

potato

Introduction to genomics 0497-
485

Fall 2020

Presented by Nehaia salem



Outline

- The genome papers
- Facts about the species
- Sequencing strategy
- Sequencing method
- Assembly
- Annotation
- Questions



The genome papers

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Genome sequence and analysis of the tuber crop potato

The Potato Genome Sequencing Consortium

Nature **475**, 189–195(2011) | [Cite this article](#)

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Abstract

Potato (*Solanum tuberosum* L.) is the world's most important non-grain food crop and is central to global food security. It is clonally propagated, highly heterozygous, autotetraploid, and suffers acute inbreeding depression. Here we use a homozygous

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Editorial Summary

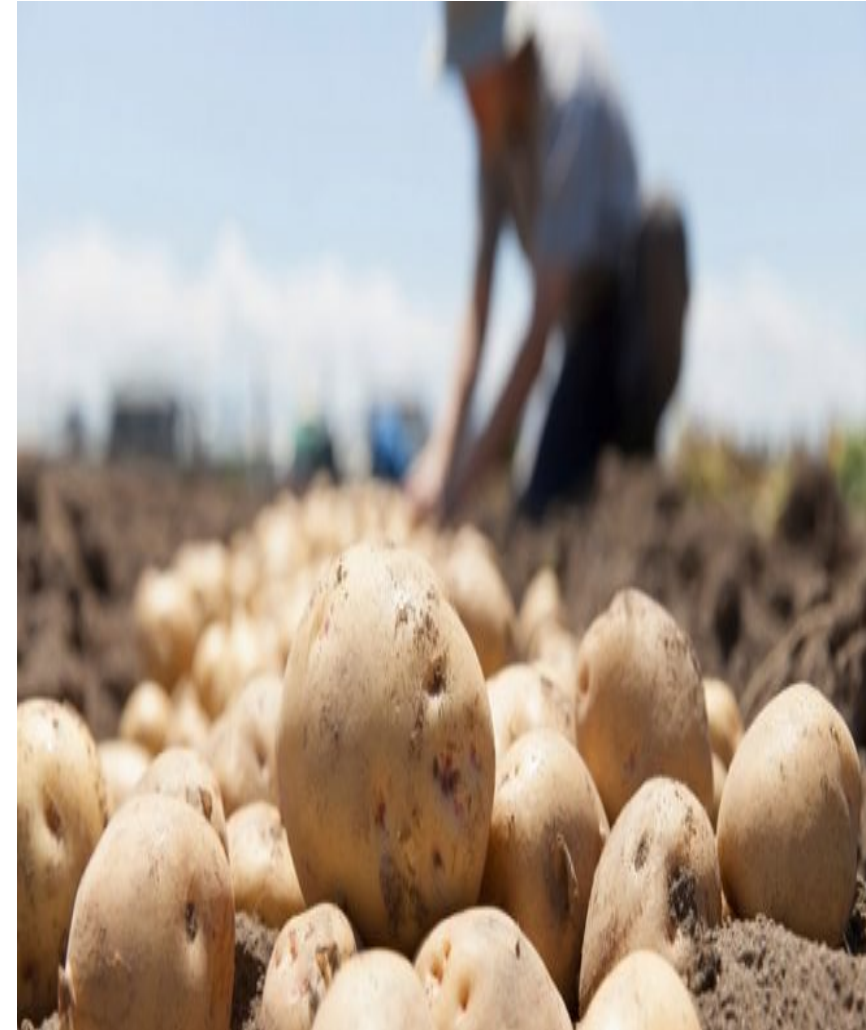
The potato genome

The genome of the potato (*Solanum tuberosum* L.), a staple crop vital to food security, has been sequenced. The Potato Genome Sequencing Consortium sequenced a homozygous doubled-monoploid potato clone as well as a heterozygous

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[Abstract](#)



Potato (*solanum tuberosum* L.)



Potato (*solanum tuberosum* L.) fact:

- Potato belongs to the asterid clade of eudicot plants that represents ~25% of flowering plant species .
- Potato occupies a wide eco-geographical range
- most important non-grain food crop and is central to global food security
- The tubers are a globally important dietary source of starch, protein, antioxidants and vitamins
- Most potato cultivars are autotetraploid ($2n = 4x = 48$), highly heterozygous, suffer acute inbreeding depression
- The potato genome sequence provides a platform for genetic improvement of this vital crop.



