Analysis of up-regulated genes during Langra mango (*Mangifera indica L.*) fruit development

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Introduction

Mango (*Mangifera indica Linn.)* fruit contains many bioactive compounds including flavonoids, carotenoids, terpenoids and anthocyanins which reduce oxidative stress.

Langra mango fruit is the export quality variety of Pakistan. This variety is well known for its taste and aroma. To better understand the temporal and spatial dynamics during the mango fruit's development, the plant's developmental genetics approach was followed and cDNA sequencing of different developmental stages of *Langra* mango fruit was carried out.

This revealed a repertoire of up-regulated genes through out the fruit's development.

Study objectives

- To characterize the trancsriptome of mango fruit development.
- To identify similar and unique genes among different stages.
- To characterize differential expression of genes involved in mango ripening, aroma, flavor, sweetness and color.
- To determine the metabolic pathways during mango fruit development.

References

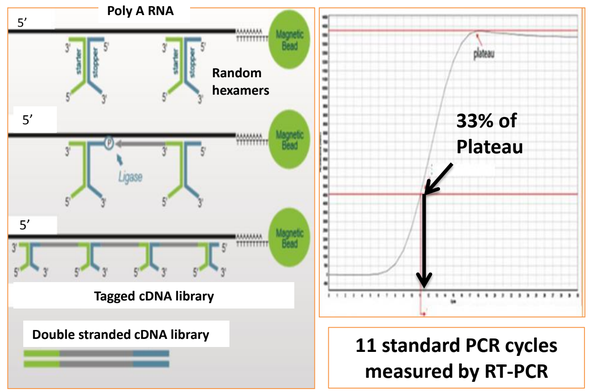
1. Azim MK, Khan IA, Zhang Y (2014) Characterization of Mango (Mangifera indica. L) transcriptome and chloroplast genome. Plant Molecular Biology.85 (1-2):193-208.
2. Davide C , Fabio G, Nicola F, Lucia M, Andrea T, Nicola V, Loriano B, Giorgio V (2015) SATRAP: SOLiD Assembler TRAnslation Program**.** PLOS ONE. http://dx.doi.org/10.1371/journal.pone.0137436PLICATIONS NOTE. 26 (6):849–850.
3. Joanna M, Abril I and Richard D. Emes (2015) Assembly, Assessment, and Availability of De novo Generated Eukaryotic Transcriptomes. Front Genet. 6: 361.
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Methodology

- High quality total RNA extraction from different Mango tissue samples.



- Total RNA quantification by **Qubit® RNA HS kit** and purity determination by **UV spectrophotometer**.
- Total RNA integrity determination by RNA integrity number (RIN) using **2100 Bioanalyser RNA kit** by **Agilent Technologies.**
- mRNA library construction by LEXOGEN SENSE kit for SOLiD™ 5500 sequencing platform.



- Clonal amplification and Fragment library sequencing by SOLiD ™ 5500 Sequencer platform.

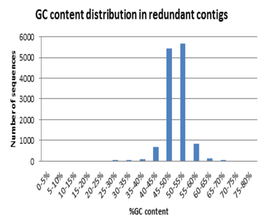
Transcriptomics and Results

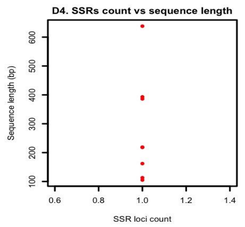
Bioinformatics pipeline

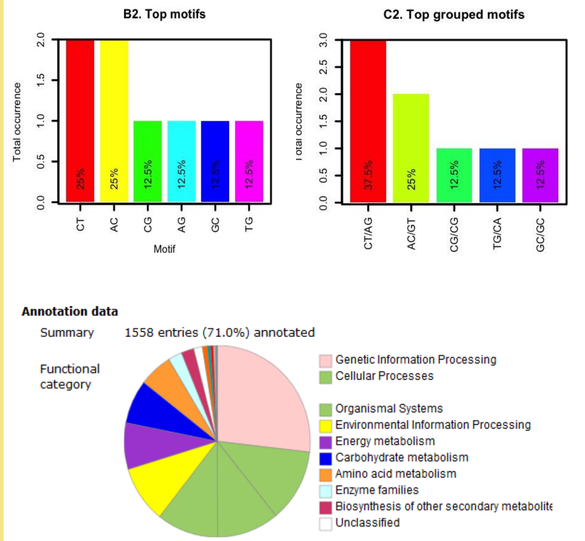
- Splitting and conversion of raw reads from XSQ format to csFASTA + QUAL format by SOLiD™ LifeScope software XSQ tools.
- Filtering of raw reads by SOLiD_preproces_ filter v2.pl Perl script.
- *De novo* transcriptome assembly by **SATRAP: SOLiD Assembler TRAslation Program.**
- Post-process assembly statistical evaluation.
- Command line tools for gene annotation, SSR mining and differential gene expression analysis.

```
>Locus_1000_Transcript_1/1_Confidence_0.000_
Length_648 FTBs=645
CcGccttggtaacctCgccAGcatATtgagcTttGGatccGGaTgg
```

Sequence type	Nucleotide length
No. of redundant sequences	12876
Longest sequence	645
Shortest sequence	111
Average length	334
N50	482







Characterized up-regulated genes during fruit development:

- Glycolytic and starch synthesis genes
- Senescence related genes
- Stress induced ethylene response factor genes
- Protein biogenesis genes
- Reactive oxygen species control genes
- Phenyl propanoid-flavonoid biosynthesis genes
- Omega -6-fatty acids synthesis genes
- Membrane transport related genes
- Antioxidant synthesis genes
- Circadian rhythm control genes
- Immune response genes

