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# Entomologi Molekuler (PCR, Sequensing DNA “Blast Gen Bank”, Tanaman Transgenik)

Kuliah Entomologi Dasar

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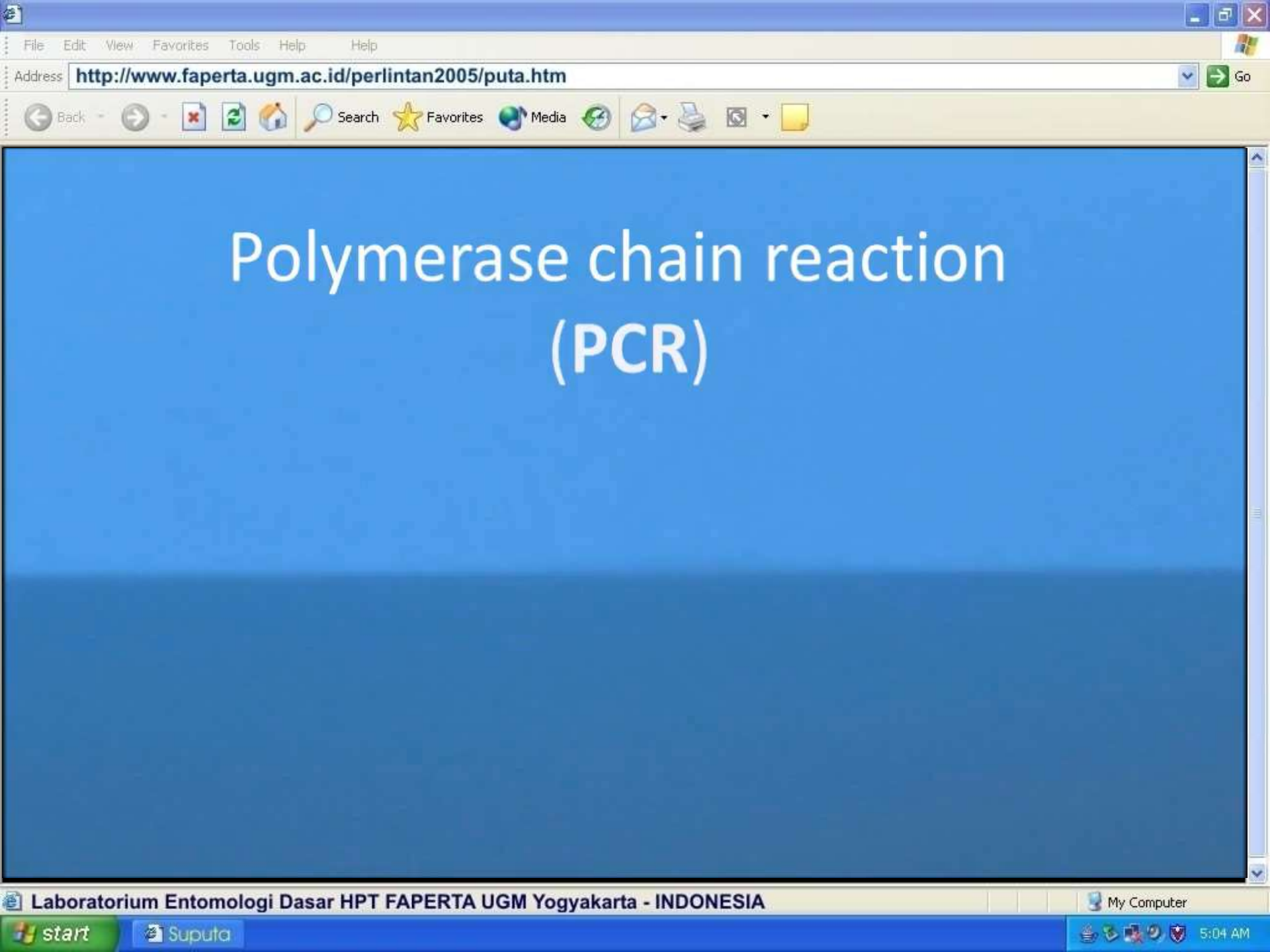
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# PCR

## *Polymerase Chain Reaction*

**Teknik atau metode perbanyak DNA secara enzimatis melalui reaksi berantai polimerase tanpa menggunakan organisme**



# Polymerase chain reaction (PCR)

# Proses Mendapatkan Basa DNA Lalat Buah

- Ekstraksi DNA akan mendapatkan Genomic DNA
- Elektroforesis Genomic DNA untuk memastikan ekstraksi DNAnya berhasil
- PCR dalam rangka melipat-gandakan DNA yang dikehendaki berdasar pada primer
- Purifikasi PCR product untuk membersihkan DNA hasil PCR dari komponen lain (sisa primer, dNTP, Taq polymerase,  $MgCl_2$ , dll.)
- Check kualitas dan kuantitas DNA
- Sequencing DNA

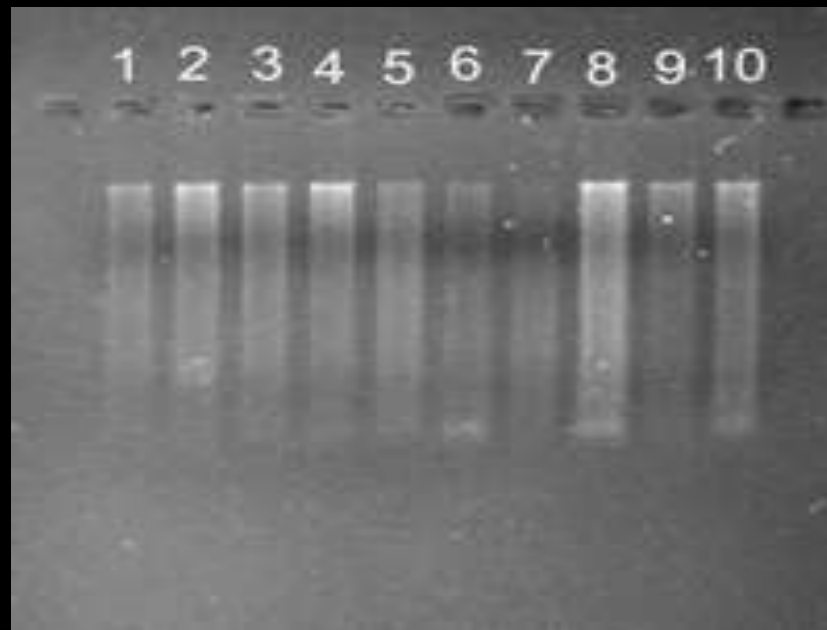
# Proses Mendapatkan Basa DNA Lalat Buah