Potato genome

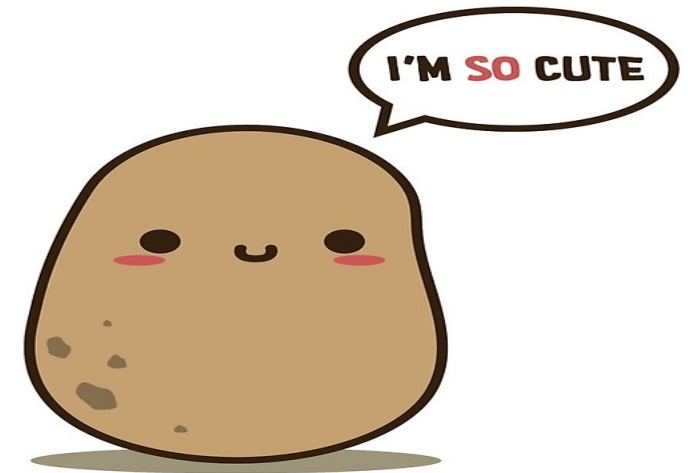
- Specimen  genome source= crop potato



- Sequencing strategy  whole genome shotgun sequencing (WGS)

Potato genome

- The primary contig N_{50} size was 697 bp and increased to 1,318 kb after gap-filling.
- which increased the N_{50} contig size to 31,429 bp with 15.4% of the gaps filled.
- Scaffold size = 1318kb=1.318 Mb
- Contig size = 31429pb= 31.429 kb

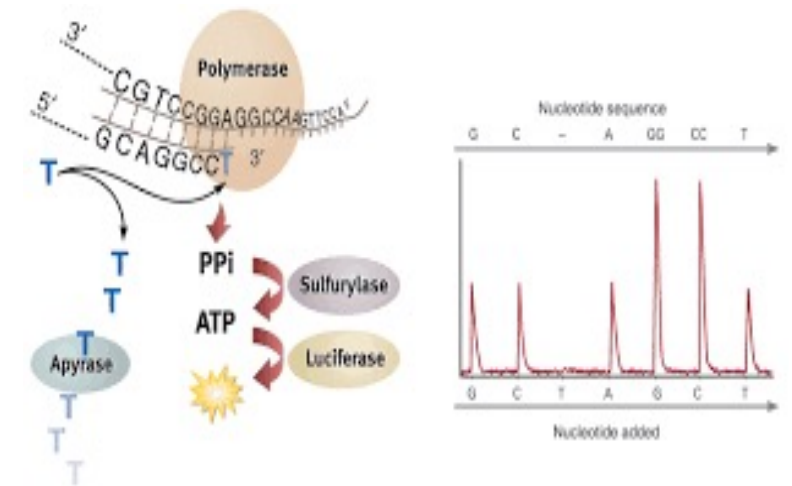
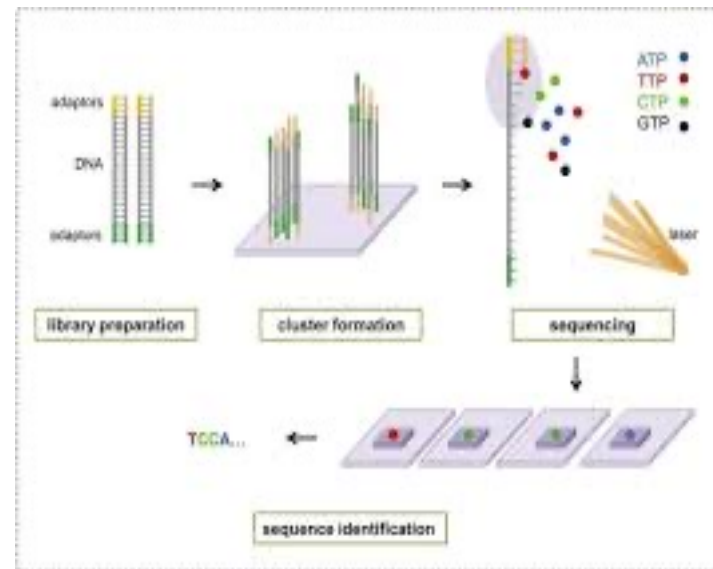
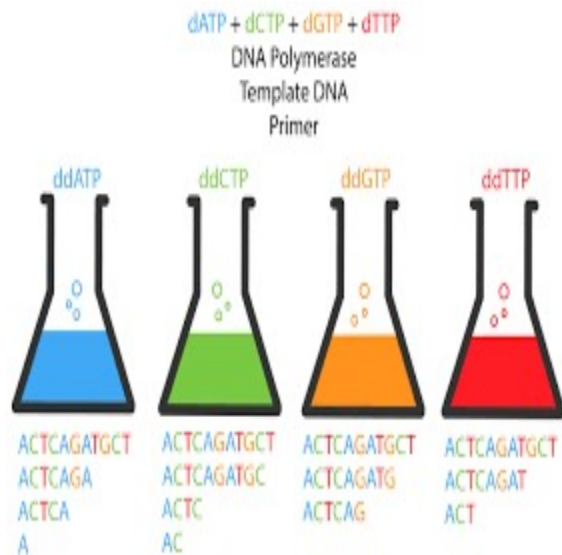


Sequencing method

• Sanger

Illumina

pyrosequencing
(Roche)



