Hu<sup>b</sup>, Huangkai Zhou<sup>d</sup>, Haijian Lin<sup>a</sup>, Sandra González-Morales<sup>g</sup>, Diana L. Trejo-Saavedra<sup>h</sup>, Hao Tian<sup>b</sup>, Xin Tang<sup>c</sup>, Maojun Zhao<sup>i</sup>, Zhiyong Huang<sup>d</sup>, Anwei Zhou<sup>b</sup>, Xiaoming Yao<sup>d</sup>, Junjie Cui<sup>c</sup>, Wenqi Li<sup>d</sup>, Zhe Chen<sup>a</sup>, Yongqiang Feng<sup>b</sup>, Yongchao Niu<sup>d</sup>, Shimin Bi<sup>b</sup>, Xiuwei Yang<sup>b</sup>, Weipeng Li<sup>c</sup>, Huimin Cai<sup>d</sup>, Xirong Luo<sup>b</sup>, Salvador Montes-Hernández<sup>j</sup>, Marco A. Leyva-González<sup>g</sup>, Zhiqiang Xiong<sup>d</sup>, Xiujing He<sup>a</sup>, Lijun Bai<sup>d</sup>, Shu Tan<sup>c</sup>, Xiangqun Tang<sup>b</sup>, Dan Liu<sup>d</sup>, Jinwen Liu<sup>d</sup>, Shangxing Zhang<sup>b</sup>, Maoshan Chen<sup>d</sup>, Lu Zhang<sup>d,k</sup>, Li Zhang<sup>c</sup>, Yinchao Zhang<sup>a</sup>, Weiqin Liao<sup>b</sup>, Yan Zhang<sup>d</sup>, Min Wang<sup>b</sup>, Xiaodan Lv<sup>d</sup>, Bo Wen<sup>d</sup>, Hongjun Liu<sup>a</sup>, Hemi Luan<sup>d</sup>, Yonggang Zhang<sup>b</sup>, Shuang Yang<sup>d</sup>, Xiaodian Wang<sup>b</sup>, Jiaohui Xu<sup>d</sup>, Xueqin Li<sup>b</sup>, Shuaicheng Li<sup>k</sup>, Junyi Wang<sup>d</sup>, Alain Palloix<sup>l</sup>, Paul W. Bosland<sup>m</sup>, Yingrui Li<sup>d</sup>, Anders Krogh<sup>e</sup>, Rafael F. Rivera-Bustamante<sup>h</sup>, Luis Herrera-Estrella<sup>g,2</sup>, Ye Yin<sup>d,2</sup>, Jiping Yu<sup>b,2</sup>, Kailin Hu<sup>c,2</sup>, and Zhiming Zhang<sup>a,2</sup>

PNAS

# Fun Facts



- Genus name '*Capsicum*' comes from the Greek *kapto* means 'to bite'.
- The heat sensation (pungency) is due to capsinoids produced by pepper.
- Birds don't have the receptor for capsinoid, so they don't feel the hot sensation as mammals.
- Pepper is the richest in vitamin C content, even than lemon.

1. YELLOW BELL PEPPERS		341.3 mg for a large pepper
2. GUAVA		125.6 mg per cup
3. LEMON/LIME		112.4 mg per cup
4. STRAWBERRIES		97.6 mg per cup
5. PAPAYA		88.3 mg per cup
6. BROCCOLI		81.2 mg per cup
7. KALE		80.4 mg per cup
8. GRAPEFRUIT		71.8 mg per cup