- Ekstraksi DNA akan mendapatkan Genomic DNA



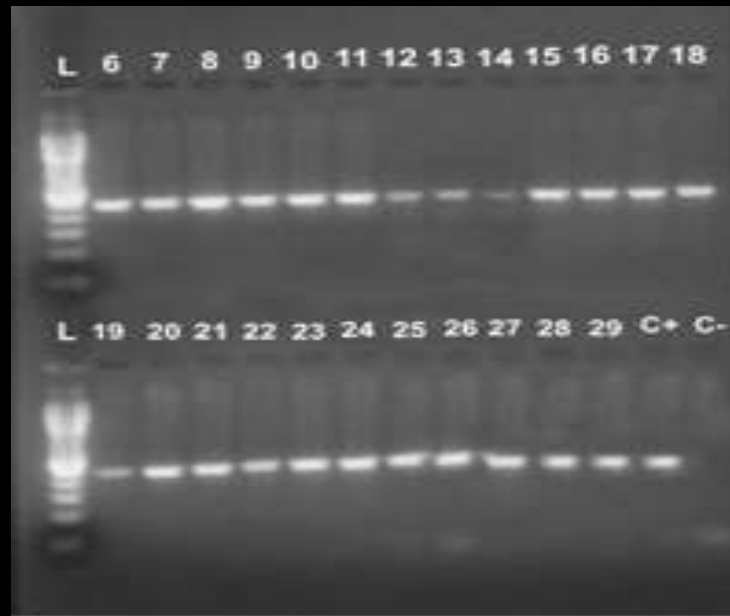
# Proses Mendapatkan Basa DNA Lalat Buah

- Elektroforesis Genomic DNA untuk memastikan ekstraksi DNAny berhasil



# Proses Mendapatkan Basa DNA Lalat Buah

- PCR dalam rangka melipat-gandakan DNA yang dikehendaki berdasar pada primer



# Proses Mendapatkan Basa DNA Lalat Buah

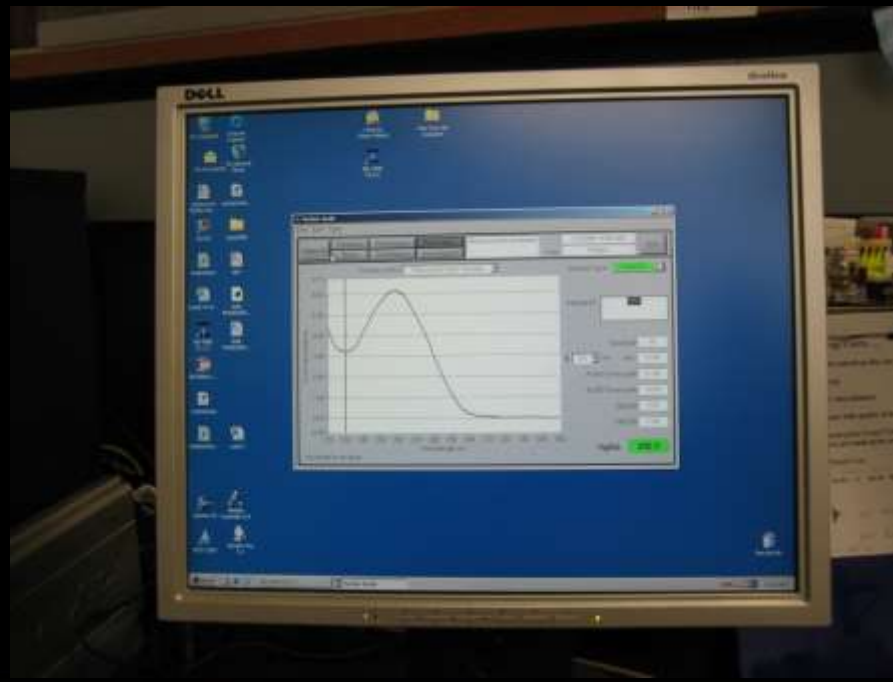
- Purifikasi PCR product untuk membersihkan DNA hasil PCR dari komponen lain (sisa primer, dNTP, Taq polymerase,  $MgCl_2$ , dll.)



