Center for
Integrated Biological &
Environmental Research

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Comparing the Transcriptomes of Three Phenotypically Different Sweetpotato Cultivars

MOLECULAR GENETICS AND EPIGENOMICS LABORATORY

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Economic Importance

http://porterbriggs.com/sweet-potatoes/

- 7th most important crop, 3rd most important root crop
- ~100 million tons produced annually worldwide
- “Strategic” crop
  - Humans consume roots and foliage
  - Foliage may be fed to animals
  - Commonly used in landscaping practice
- Extremely Healthy
  - Rich in vitamin C and beta-carotene
  - Antioxidant rich
  - Good for eye health

Combating Symptoms of Climate Changes

- Can be a no-till crop
  - Less erosion of fertile growth media
  - No need for fossil fuel-powered machinery
- Extensive root system that could protect wetland areas from erosion
- Massive biomass yield that can be used for plastics and fuel production

https://sweetpotatoproject.wordpress.com/2013/10/18/1000-pounds-goodman-youth-grow-local-farm/

Challenges to Creating Genetically Superior Crop

- Sweetpotato is typically sterile, difficult to cross
- Vegetatively reproduced through cuttings or slips
- Any resulting seeds are often not viable
- Thought to be due to polyploidy nature
- Complex hexaploid genome
- Genome not sequenced

https://www.simplycanning.com/growing-sweet-potato-slips.html
https://www.mpimp-golm.mpg.de/2154967/sweet-potato

Project Questions

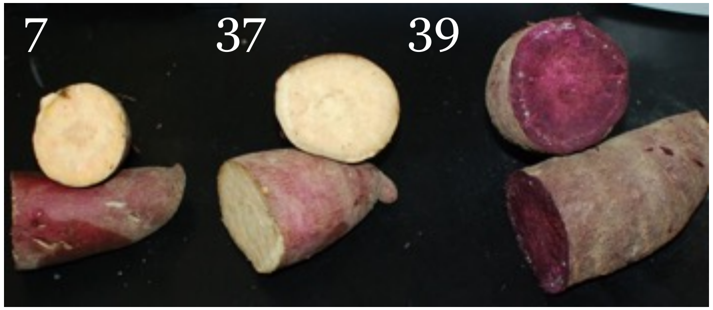
- What is normal gene expression in fully matured sweetpotato plants?
- What are major genes involved in biomass accumulation, nutritional content, starch and sugar accumulation, etc.?
- What genes are involved in changing fibrous roots into storage roots?
- What other phenotypic differences have to do with not differences in genes, but in the expression levels of genes?