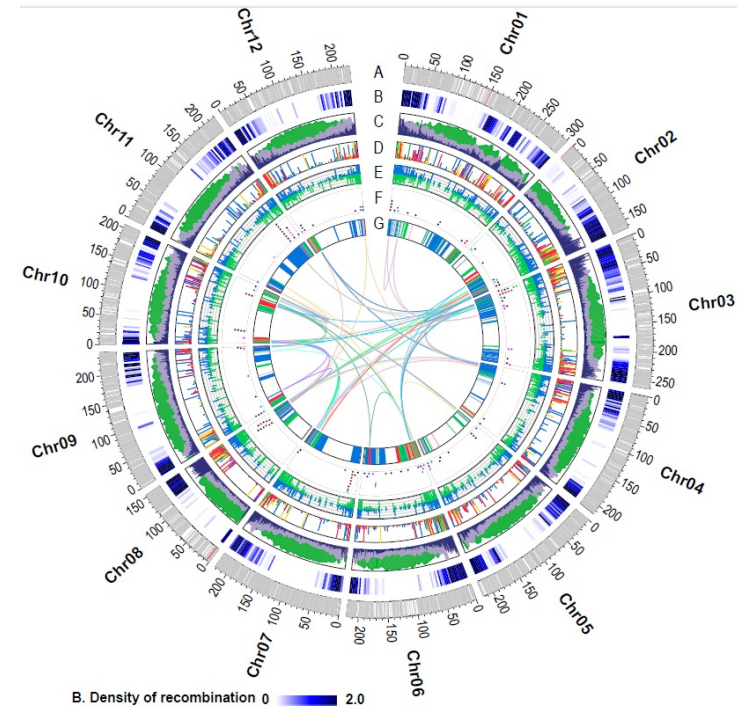
# General information about the genome

- Belong to Solanacea family, with tomato and potato.
- 12 pairs of chromosomes (diploid).
- Linear, dsDNA.
- Genome size: 3.48 Gb for *Capsicum annuum* specie



# General information about the genome

- Around 35,000 protein coding genes → 3,143 genes of them are specific for pepper, and over 31% of the protein coding genes are housekeeping, located almost near the telomeres.
- The genome transposable elements (TE)  $\approx$  2.7Gb larger than human genome!



# General information about the genome

- The genomes sequenced are for:
  - *Capsicum annuum* L.