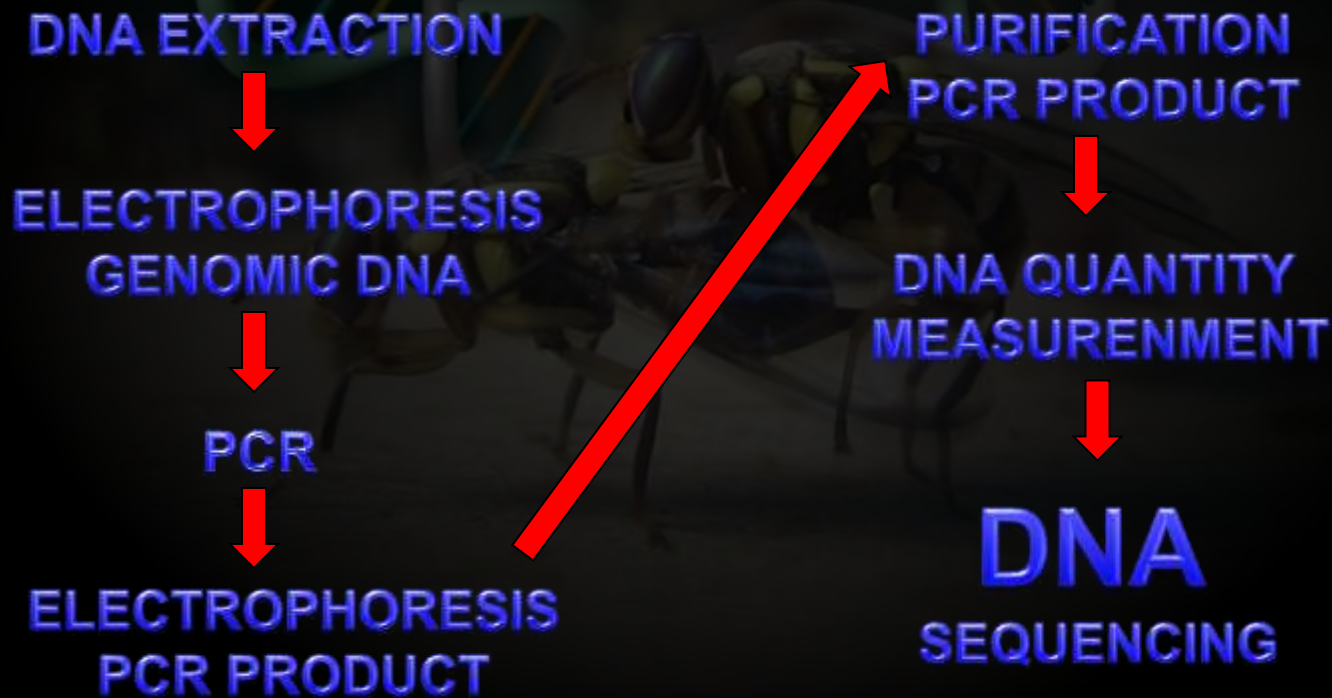


# Proses Mendapatkan Basa DNA Lalat Buah

- Check kualitas dan kuantitas DNA

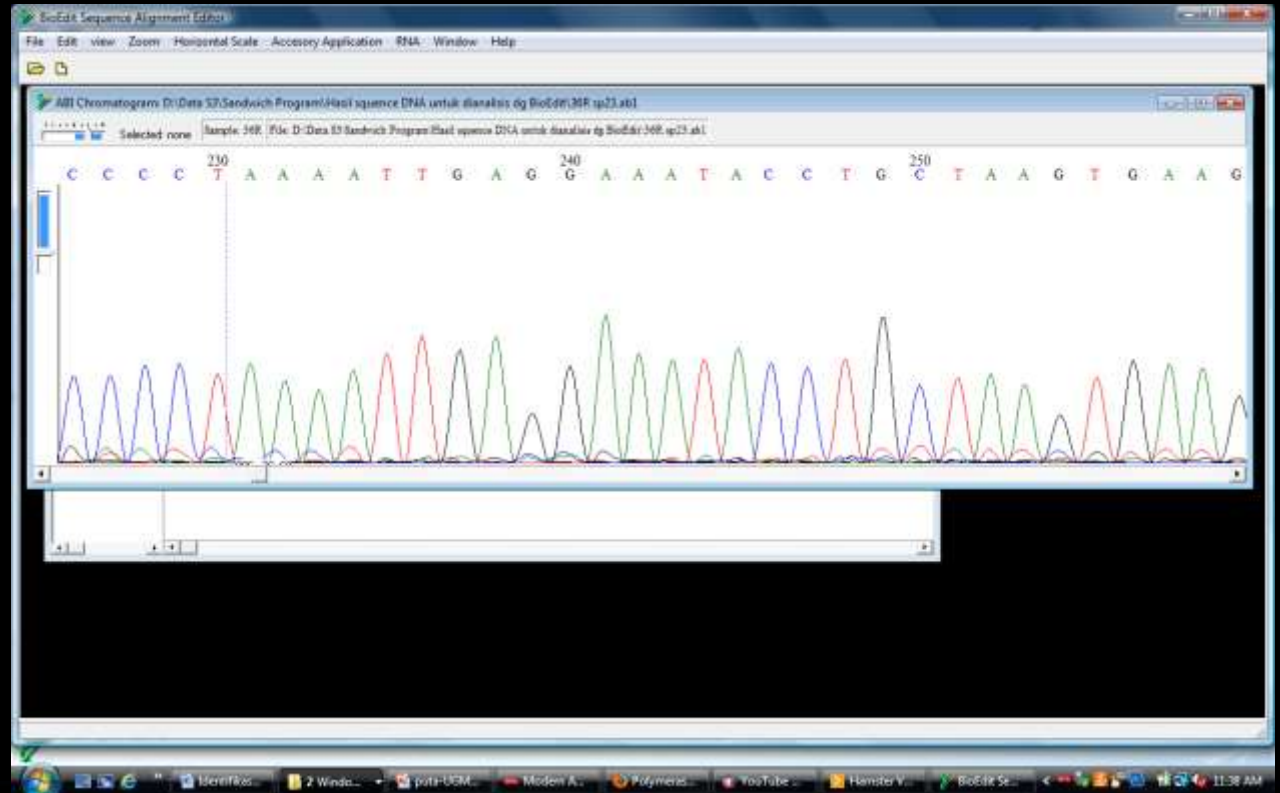


# Proses Mendapatkan Basa DNA Lalat Buah



# Urutan Proses Mendapatkan Urutan Basa DNA

- Sequencing DNA



# Identifikasi Lalat Buah berdasarkan DNAny

NCBI Blast Nucleotide Sequence (422 letters) - Windows Internet Explorer

http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=GetALIGNMENTS&100&ALIGNMENT\_VIEW=Pairwise&DATABASE\_SORT=0&DESCRIPTIONS=100&FIRST\_QUERY\_NI...

