Genome "dactyloscopy " (DNA finger - printing) and gene expression: Polymerase Chain Reaction (PCR) and Real Time Polymerase Chain Reaction (RT- PCR) in action

Erin Sharkawy and Yasmin Osman

Under Supervision : Dr. E. Kravchenko



Artyom

Styesha

Erin

Yasmine

Dr. E. Kravchenko

Content:

Aim of the project.
Materials.
Methods, Results and discussion
Conclusion.

Aim of the work

 Provide a genomic identification and determine predisposition to several diseases in the genes of human samples.

 Estimate the expression levels for the yellow gene and elongation factor Drosophila melanogaster

Materials



RNA work box

Agarose gel electrophoresis

Methods

First: Human DNA

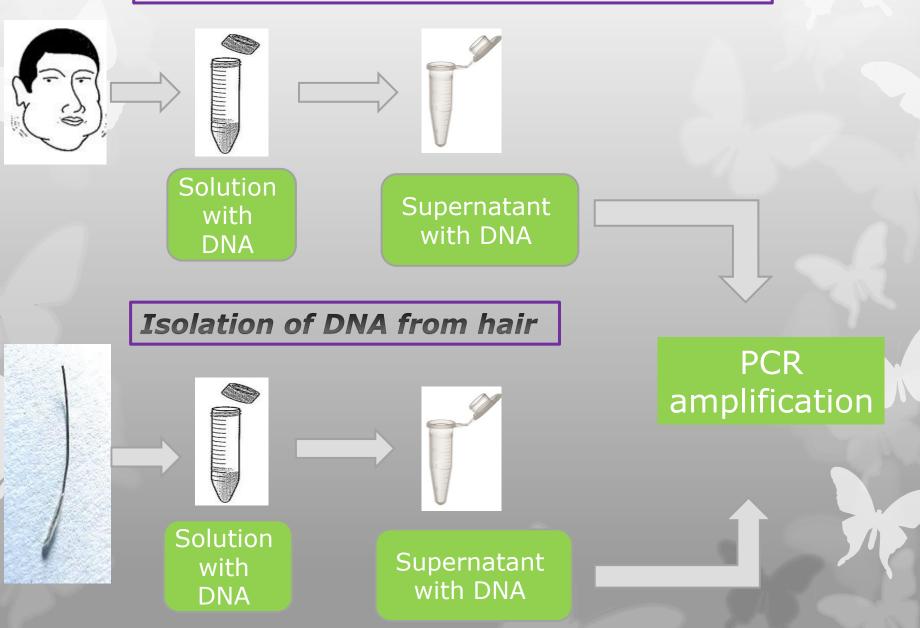
* **Isolation of DNA:**

- Isolation of DNA from buccal epithelium
- Isolation of DNA from hair
- PCR reaction
- Gel electrophoresis

Human finger printing :ALU PCR

- Isolation of DNA
- PCR reaction
- Gel electrophoresis
- * <u>Allelic discrimination :</u>
 - Isolation of DNA
 - Using TaqMan PCR