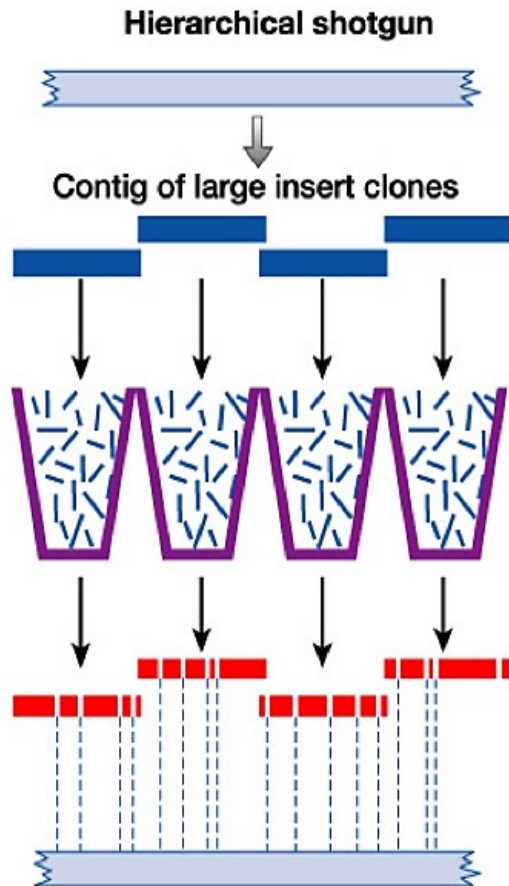
□ *C.annuum* Zunla-1

□ *C.annuum* Chiltepin

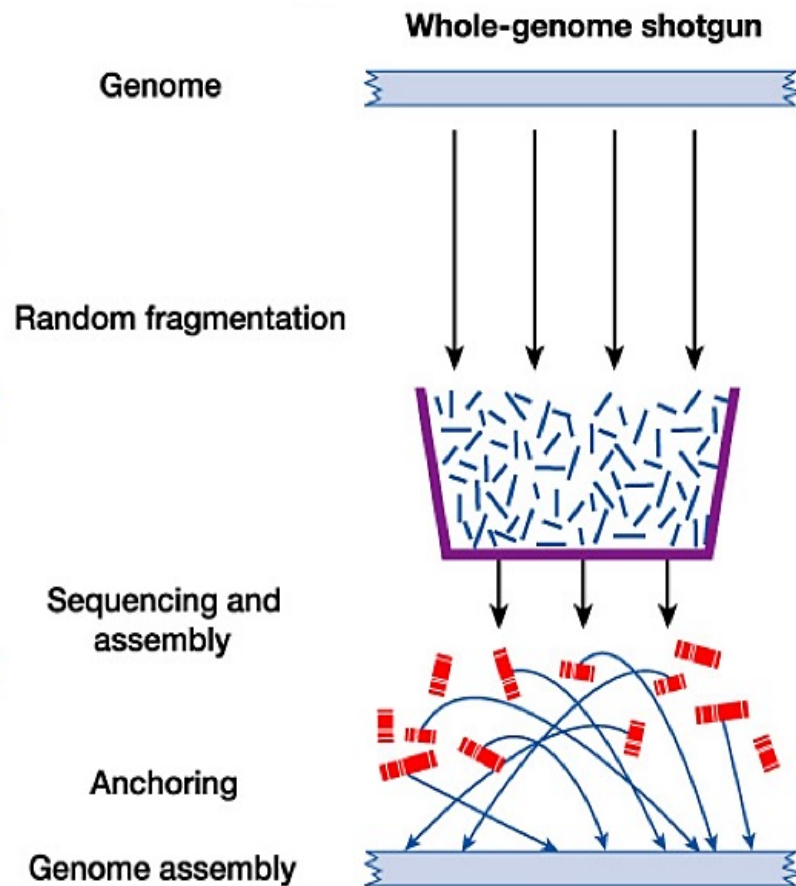


# Sequencing Strategy

Hierarchical- BAC clones  
libraries (for validation)



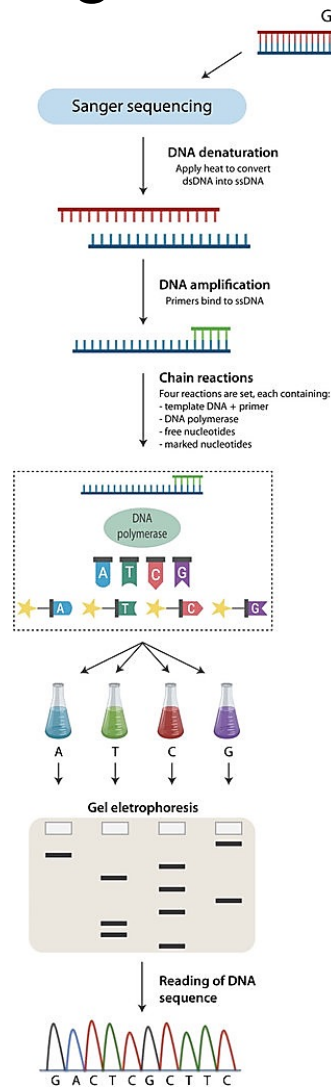
Whole Genome Shotgun  
(WGS)