Google

NCBI Blast Nucleotide Sequence (422 letters)

Descriptions

Legend for links to other resources: UniGene, GEO, Genes, Structure, Map Viewer, PubChem BioAssay

Sequences producing significant alignments:

Accession	Description	Max score	Total score	Query coverage	E value	Max ident	Link
DQ116237.1	Bactrocera carambolae isolate FF1039 cytochrome oxidase subunit I	786	786	100%	0.0	100%	
DQ116238.1	Bactrocera carambolae isolate FF1041 cytochrome oxidase subunit I	774	774	100%	0.0	99%	
DQ116414.1	Bactrocera carambolae mitochondrion, complete genome	769	769	100%	0.0	99%	
DQ116233.1	Bactrocera carambolae isolate FF675 cytochrome oxidase subunit I (	763	763	100%	0.0	99%	
DQ116236.1	Bactrocera papayae isolate FF1074 cytochrome oxidase subunit I (C	758	758	100%	0.0	99%	
DQ006671.1	Bactrocera carambolae voucher Q017_1 cytochrome oxidase subunit	758	758	100%	0.0	99%	
HQ262394.1	Diptera sp. BOLD:AAA2295 voucher BainF12 cytochrome oxidase sub	752	752	100%	0.0	98%	
HQ262392.1	Diptera sp. BOLD:AAA2295 voucher BainF11 cytochrome oxidase sub	752	752	100%	0.0	98%	
HQ262391.1	Diptera sp. BOLD:AAA2295 voucher BainF09 cytochrome oxidase sub	752	752	100%	0.0	98%	
HQ262389.1	Diptera sp. BOLD:AAA2295 voucher BainF07 cytochrome oxidase sub	752	752	100%	0.0	98%	
G5682013.1	Diptera sp. BOLD:AAA2295 voucher NB8GE IMB-00202 cytochrome o	752	752	100%	0.0	98%	
FM20482.1	Bactrocera papayae isolate MY001COI cytochrome oxidase subunit I	752	752	100%	0.0	98%	
DQ0912578.1	Bactrocera papayae isolate SH63 mitochondrion, complete genome	752	752	100%	0.0	98%	
DQ116271.1	Bactrocera papayae isolate FF705 cytochrome oxidase subunit I (CC	752	752	100%	0.0	98%	
DQ116281.1	Bactrocera dorsalis isolate FF1094 cytochrome oxidase subunit I (CC	752	752	100%	0.0	98%	
DQ116280.1	Bactrocera dorsalis isolate FF1092 cytochrome oxidase subunit I (CC	752	752	100%	0.0	98%	
DQ116276.1	Bactrocera dorsalis isolate FF990 cytochrome oxidase subunit I (COI	752	752	100%	0.0	98%	
DQ116275.1	Bactrocera dorsalis isolate FF989 cytochrome oxidase subunit I (COI	752	752	100%	0.0	98%	
DQ116273.1	Bactrocera dorsalis isolate FF986 cytochrome oxidase subunit I (COI	752	752	100%	0.0	98%	
DQ116269.1	Bactrocera dorsalis isolate FF901 cytochrome oxidase subunit I (COI	752	752	100%	0.0	98%	
HQ260727.1	Bactrocera dorsalis isolate E2010-5235-1 clone 2 tRNA-Tyr gene, ps	747	747	100%	0.0	98%	
HQ260726.1	Bactrocera dorsalis isolate E2010-5235-1 clone 1 tRNA-Tyr gene, ps	747	747	100%	0.0	98%	
DQ0843288.1	Bactrocera dorsalis mitochondrion, complete genome	747	747	100%	0.0	98%	
DQ116217.1	Bactrocera philippinensis isolate FF1028 cytochrome oxidase subunit	747	747	100%	0.0	98%	
DQ116216.1	Bactrocera philippinensis isolate FF1020 cytochrome oxidase subunit	747	747	100%	0.0	98%	

