# The Golden Fruit of Vegetables

Presented by: Abeer Ali Al-lehdan Introduction to genomics (485) Spring 2020

### **Outline:**

- The genome papers'
- Introducing tomato plant species
- Fun facts about tomato's
- Sequencing strategy
- Sequencing methods
- Assembly
- Annotations
- Questions



#### **Genome papers**

#### l"I'H'R

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#### The tomato genome sequence provides insights into fleshy fruit evolution

The Tomato Genome Consortium\*

Tomato (Solanum lycopersicum) is a major crop plant and a model The pipeline used to annotate the tomato and potato<sup>\*</sup> genomes is system for fruit development. Solanum is one of the largest described in Supplementary Information section 2. It predicted 34,727 angiosperm genera1 and includes annual and perennial plants and 35,004 protein-coding genes, respectively. Of these, 30,855 and from diverse habitats. Here we present a high-quality genome 32,988, respectively, are supported by RNA sequencing (RNA-Seq) data, sequence of domesticated tomato, a draft sequence of its closest and 31,741 and 32,056, respectively, show high similarity to Arabidopsis wild relative, Solanum pimpinellifolium<sup>2</sup>, and compare them to genes (Supplementary Information section 2.1). Chromosomal organeach other and to the potato genome (Solanum tuberosum). The ization of genes, transcripts, repeats and small RNAs (sRNAs) is very two tomato genomes show only 0.6% nucleotide divergence and similar in the two species (Supplementary Figs 2-4). The proteinsigns of recent admixture, but show more than 8% divergence from coding genes of tomato, potato, Arabidopsis, rice and grape were potato, with nine large and several smaller inversions. In contrast clustered into 23,208 gene groups (≥2 members), of which 8,615 are to Arabidopsis, but similar to soybean, tomato and potato small common to all five genomes, 1,727 are confined to eudicots (tomato, RNAs map predominantly to gene-rich chromosomal regions, potato, grape and Arabidopsis), and 727 are confined to plants with including gene promoters. The Solanum lineage has experienced fleshy fruits (tomato, potato and grape) (Supplementary Information two consecutive genome triplications: one that is ancient and section 5.1 and Supplementary Fig. 5). Relative expression of all tomato shared with rosids, and a more recent one. These triplications set genes was determined by replicated strand-specific Illumina RNA-Seq the stage for the neofunctionalization of genes controlling fruit of root, leaf, flower (two stages) and fruit (six stages) in addition to leaf characteristics, such as colour and fleshiness,

and fruit (three stages) of S. pimpinellifolium (Supplementary Table 1).

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#### **Full Paper**

#### Whole-genome re-sequencing of two Italian tomato landraces reveals sequence variations in genes associated with stress tolerance, fruit quality and long shelf-life traits

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### Introducing tomato's



This study focus on 3 types of tomato's (Solanum *lycopersicum*), their fleshy fruit and ripening evolutions. The genome size for the different Tomato: For S.Corbarino (COR): 823,643,567 bp ~ 823.6 Mb ✤ For S.lucariello (Luc): 823,719,672 bp ~823.7 Mb For S.pimpinellifolium : 739 Mb Composed of 12 chromosomes

All are from same Order : Solanales

### **Fun Facts**

Common names for tomato:

50

- Love apple
- Golden apple
- Wolf peach

#### **Fun Facts**

- •Tomatoes' are fruit Not vegetables.
- It contain vitamin A,B,C and  $Mg^{+2}$  also  $Ca^{+2}$  and iron. Its recommended to consume after cooking due to the releasing of enzymes and nutrient more when its in raw state.
- •Its thought to be originally came from the "Aztec" Peru and introduced to Europe and America in the 16<sup>th</sup> and 19th century.
- •Tomato plant is considered as type variety of nightshade plant in which its poisonous thus it wasn't popular in the past.

•The plant leave, stem and root are poisonous, when a 900 g is consumed it will cause death.

•Tomato have large varieties reach up to 10,000. In Italy they have more than 300 different types

•Unfortunately, there is annual festival in Spain called "La Tomatina" in which more than 150,000 kg of tomato is wasted.



![](_page_6_Picture_4.jpeg)

# Sequencing methods

![](_page_7_Picture_1.jpeg)

![](_page_8_Picture_0.jpeg)

#### **Sequencing methods**

Whole plant was used: stem, leaf, roots & fruits.

- Sanger sequencing of selected BAC clone:
- SOLiD sequencing:
- Illumina sequencing:

![](_page_8_Picture_6.jpeg)

#### **Interesting facts**

- <u>Solanum</u> is one of the largest angiosperm genera.
- <u>Solanum lycopersicum</u> and <u>Solanum pimpinellifolium</u> are consider as close relatives and share 0.6% SNPs divergence
- Tomato chromosomes composed mainly by pericentric heterochromatin and distal euchromatin. Also contains fewer high copy and (LTR). Thus is considered as unusual angiosperm with low copy of DNA.

#### **Sequencing strategies**

The research used: shotgun, BAC clone, Roche/454 shotgun and mate paired ends

![](_page_10_Picture_2.jpeg)

#### **Interesting facts**

Comparison between tomato and potato genome sharing same coding genes paired against *Arabidopsis*.

Tomato	Potato (solanum tuberosum)				
34,727 protein coding genes	35,004 protein coding genes				
RNA-seq data :30,855	RNA-seq data:32,988				
sRNA-seq: 96 conserved miRNA	sRNA-seq: 120 conserved miRNA				
They share 18,320 orthologous gene pairs Example: self pruning gene (SP)					

![](_page_12_Picture_0.jpeg)

## Assembly

#### • De novo shotgun assembly

Name	Genome size	coverage	#of contig	#of scafolds	N50 contig	N50 scafold	G-C content
S.Corbarino	823,6 Mb	15.34x	-	-	-	-	-
S.lucariello	823,7Mb	13.42x	-	-	-	-	-
S.pimpinellif olium	900 Mb	40x	76,534	48,863	27,860	85,811	32%-

## Annotations

De novo gene prediction & RNA-seq alignment

Name	#genes	Coding genes	Noncoding genes	SNP
S.Corbarino	43,054	46,065	-	68.8%
S.lucariello	44,579	45,815	-	69.9%
S.pimpinellif olium	34,771	-	-	-

#### More interesting facts

- Due to genome triplication added new gene family responsible for fruit specific function such as:
- transcription factors & enzymes for ethylene synthesis.
- Red light photoreceptors for fruit quality
- Regulated genes for lycopene synthesis.
- There is >50 protein genes spread in the whole genome controlling the structure of cell wall such as Xyloglucan endotransglucosylase/hydrolases.
  In which its responsible for the fleshiness of tomatoes.

# AND FΑ TOMATOES

## Questions

- What causes the tomatoes repining ? Type of hormone?
- What is reasons for 'Heinze 1706' to choose those tomatoes? What special about them.
- Dose it share certain genes with potato plant?