Isolation of DNA from buccal epithelium

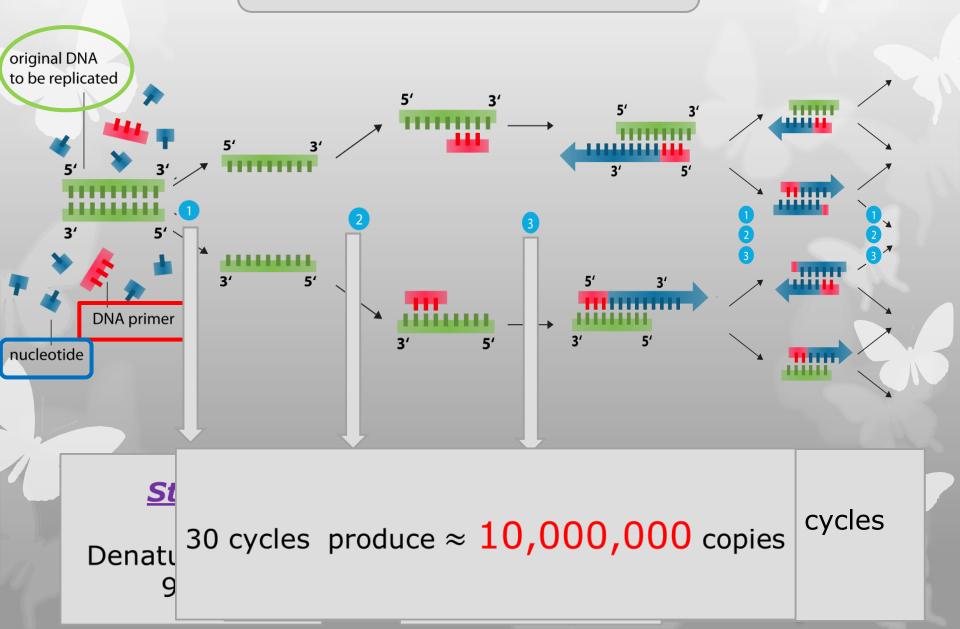




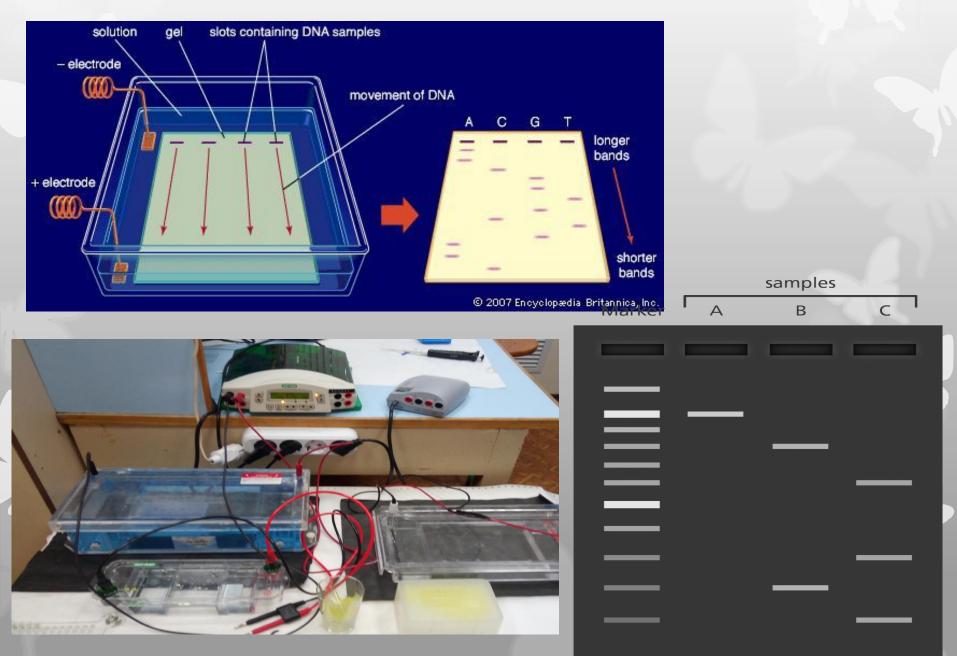
- ✤ A technique to **AMPLIFY** specific DNA fragments
- Only a single DNA fragment needed to generate a million to billion copies

PCR componer	nts:	
AGCT DNA Nucleotides Nucleotides Taq polymerase Reaction buffer	Primer	

Steps of PCR



Agarose gel electrophoresis



Methods

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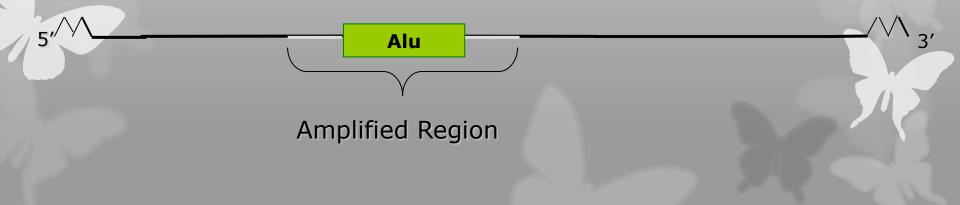
* <u>Human finger printing :ALU PCR</u>

- Isolation of DNA
- PCR reaction
- Gel electrophoresis
- * <u>Allelic discrimination :</u>
 - Isolation of DNA
 - Using taqMan RT-PCR

Human finger printing :ALU PCR

What is ALU?