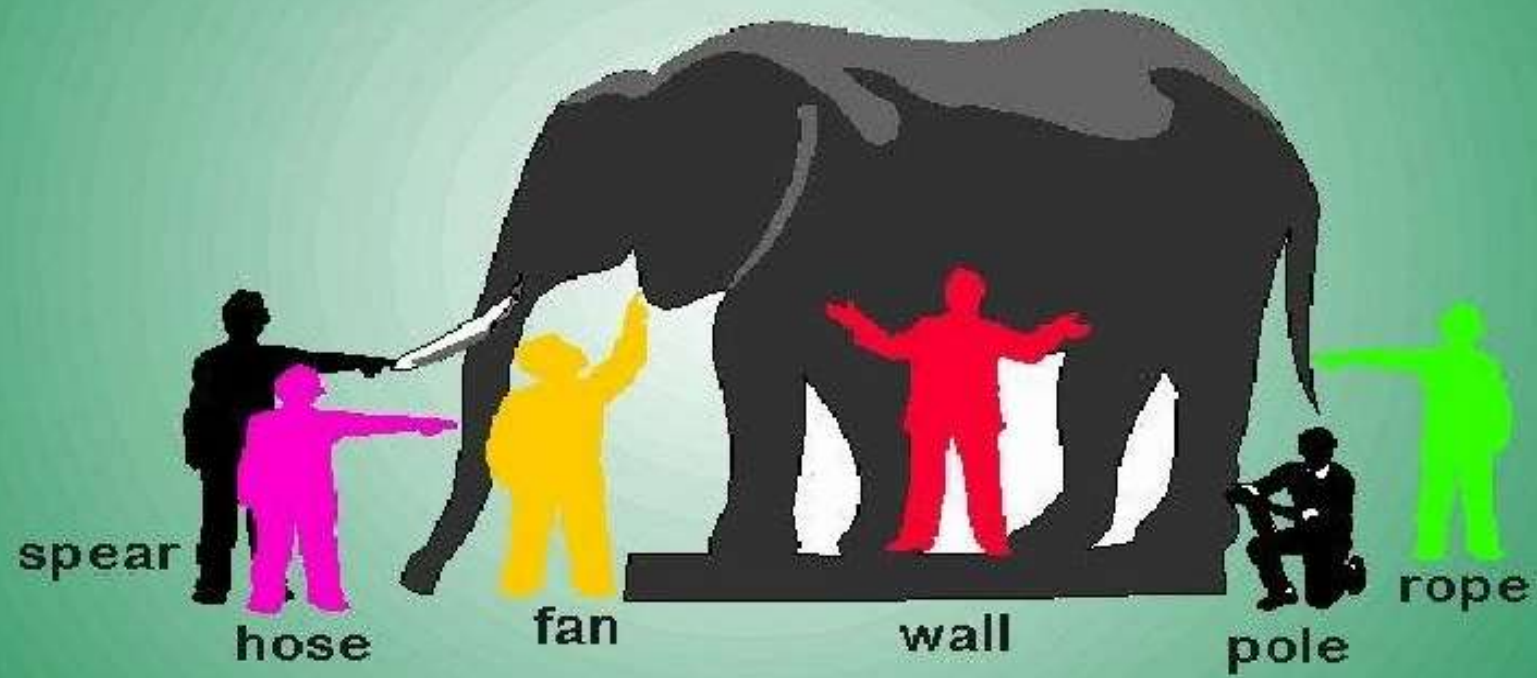


By  
**SUPUTA**

**GMOS**  
Genetically Modified Organisms

JURUSAN HAMA & PENYAKIT TUMBUHAN  
FAKULTAS PERTANIAN  
UNIVERSITAS GADJAH MADA

# THE ELEPHANT METAPHOR OF REALITY



# Genetic Engineering is an Extension of Traditional Plant Breeding

## TRADITIONAL PLANT BREEDING

DNA is a strand of genes, much like a strand of pearls. Traditional plant breeding combines many genes at once.



## GENETIC ENGINEERING

Using genetic engineering, we can add a single gene to the strand.