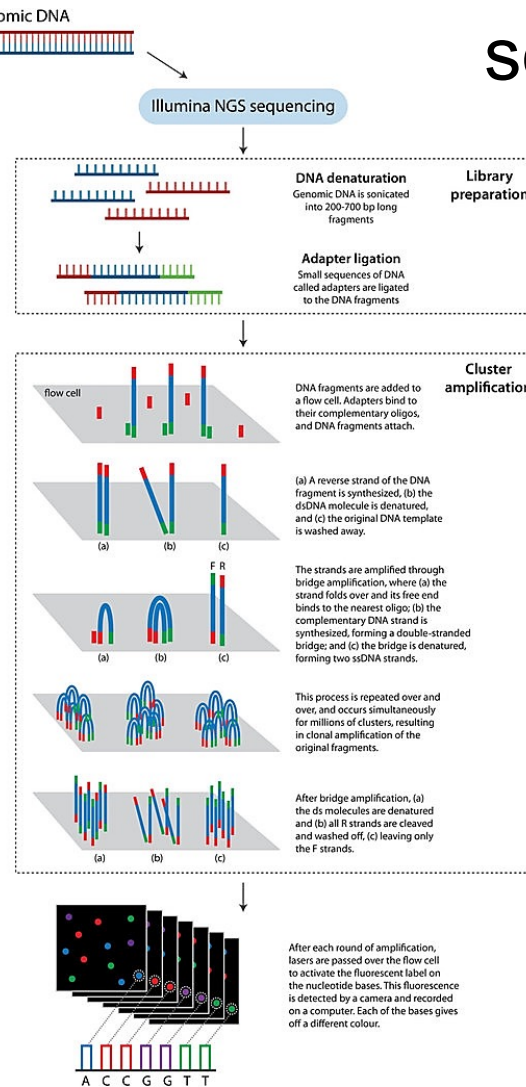


# Sequencing Method

## Sanger sequencing



## Illumina (current) sequencing



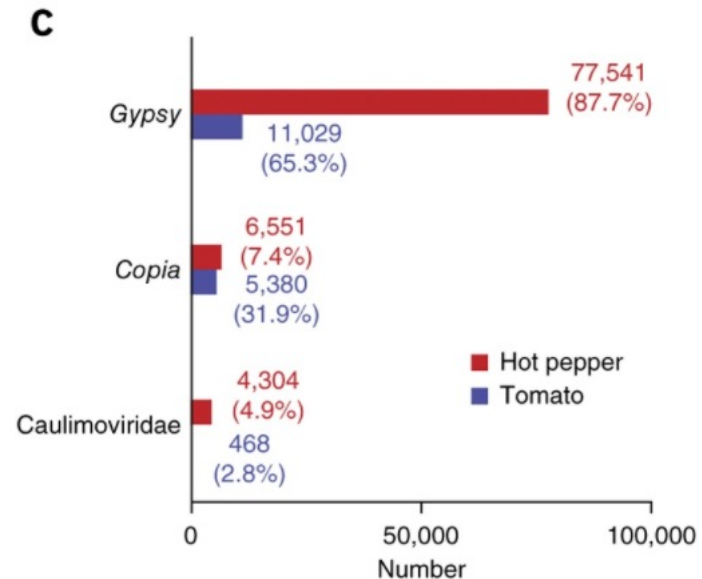
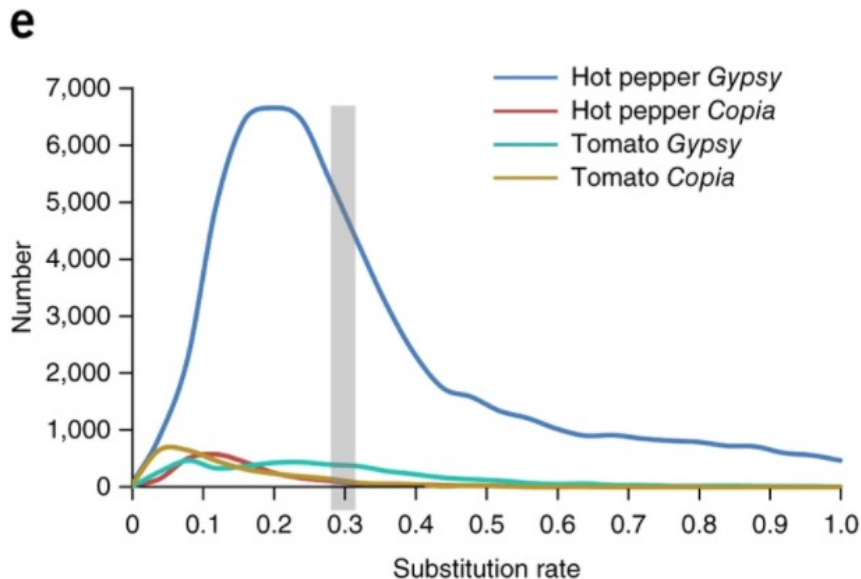
# Assembly