- The genome contains small repetitive DNA elements that have become randomly inserted into the human genome.
- Classified as SINEs (Short INterspersed Repetitive Element) and about 300 base pairs long repeated Approx.
- Useful as a measure of genetic variation, associated with disease or used for DNA typing



Alu inserted genes

TPA25

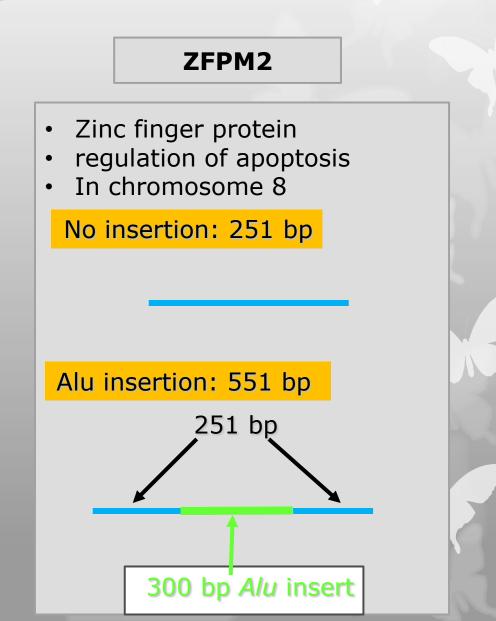
- Tissue plasminogen activator
- An Enzyme to dissolve blood clot
- In chromosome 8

No insertion: 112 bp

Alu insertion: 412 bp

112 bp

300 bp Alu insert



Alu inserted genes

XPR1

- Xenotropic and polytropic retrovirus receptor
- Plays a role in phosphate homeostasis
- In chromosome 1

No insertion: 223 bp

Alu insertion: 523 bp

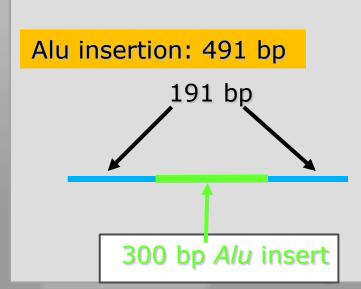
300 bp Alu insert

223 bp

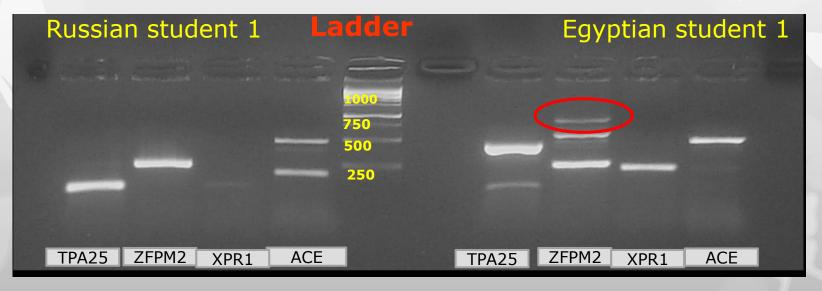
ACE

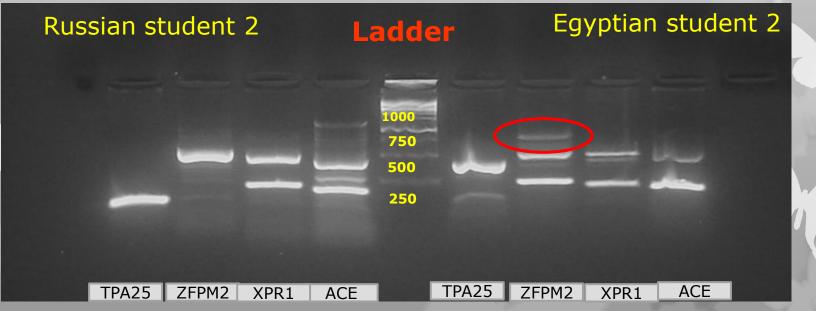
- Angiotensin converting enzyme
- inactivate the vasodilator, proinflammatory peptide, bradykinin.
- In chromosome 17