# INTRODUCTION

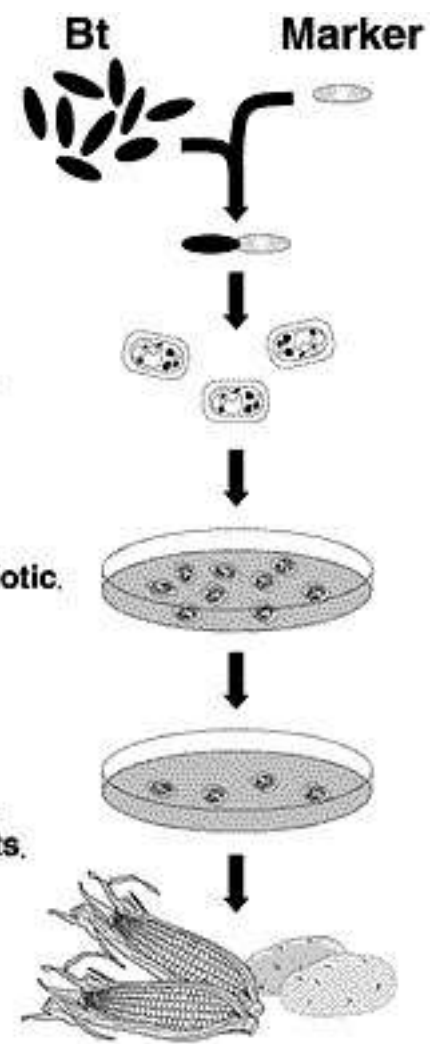


1. The Bt gene that produces the desired lethal protein is joined to a marker gene for antibiotic resistance.

2. Bt gene + marker is inserted into plant cells.

3. Plant cells are grown in the presence of antibiotic.

4. Cells that carry the Bt gene + antibiotic resistance gene survive and are grown into plants.





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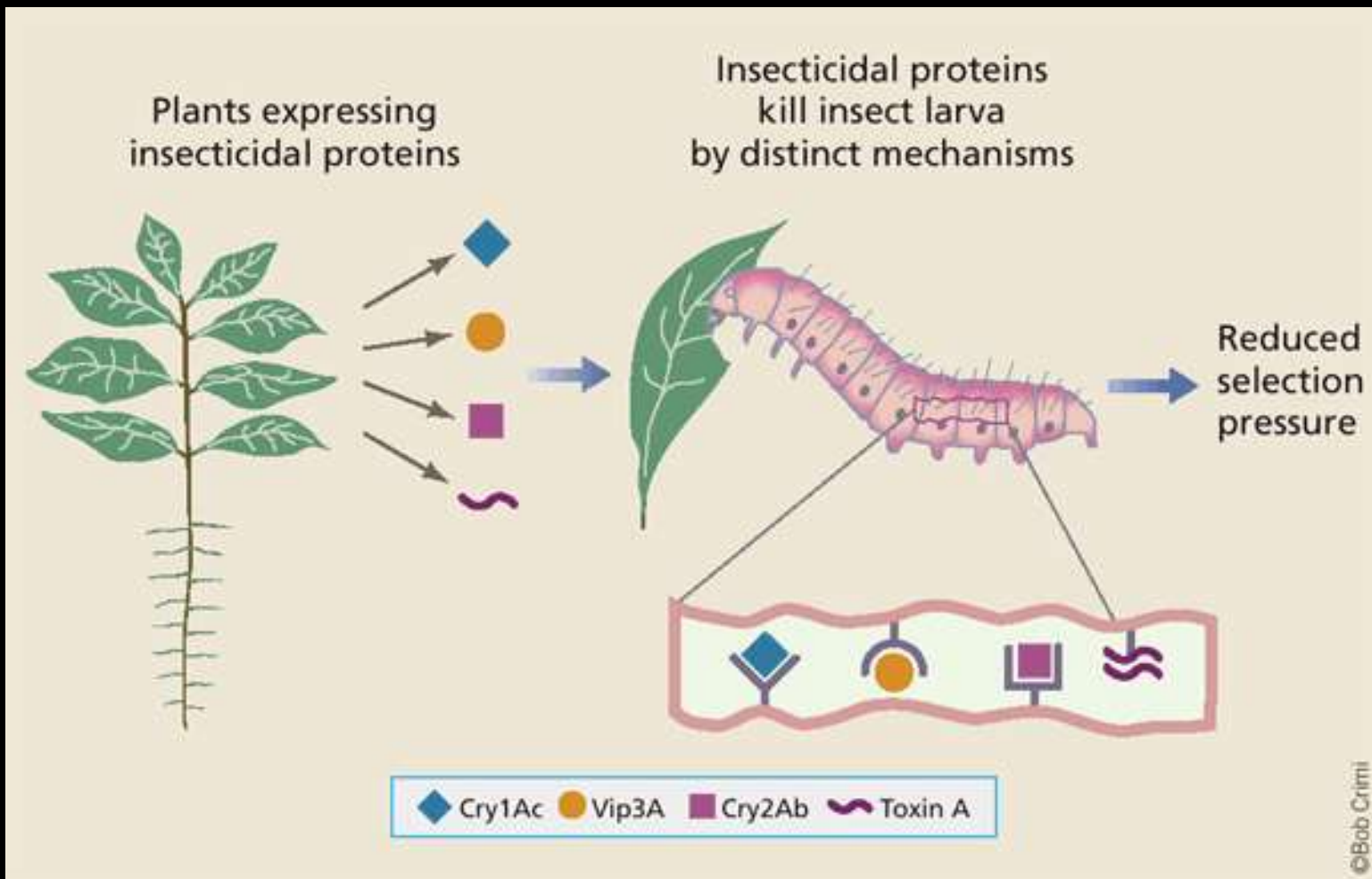
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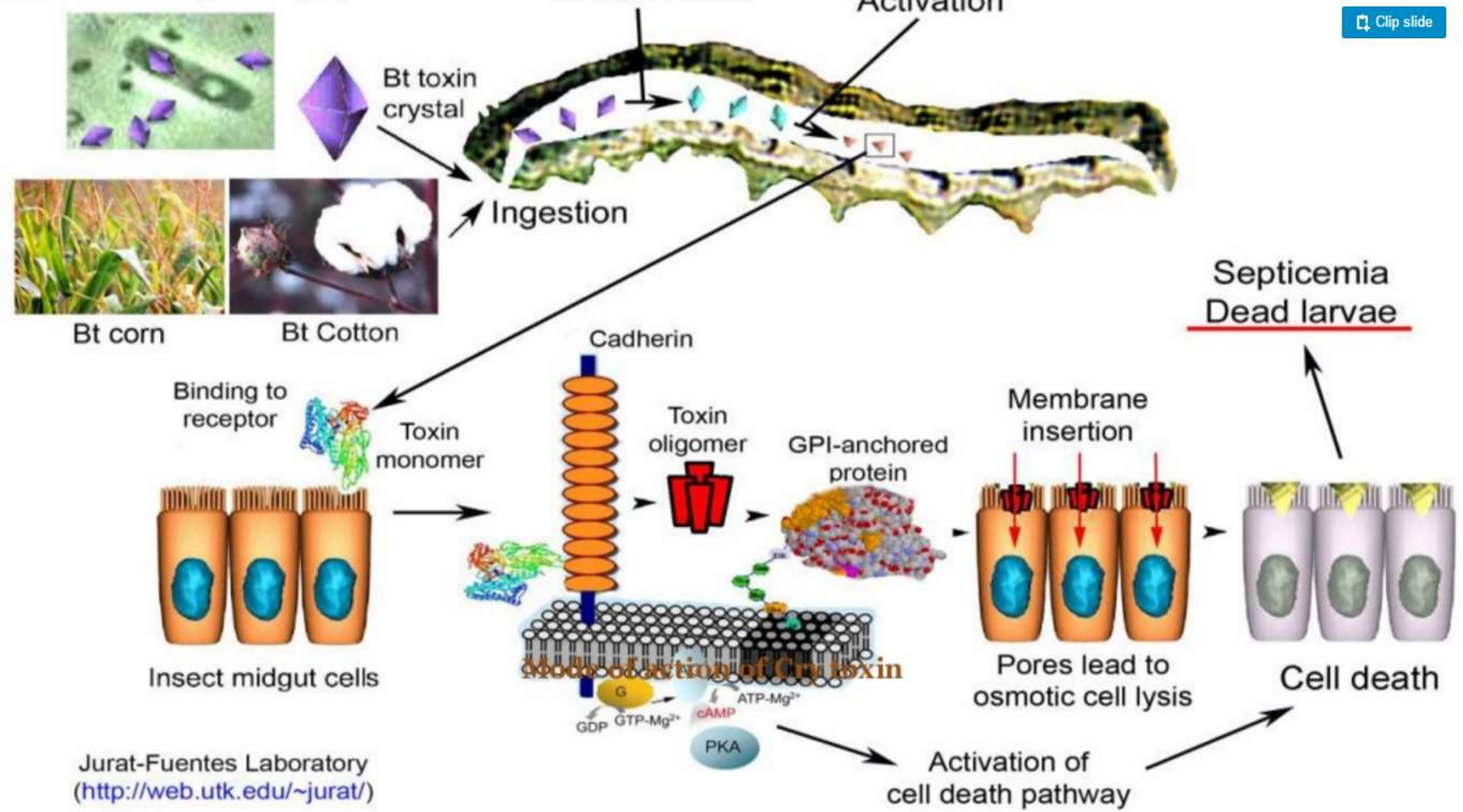
# INTRODUCTION