	Assembly method	Genome size	Coverage	GC%	N50 contig	N50 scaffold
<i>Capsicum annuum</i> (hot)	SOAPdenovo & SSPACE	3.48 Gb	186.6 x	35.03 %	30 kb	2.47 Mb
<i>C. annuum</i> Zunla-1 (cultivated)	SOAPdenovo	3.26 Gb	99 x	34.9 %	55.4 kb	1.23 Mb
<i>C. annuum</i> Chiltepin (wild)	SOAPdenovo	3.07 Gb	67 x	35 %	52.2 kb	0.445 Mb



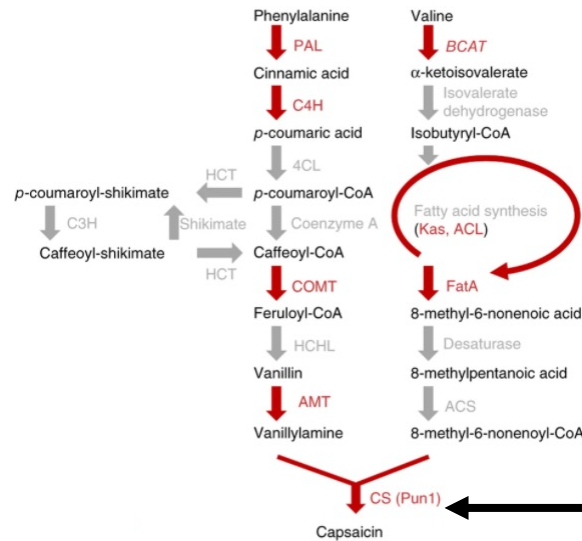
# Genome Outcome

- Genome size much larger than its family members due to rapid amplification of retrotransposable elements.
- 81% of the genome are transposable elements (TE)!
- LTR is the most, 70% parallel the maize genome, 75%.
- Most of the LTRs are *Gypsy* that are the main cause of genome expansion.
- *Gypsy* is loaded with reverse transcriptase domains (12 fold than other types of LTRs).



# Genome Outcome

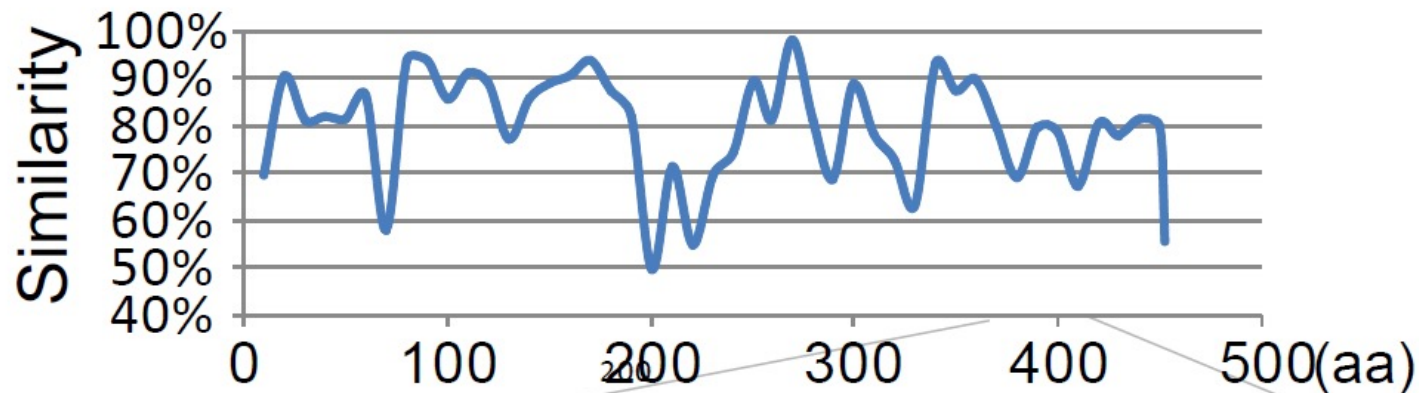
- Whole genome triplication happen ➤ most genes lost one or two copies ➤ few remaining triplicated genes.
- Example: **AT3 (Pun1)** gene code for capsaicin synthase (CS) that have a conserved motif.
- The gene have two alleles:
  - **AT3-D1** ➤ non-pungent, due to deletions in the promoter and first exon (pseudogene)
  - **AT3-D2** ➤ Pungent, code for CS that contribute in the capsaicinoid synthesis pathway.