No insertion: 191 bp

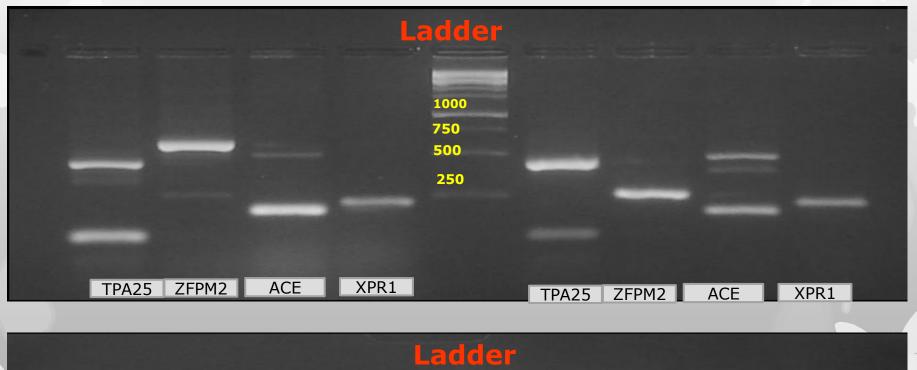


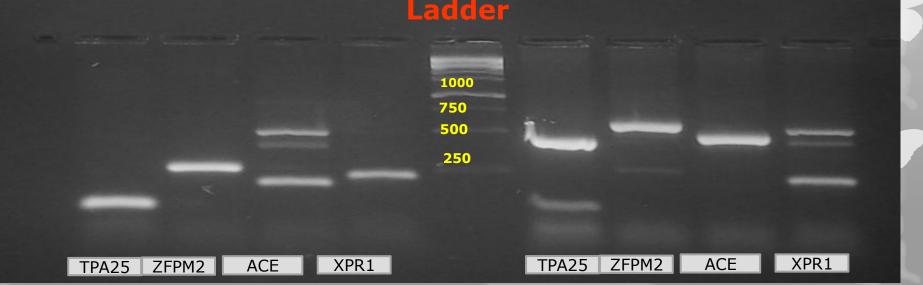
PCR reaction and gel



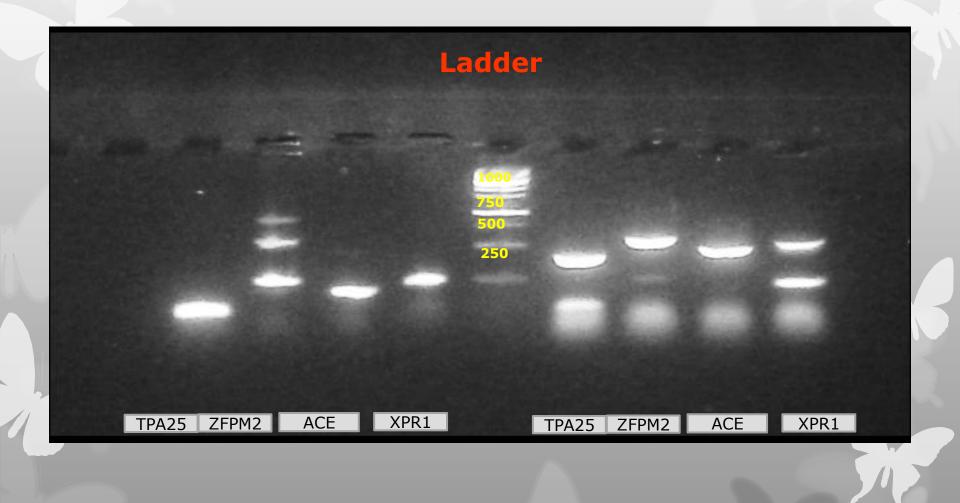


Other Egyptian students





Other Egyptian students



Methods

First: Human DNA

* **Isolation of DNA:**

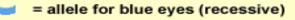
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* <u>Human finger printing :ALU PCR</u>

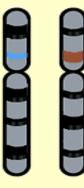
- Isolation of DNA
- PCR reaction
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- * <u>Allelic discrimination :</u>
 - Isolation of DNA
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Allelic discrimination with TaqMan probes RT-PCR

What is allele?



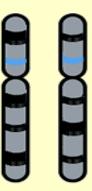
= allele for brown eyes (dominant)



Individual A:

heterozygous

Individual B: homozygous



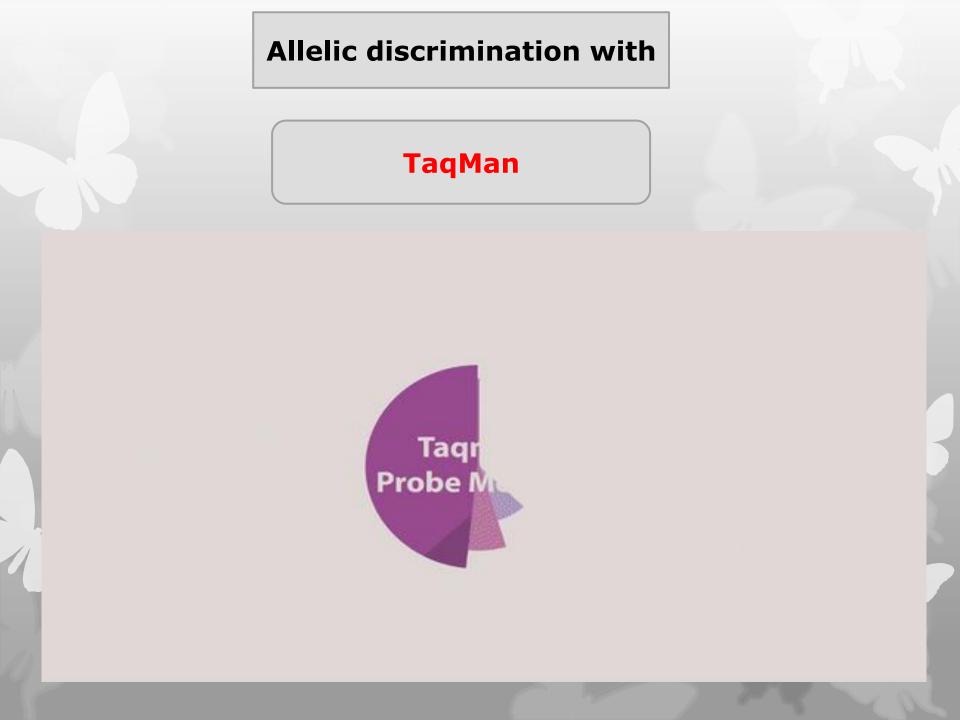
Individual C: homozygous recessive





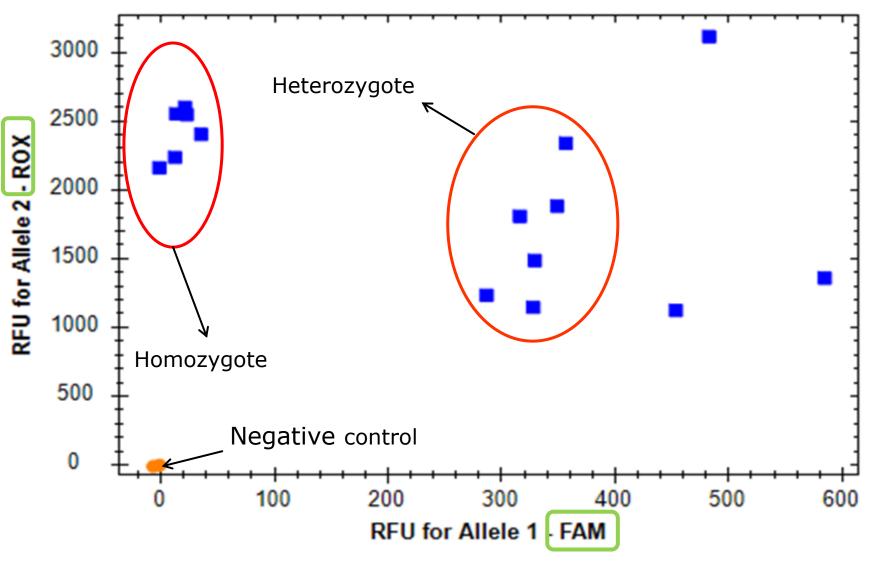
Q-PCR amplifies a specific target sequence in a sample then monitors the amplification progress using **fluorescent technology**

In real-time PCR, the amount of DNA is measured after each cycle via fluorescent dyes that yield increasing fluorescent signal in direct proportion to the number of PCR product molecules (amplicons) generated.