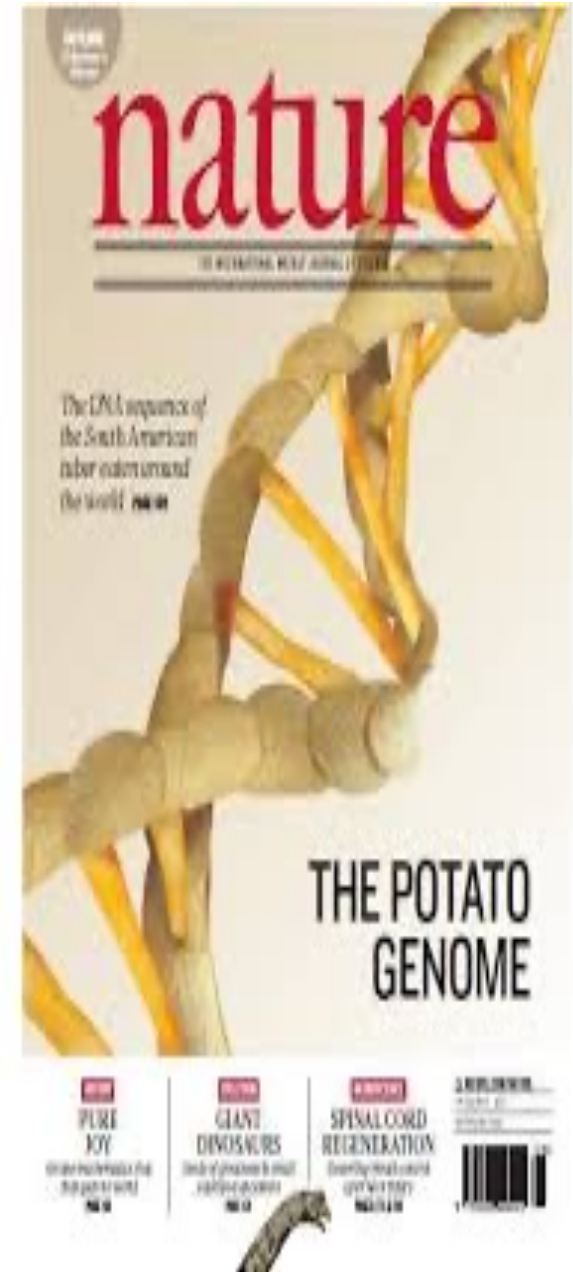
Assembly

	Assembly method	Genome size	N50 contig	N50 scaffold	GC%	Number of chromosome	coverage
Crop potato	SOAPdenovo	844Mb	697pb	22.4Kb	34.80%	12	84X

Annotation

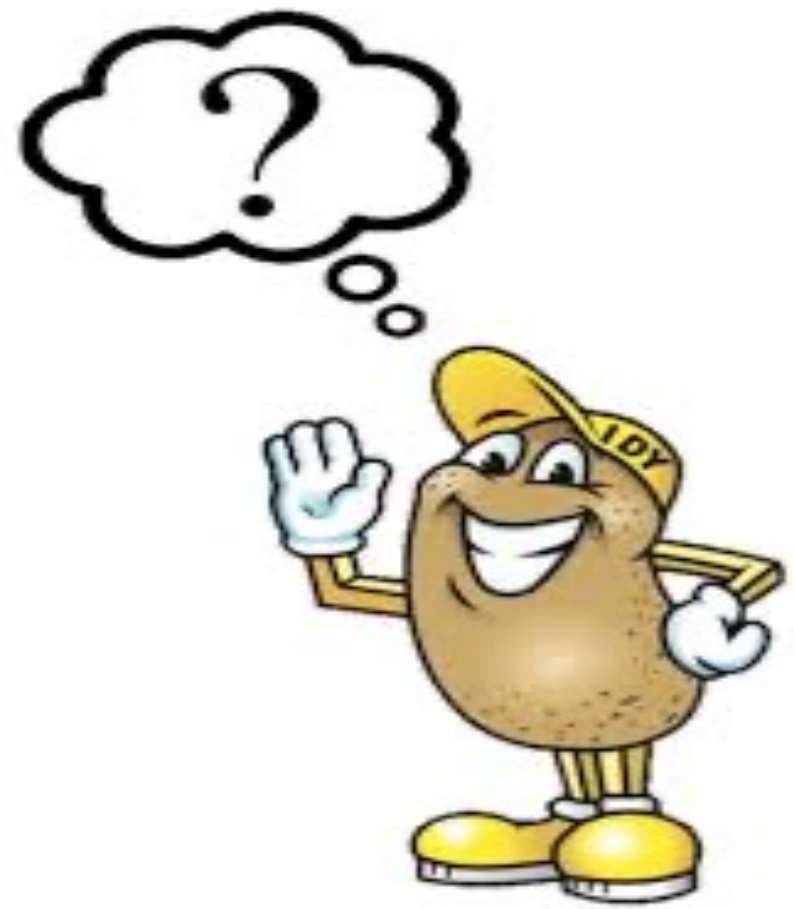
- We generated 31.5 Gb of RNA-seq data from 32 DM
- and 16 RH libraries representing all major tissue types

- Reads were mapped against the DM genome sequence
- (90.2% of DM and 88.6% of RH)



Questions

- What the methode used ?
- What the scientific name ?



- What the sequencing strategy?