**Capsaicin  
Synthase**



# Genome Outcome



Pun 1_C. chinense	362	NMDGY-ENVY <b>T</b> CSNLCKYP <b>Y</b> Y <b>T</b> VDFGWGR <b>P</b> ERV <b>C</b> LGNGPSK <b>N</b> AFFLKDY <b>K</b> A
AT3-D1_Zunla-1	362	NMDGY-KNVY <b>T</b> CSNLCKYP <b>Y</b> Y <b>T</b> VDFGWGR <b>P</b> ERV <b>C</b> LGNGPSK <b>N</b> AFFLKDY <b>K</b> A
AT3-D2_Zunla-1	362	N <b>K</b> DGYHENVY <b>I</b> CSNLCKYP <b>Y</b> D <b>T</b> VDFGWGR <b>P</b> ESV <b>C</b> IANGPFK <b>N</b> AFFLKDY <b>K</b> A
AT3-D3_Zunla-1	369	N <b>K</b> DEY-ENVYSCSNVCGYPFYNVDFGWGK <b>P</b> VR <b>M</b> S <b>I</b> PNGPFK <b>N</b> LFFLNDY <b>Q</b> T
AT3-D1_Chiltepin	362	NMDGY-ENVY <b>T</b> CSNLCKYP <b>Y</b> Y <b>T</b> VDFGWGR <b>P</b> ERV <b>C</b> LGNGPSK <b>N</b> AFFLKDY <b>K</b> A
AT3-D2_Chiltepin	362	N <b>K</b> DGYHENVY <b>I</b> CSNLCKYP <b>Y</b> D <b>T</b> VDFGWGR <b>P</b> ESV <b>C</b> IANGPFK <b>N</b> AFFLKDY <b>K</b> A
AT3-D3_Chiltepin	366	N <b>K</b> DEY-ENVYSCSNVCGYPFYNVDFGWGK <b>P</b> VR <b>M</b> S <b>I</b> PNGPFK <b>N</b> LFFLNDY <b>Q</b> T
AT3-D1_Potato	366	--DDY-ENVYSCSNVCRYPFYNVDFGWGK <b>P</b> ERV <b>G</b> LPNGPFK <b>N</b> LFFLKD <b>Y</b> K <b>I</b>
AT3-P2_Potato	317	TGDDE-CDMYFCSNVC-----SVDFGWGK <b>P</b> ERGGVPNGPFK <b>K</b> MFFLFD <b>Y</b> Q <b>T</b>
AT3-P3_Potato	365	--DEY-ENVYACSNLCKYPDYNVDFGWGK <b>P</b> KRV <b>G</b> LPNGPFK <b>N</b> VFFLKD <b>Y</b> K <b>I</b>
AT3-D1_Tomato	359	--DEY-ENVYSCSNLCRFPLYKVDFGLGK <b>P</b> ERS <b>L</b> PNGPFK <b>N</b> FFLKD <b>Y</b> K <b>I</b>
AT3-D2_Tomato	360	--EEY-ENVYSCSNVCRFPFYNVDFGWGK <b>P</b> ERV <b>G</b> LPNGPFK <b>N</b> LFFLKD <b>L</b> K <b>I</b>
AT3-D3_Tomato	362	--DDY-ENVYSCCNLCKFPLYKVDFGWGK <b>P</b> ERS <b>L</b> PNGPFK <b>N</b> FFLND <b>Y</b> K <b>I</b>

:        ::\* \*.\*:\*        .\*\*\*\* \*.\*        : \*\*\* \*: \*\*\* \* :

DFGWGKP motif

# Genome Outcome


- You may ask, why presenting a lot of **red** in the although you see variation in pepper colors in you Salad?
- This is because of the level of *CaPSY1* gene expression level that thought to be associated with the red and yellow colors of the pepper specie.