Results

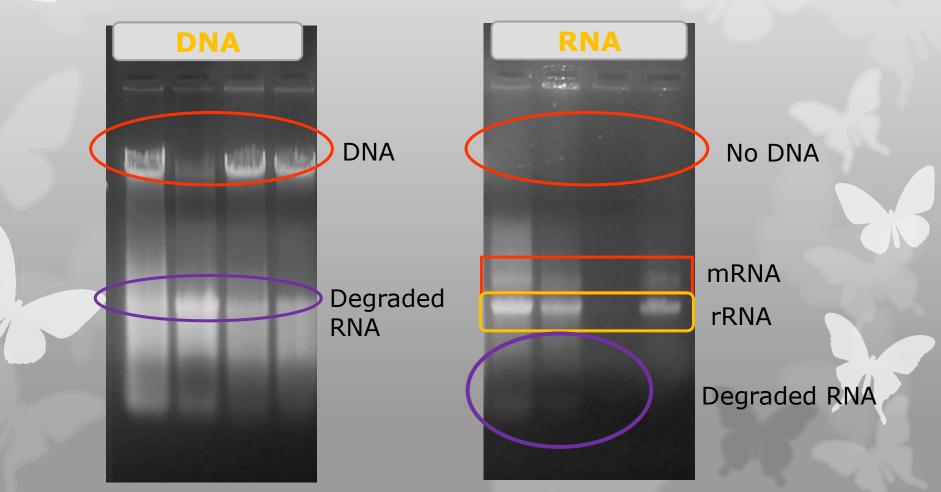
Allelic Discrimination



second

Experiments with Drosophila Melanogaster

Isolation of DNA & RNA each one aloneAgarose gel electrophoresis for both

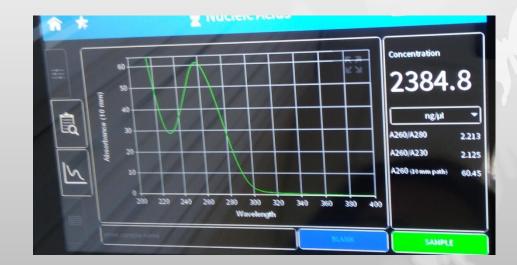


Determine the concentration and purity of an DNA and RNA samples by using Nanovolume



Concentration of RNA samples







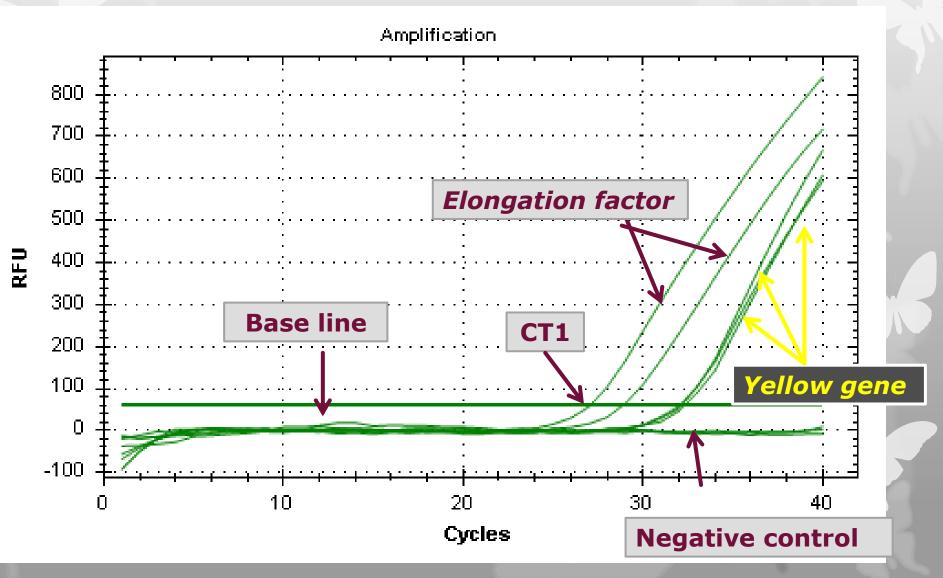


Reverse Transcription with RT kit tissue **RNA cDNA** PCR sample nucleic acid real-time PCR RT sampling isolation amplification

SYBR green

SYBR Green based Method

Quantification of RT-PCR for yellow gene and elongation factor



Calculations

Sample

<u>1. The average of yellow gene :</u>						
$\frac{32.32+32.15+32.06}{3} = 32.17$						
<u>1. The average of elongation gene :</u>	Fluor ∆	Target 🔇	Content 🔇	Cq ≬	Well ≬	
29.89+27.08	SYBR		Unkn	N/A	A03	
$\frac{29.89+27.08}{2} = 27.98$	SYBR		Unkn	N/A	B03	
2	SYBR		Unkn	32,32	205	
2. Subtract both results	SYBR		Unkn	32,15	8(<mark>6</mark>	
(Y - EF) =	SYBR		Unkn	32,06	<mark>5,</mark> 07	
32.17 - 27.98 = 4.19	SYBR		Unkn	hit.	C03	
32.17 - 27.90 - 4.19	SYBR		Unkn	28,89	617	
Number of Cucles	SYBR		Unkn	27,08	2 08	
$\frac{Number of Cycles :}{4.19^2 = 17.55 \text{ cycle}}$						

copies of elongation factor > copies of yellow gene

Conclusion :

- According to the result we measure fluoresce from SYBR DNA complex that reflects the starting amount of RNA in our samples.
- The relative expression level of *elongation factor* gene is approx. 18 times more than *yellow* gene.
- That is because all living cells need *elongation factor* but only cuticula cells need product of *yellow* gene

THAN YOU FOR YOUR ATTENTION