Transcriptome Sequencing

7

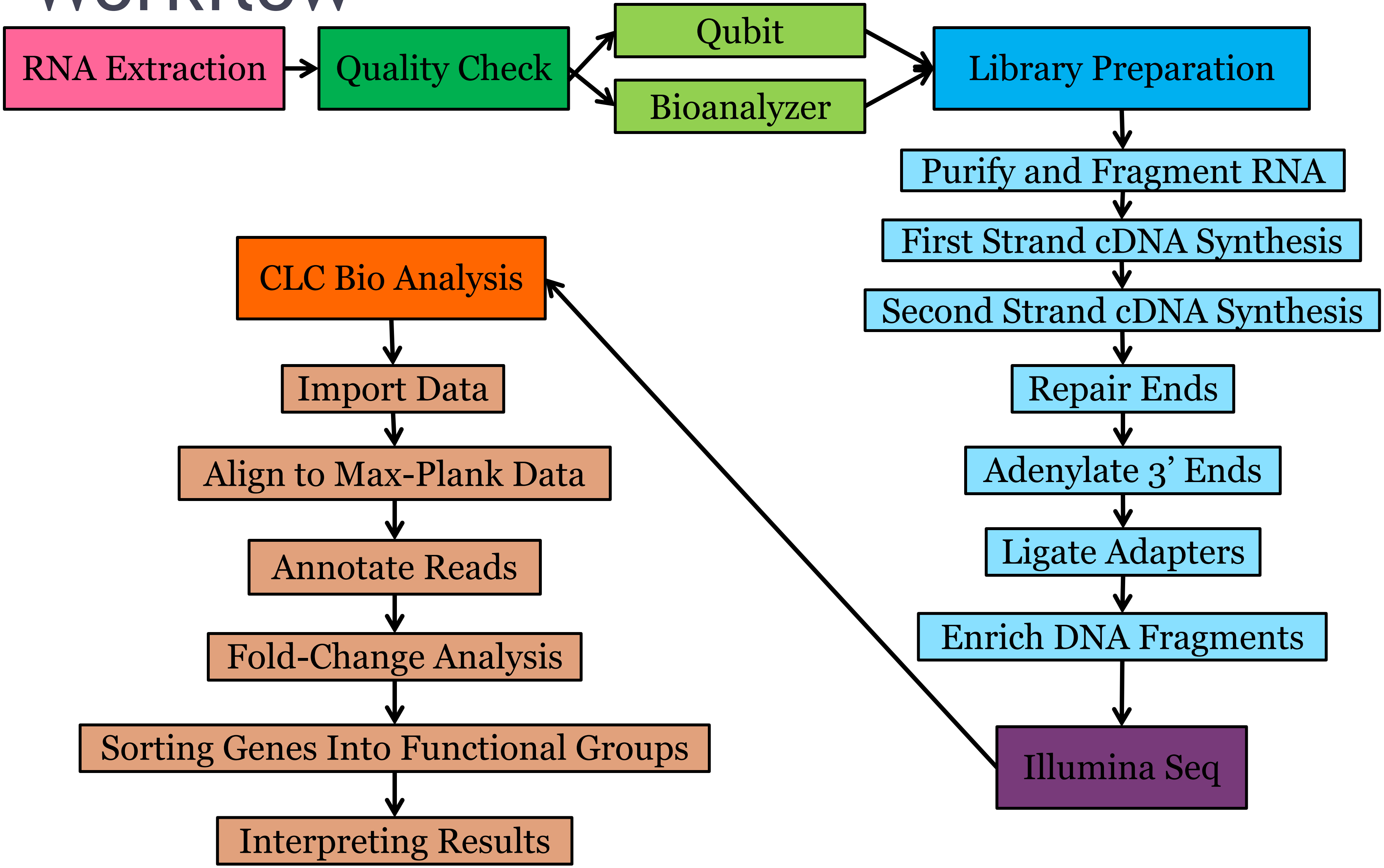
37

39



- Three genotypes
- mRNA isolated from leaf tissue
- Library preparation
- Sequenced on Illumina HiSeq2500 platform
- Comparison of gene expression between the three genotypes
- Mapping and fold-change carried out with CLC Bio
- Transcriptome data from Max-Planck Institute

Workflow



RNA Extraction

Quality Check

Qubit

Bioanalyzer

Library Preparation

Purify and Fragment RNA

First Strand cDNA Synthesis

Second Strand cDNA Synthesis

Repair Ends

Adenylate 3’ Ends

Ligate Adapters

Enrich DNA Fragments

Illumina Seq

CLC Bio Analysis

Import Data

Align to Max-Plank Data

Annotate Reads

Fold-Change Analysis

Sorting Genes Into Functional Groups

Interpreting Results

Comparison of Sequences

- Expression profiles across three different genotypes
- Closely examine genes related to:
  - Disease resistance
  - Stress resistance
  - Starch accumulation
  - Sugar accumulation
- May explain variation in storage root size, biomass accumulation, etc.

Sweetpotato Viruses

- Viruses are able to accumulate
- Many viruses can be mistaken for other pests and pathogens
- No treatment
- By the time infection is known, it is too late in the season to take action
- Spread mostly by aphids and whiteflies
- Pesticides are only effective preventative measure

Leaf Distortion/Puckering

Vein clearing

Leaf strapping

Chlorosis

https://keys.lucidcentral.org/keys/sweetpotato/key/Sweetpotato%20Diagnotes/Media/Html/TheProblems/DiseasesViral/Vi
alInfectionUnspecified/VirusUnspecified.htm
https://keys.lucidcentral.org/keys/sweetpotato/key/Sweetpotato%20Diagnotes/Media/Html/TheProblems/MineralDeficienc
es/CopperDeficiency/Copper%20%20deficiency.htm
https://cals.arizona.edu/crop/weeds/key/parttwoA.html
https://en.wikipedia.org/wiki/Chlorosis

Sweetpotato Viruses

- Infection with multiple diseases could lead to the development of viral disease complexes
- Synergistic relationship exists between viruses

- Sweet Potato Chlorotic Stunt Virus (SPCSV) + Sweet Potato Feathery Mottle Virus (SPFMV) = Sweet Potato Virus Disease (SPVD)

- SPVD may cause up to 100% yield loss

University of Arkansas-Pine Bluff Collaborative Work

- Multiple generations arising from the same plant
- Viruses accumulate in plants from vegetative regeneration
- Compare infections, RNA expression profiles, and Epigenome between generations

- Screen for viruses using reverse transcriptase PCR
- Quantify virus copies using real time PCR
- RNA-Sequencing and ChIP-Sequencing

Impact

- Find which genes are related to important phenotypic qualities like starch accumulation, and root differentiation, biomass accumulation, etc.
- Reference transcriptome for future work
- Give farmers an edge when planning
- Make sweetpotato a more favorable crop, especially in isolated regions

https://keys.lucidcentral.org/keys/sweetpotato/key/Sweetpotato%20Diagnotes/Media/Html/TheCrop/AboutTheCrop/growing_environments.htm
http://www.farmerstrend.co.ke/complete-guide-sweet-potato-farming-kenya/

Connection to Climate Change

- No-till
- Prevents water erosion
- Prevents wind erosion
- Large biomass for plastics and fuel production
- Tolerant to many adverse conditions
- Highly nutritious, keep people healthy in more rural environments

https://www.google.com/search?biw=969&bih=834&tbm=isch&sa=1&ei=SQ60WsuvDvCpggeX2pfYBw&q=digging+up+sweet+potatoes+with+pitch+fork&oq=digging+up+sweet+potatoes+with+pitch+fork&gs_l=psy-ab.3...27504.32177.0.32423.16.16.0.0.0.0.87.1021.16.16.0....0...1c.1.64.psy-ab..0.1.80...0i30k1.0.0a1IEl7JX40#imgrc=vIWXF1zVwym1bM:
https://www.google.com/search?q=wind+erosion&source=lnms&tbm=isch&sa=X&ved=0ahUKEwizic-D7unZAhUjiOAKHTqWAXcQ_AUICigB&biw=969&bih=834#imgrc=CTcRMVBhM7V60M:
https://www.pinterest.com/pin/408631366160845584/?autologin=true
http://www.greenishthumb.net/2011/09/growing-buying-cooking-sweet-potato.html

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Questions?