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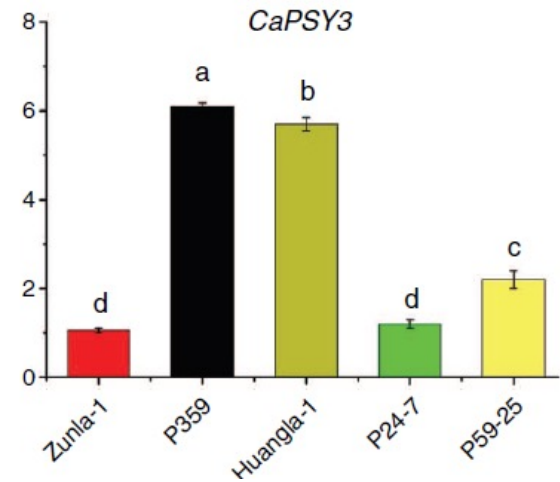
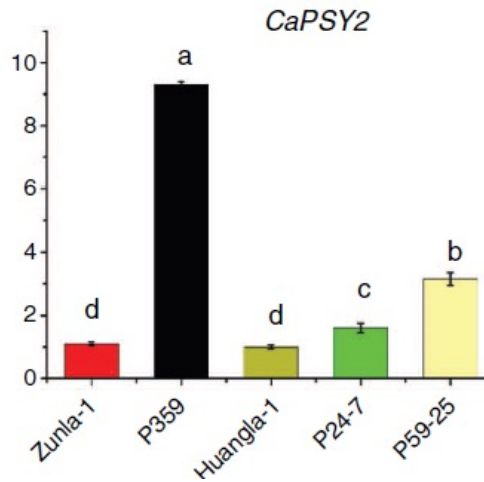
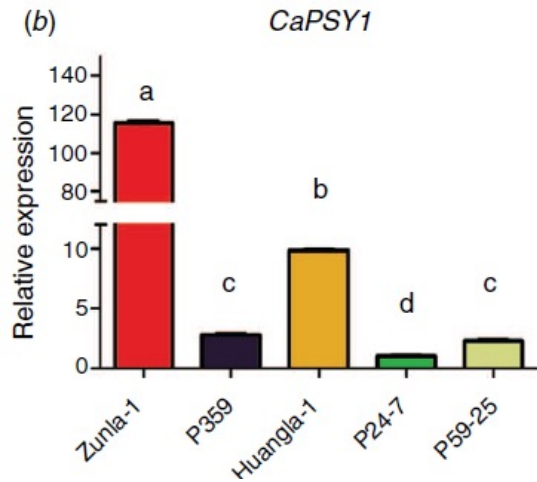
*Functional Plant Biology*

<https://doi.org/10.1071/FP19287>

***CaPSY1* gene plays likely the key role in carotenoid metabolism of pepper (*Capsicum annuum*) at ripening**

Xiaochun Wei<sup>A,B,\*</sup>, Chunyang Meng<sup>A,B,\*</sup>, Yuxiang Yuan<sup>A,\*</sup>, Ujjal Kumar Nath<sup>C</sup>,  
Yanyan Zhao<sup>A</sup>, Zhiyong Wang<sup>A</sup>, Shuangjuan Yang<sup>A</sup>, Lin Li<sup>A</sup>, Liuqing Niu<sup>A</sup>, Qiuju Yao<sup>A</sup>,  
Fang Wei<sup>B,D</sup> and Xiaowei Zhang<sup>A,B,D</sup> 

# Genome Outcome



# Questions

- Order the assembly quality for the three strains starting from the best. Justify the answer.
- What is the reason behind variation in the pungency (hot sensation) of different pepper species?