## Mechanism of *Agrobacterium*

# INSECT KILLED BY Bt



*Bacillus thuringiensis* (Bt)



Jurat-Fuentes Laboratory  
<http://web.utk.edu/~jurat/>

# Selective action of *Bt* in insects

Ingestion (occurs while feeding plant tissues)

Solubilization (Alkalinity)

Activation (pH >9.5)

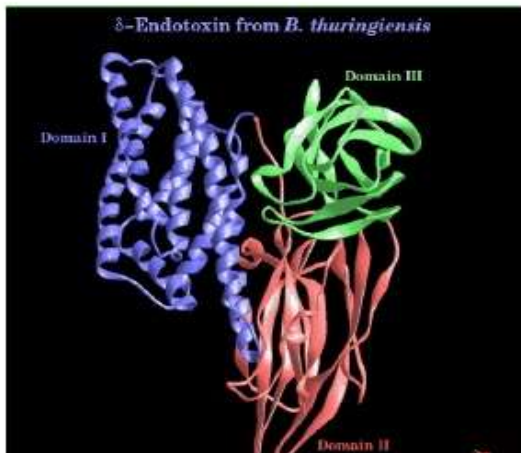
Binding (Specific receptor)

Insertion (Damage gut wall)

Pore formation

Cell lyses

**Deat**



# Crystal protein of *Bacillus thuringiensis* and their specificity

Crystal proteins	Order(s) specific
Cry-I	Lepidoptera
Cry-II	Lepidoptera & Diptera
Cry-III	Coleoptera
Cry-IV	Diptera
Cry-V	Lepidoptera & Coleoptera

# Transgenic plants expressing foreign gene for insect resistance

Crop	Foreign gene	Origin of gene	Target Insect Pest (s)
Cotton	<i>Cry1Ab</i> , <i>Cry1Ac</i> , <i>Cry2Ab</i>	<i>Bacillus thuringiensis</i>	<i>Helicoverpa zea</i> (Boddie) <i>Spodoptera exigua</i> (Hubner) <i>Trichoplusia ni</i> (Hubner)
Brinjal	<i>CryIIIb</i>	<i>B. thuringiensis</i>	<i>Leptinotarsa decemlineata</i> (say)
Maize	<i>Cry1Ab</i>	<i>B. thuringiensis</i>	<i>Ostrinia nubilalis</i> (Hubner)
Rice	<i>Corn cystatin (cc)</i>	Corn	<i>Sitophilus zeamais</i> (Motschulsky)
	<i>Pin 2</i>	Potato	<i>Chilo suppressalis</i> (Walker)
	<i>CpTi</i>	Cowpea	<i>C. suppressalis</i>
	<i>Cry1Ab</i>	<i>B. thuringiensis</i>	<i>C. suppressalis</i> , <i>Cnaphalocrosis medinalis</i> (Guenee), <i>Scirpophaga incertulas</i> (Walker)

Contd..

Crop	Foreign gene	Origin of gene	Target Insect Pest (s)
Potato	<i>Cry1Ab</i>	<i>B. thuringiensis</i>	<i>Phthorimaea operculella</i> (Zeller)
	<i>Oryza cystatin 1 (oc1)</i>	Rice	<i>L. decemlineata</i>
Sugarcane	<i>Cry1Ab</i>	<i>B. thuringiensis</i>	<i>Diatraea sachharalis</i> (Fabricius)
Tobacco	<i>Cry1Ab</i>	<i>B. thuringiensis</i>	<i>Heliothis virescens</i> (Fabricius)
	$\alpha$ -ai	Pea	<i>Tenebrio molitor</i> (Linnaeus)
	<i>CpTi</i>	Cowpea	<i>H. virescens</i> , <i>Manduca sexta</i> (L.)
Tomato	<i>Cry1Ac</i>	<i>B. thuringiensis</i>	<i>M.Sexta</i>
	<i>B.t. (k)</i>	<i>B.thuringiensis</i>	<i>H.zea</i> , <i>M.sexta</i> , <i>Keifera lycopersicella</i> (Walsingham)

# Comparison of breeding and transgenic technology

## Breeding

Exchange of genes within a species

Gene of interest with flanking sequence transferred

Simple Technology

## Transgenic Technology

No barrier

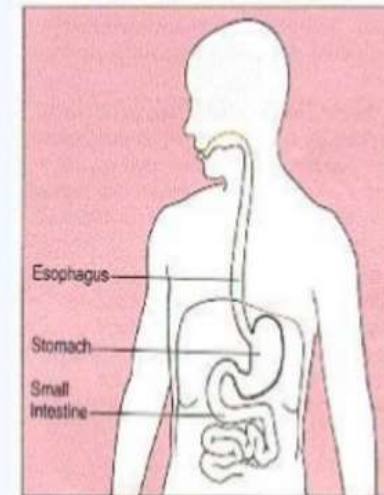
Only Gene of Interest

Intensive Technology



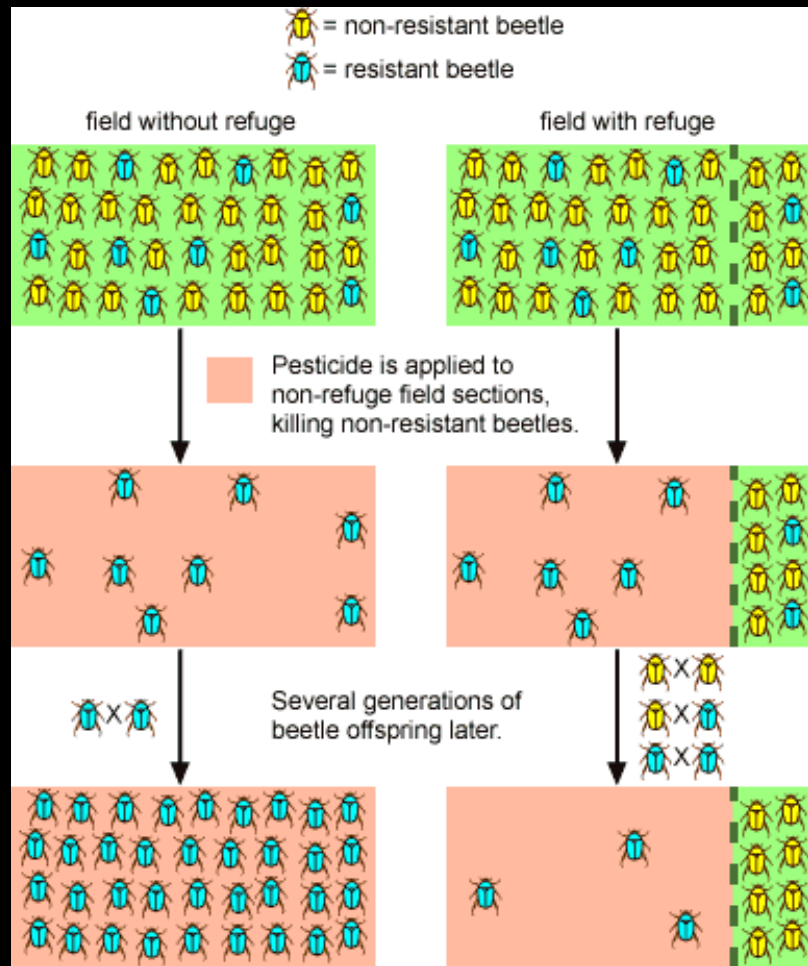
*Bt* has no toxic impact in higher animals  
(HUMAN) because of...

- Acidic stomach
- Very low pH ( $\approx 1.5$  in humans)
- Absence of required receptors

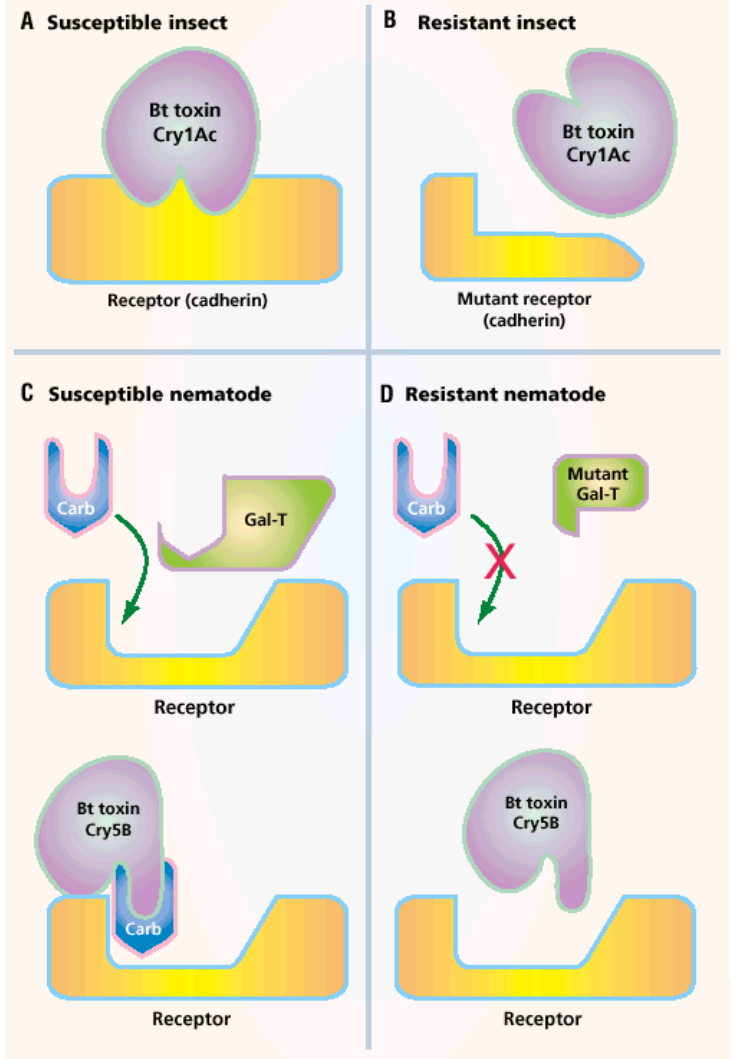


*Bt* is safe to non-target organisms-  
HUMAN

# THE PROBLEM IS INSECT RESISTANT



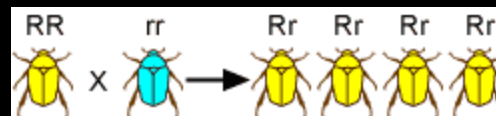
# INSECT RESISTANT TO Bt



# SOLVE THE PROBLEM

Refugia → the non-resistant insects survive. The allele for Bt resistance happens to be recessive = that means that the resistant allele can be masked by the dominant non-resistant allele.

**So if a resistant insect (rr) surviving in the Bt-producing field mates with a non-resistant insect (RR) surviving in the refuge, all of their offspring will be non-resistant (Rr).**



When two heterozygous pests mate, only one in four offspring (on average) will be homozygous recessive (rr) and therefore resistant to the pesticide.

