

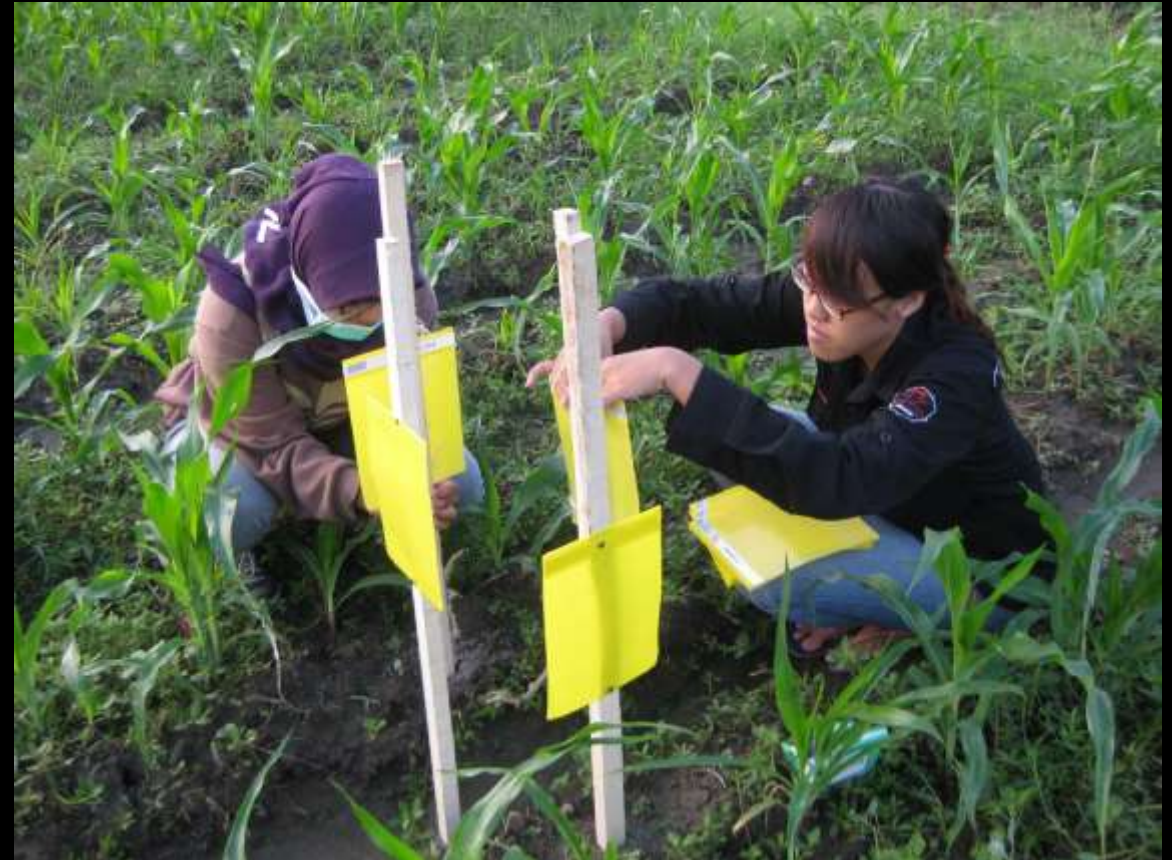
# Identifikasi Hama Tanaman Berdasarkan Gejala Serangan

# Identifikasi Hama Tanaman





# Identifikasi Hama Tanaman





# Identifikasi Hama Tanaman



# Identifikasi Hama Tanaman





# Tanda dan Gejala Serangan Hama hubungannya dengan morfologi dan perilaku OPT



# Tanda dan Gejala Serangan Hama hubungannya dengan morfologi dan perilaku OPT





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# Tanda dan Gejala Serangan Hama hubungannya dengan morfologi dan perilaku OPT





# Tanda dan Gejala Serangan Hama hubungannya dengan morfologi dan perilaku OPT



**Berdasarkan Bagian Tanaman yang diserang  
(Contoh Penggerek dan Pengorok)**

**HAMA?**



**Berdasarkan Fase Tanaman yang Diserang  
(Contoh Penggerek Batang Padi)**

**HAMA?**

# Berdasarkan Tanda Serangan





# Berdasarkan Tanda Serangan



# Berdasarkan Tanda Serangan





# Berdasarkan Tanda Serangan



# Berdasarkan Tanda Serangan







The image shows a screenshot of a web browser window. The address bar contains the URL <http://hpt.faperta.ugm.ac.id/suputa/>. The browser's menu bar includes File, Edit, View, Favorites, Tools, and Help. The toolbar contains icons for Back, Forward, Stop, Refresh, Home, Search, Favorites, Media, and other functions. The main content area is a black rectangle with the following text in yellow:

# Identifikasi Hama Tanaman Berdasarkan Organisme Hamanya

At the bottom of the browser window, the Windows taskbar is visible, showing the Start button, a taskbar with 'Suputa', and the system tray with 'My Computer', a clock showing 5:04 AM, and other icons.

# Berdasarkan Organisme Hama





# Berdasarkan Organisme Hama



# Berdasarkan Organisme Hama





# Berdasarkan Organisme Hama



# Berdasarkan Organisme Hama





# Berdasarkan Organisme Hama



# Berdasarkan Organisme Hama





# Berdasarkan Organisme Hama



# Berdasarkan Organisme Hama





# Berdasarkan Organisme Hama





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# Berdasarkan Organisme Hama





# Berdasarkan Organisme Hama



# Berdasarkan Organisme Hama





# Berdasarkan Organisme Hama



# Berdasarkan Organisme Hama





# Berdasarkan Organisme Hama

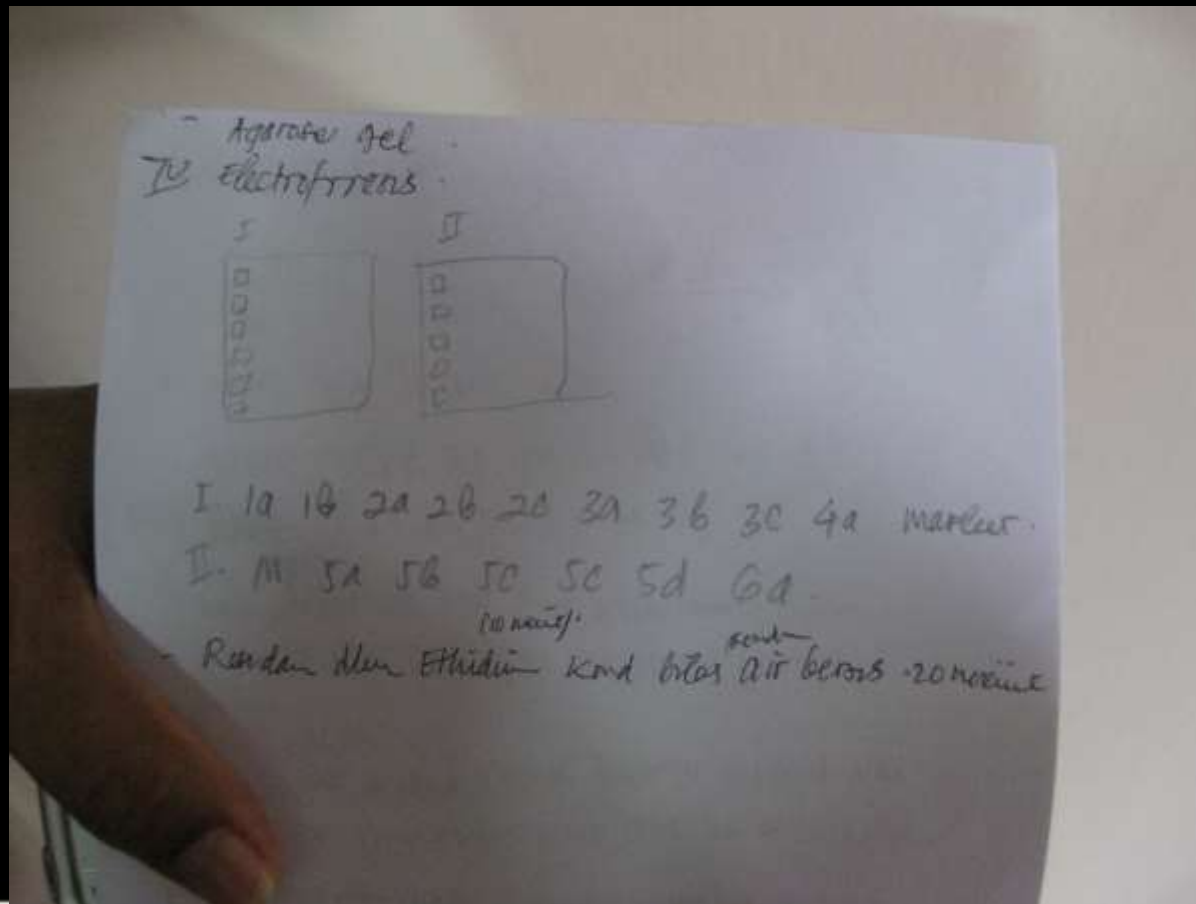


# Berdasarkan Organisme Hama

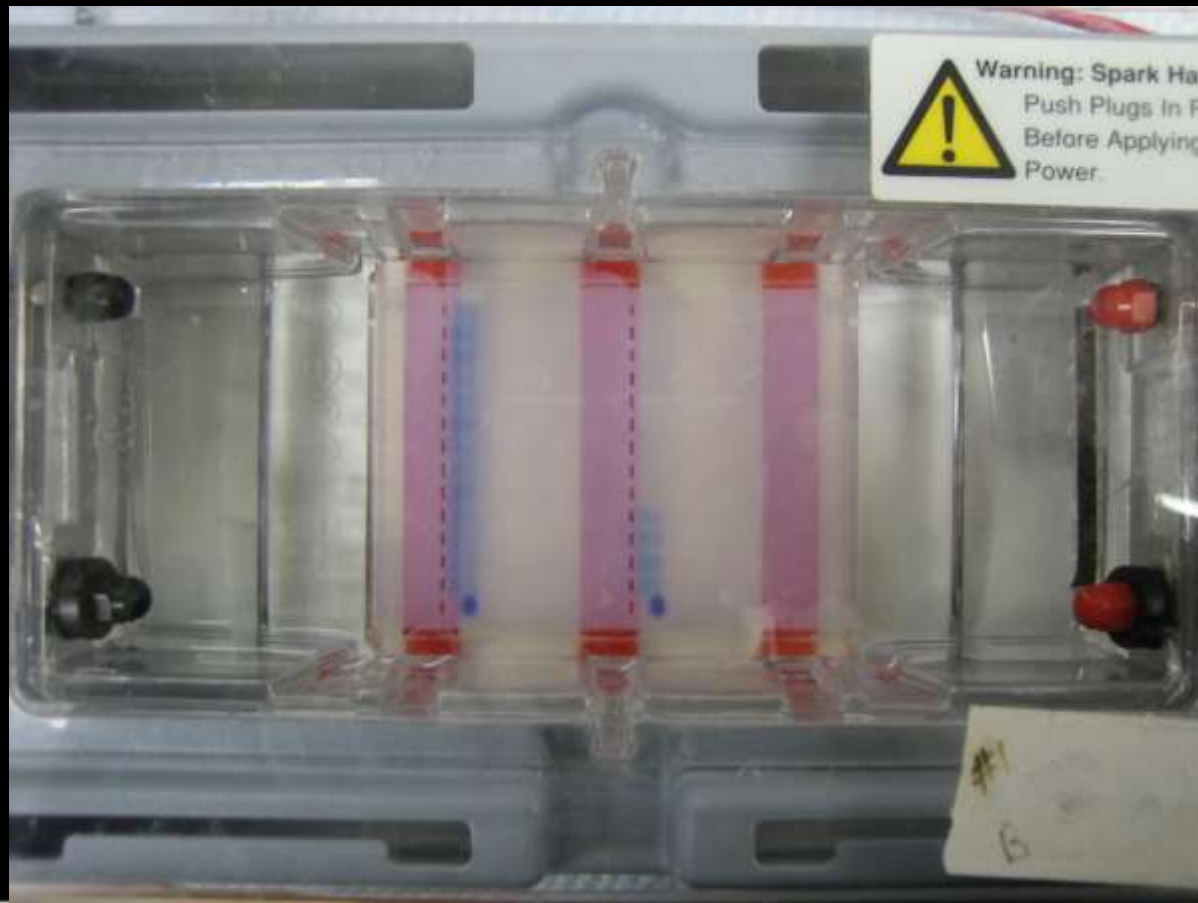




# Molekuler (PCR, Sequencing DNA "Blast Gen Bank")

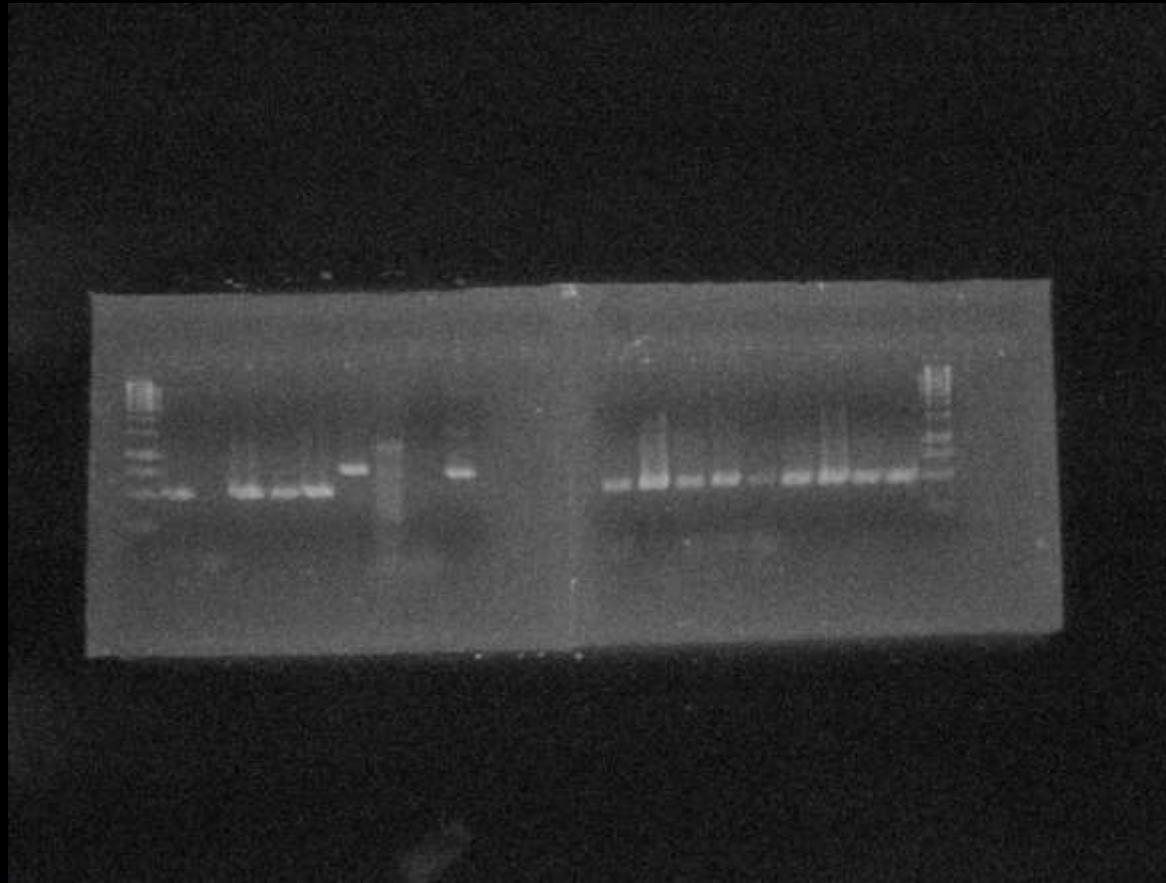


# Molekuler (PCR, Sequensing DNA "Blast Gen Bank")





# Molekuler (PCR, Sequencing DNA "Blast Gen Bank")



# Molekuler (PCR, Sequencing DNA "Blast Gen Bank")

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

http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Get&ALIGNMENTS=100&ALIGNMENT\_VIEW=Pairwise&DATABASE\_SORT=05&DESCRIPTIONS=100&FIRST\_QUERY\_NI

Google

NCBI Blast:Nucleotide Sequence (422 letters)

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

Sequences producing significant alignments:

Accession	Description	Max score	Total score	Query coverage	E value	Max ident	Links
DQ116257.1	Bactrocera carambolae isolate FF1039 cytochrome oxidase subunit I	780	780	100%	0.0	100%	
DQ116238.1	Bactrocera carambolae isolate FF1041 cytochrome oxidase subunit I	774	774	100%	0.0	99%	
EF014414.1	Bactrocera carambolae mitochondrion, complete genome	769	769	100%	0.0	99%	
DQ116255.1	Bactrocera carambolae isolate FF675 cytochrome oxidase subunit I (	763	763	100%	0.0	99%	
DQ116226.1	Bactrocera papayae isolate FF1074 cytochrome oxidase subunit I (C	758	758	100%	0.0	99%	
DQ006821.1	Bactrocera carambolae voucher Q017_1 cytochrome oxidase subunit	758	758	100%	0.0	99%	
NC096259.1	Diptera sp. BOLD:AAA2295 voucher BainF12 cytochrome oxidase sub	752	752	100%	0.0	98%	
NC096259.1	Diptera sp. BOLD:AAA2295 voucher BainF11 cytochrome oxidase sub	752	752	100%	0.0	98%	
NC096259.1	Diptera sp. BOLD:AAA2295 voucher BainF09 cytochrome oxidase sub	752	752	100%	0.0	98%	
NC096258.1	Diptera sp. BOLD:AAA2295 voucher BainF07 cytochrome oxidase sub	752	752	100%	0.0	98%	
GU682019.1	Diptera sp. BOLD:AAA2295 voucher NIBGE IMB-00202 cytochrome ox	752	752	100%	0.0	98%	
FJ802487.1	Bactrocera papayae isolate MY001C01 cytochrome oxidase subunit I	752	752	100%	0.0	98%	
DQ917578.1	Bactrocera papayae isolate SH63 mitochondrion, complete genome	752	752	100%	0.0	98%	
DQ116321.1	Bactrocera papayae isolate FF706 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%	
NC026022.1	Bactrocera dorsalis isolate E2010-5235-1 clone 2 tRNA-Tyr gene, pa	747	747	100%	0.0	98%	
NC026022.1	Bactrocera dorsalis isolate E2010-5235-1 clone 1 tRNA-Tyr gene, pa	747	747	100%	0.0	98%	
DQ845759.1	Bactrocera dorsalis mitochondrion, complete genome	747	747	100%	0.0	98%	
DQ116317.1	Bactrocera philippinensis isolate FF1028 cytochrome oxidase subunit	747	747	100%	0.0	98%	
DQ116316.1	Bactrocera philippinensis isolate FF1020 cytochrome oxidase subunit	747	747	100%	0.0	98%	

Internet | Protected Mode: On

100%

My Computer

5:04 AM



# Molekuler (PCR, Sequencing DNA "Blast Gen Bank")

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

Address: <http://blast.ncbi.nlm.nih.gov/Blast.cgi>

BLAST Basic Local Alignment Search Tool

My NCBI [Sign In] [Register]

NCBI BLAST | blastn suite | Formatting Results - SMJNHR3015

[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

### Nucleotide Sequence (422 letters)

Query ID	Idj44207	Database Name	nr
Description	None	Description	All GenBank+EMBL+DBJ+POB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)
Molecule type	nucleic acid	Program	BLASTN 2.2.25+ <a href="#">Citation</a>
Query Length	422		

Other reports: [Search Summary](#) [Taxonomy reports](#) [Distance tree of results](#)

#### Graphic Summary

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the define, click to show alignments

Color key for alignment scores	
Score Range	Color
<40	Black
40-80	Blue
80-160	Green
160-240	Yellow
240-320	Pink
320-400	Red
>=200	Dark Red

Query

1 80 160 240 320 400

# Molekuler (PCR, Sequencing DNA "Blast Gen Bank")





# Molekuler (PCR, Sequensing DNA "Blast Gen Bank")

Nucleotide BLAST: Search nucleotide databases using a nucleotide query - Windows Internet Explorer

Address: <http://hpt.faperta.ugm.ac.id/suputa/>

BLAST Basic Local Alignment Search Tool

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s)

TGCTCAAACGAATAGAGGTATTCGATCAAGGTGATTCCTGTGATCGTATATTAATTACTGTTSTA  
ATGAAATTTACTGCTCCTAAAATTGAGGAAATACCTGCTAAGTGAAGTGAAGGAAATAGCTAGATCAA  
CTGAACTCCTCCGTCCCAATAACASATGATAGGGTGGTAAACTGTTCAACTGTACCACTCC  
GTTTCTACTACTTCTACTAATAGTAATGTAAGGAAAGGTAATAATCAAAATCTTATATTA  
TTCAATCGTGGAAATGCTAT

Or, upload file

Job Title

Align two or more sequences

Choose Search Set

Database:  Human genomic + transcript  Mouse genomic + transcript  Others (nr etc.)

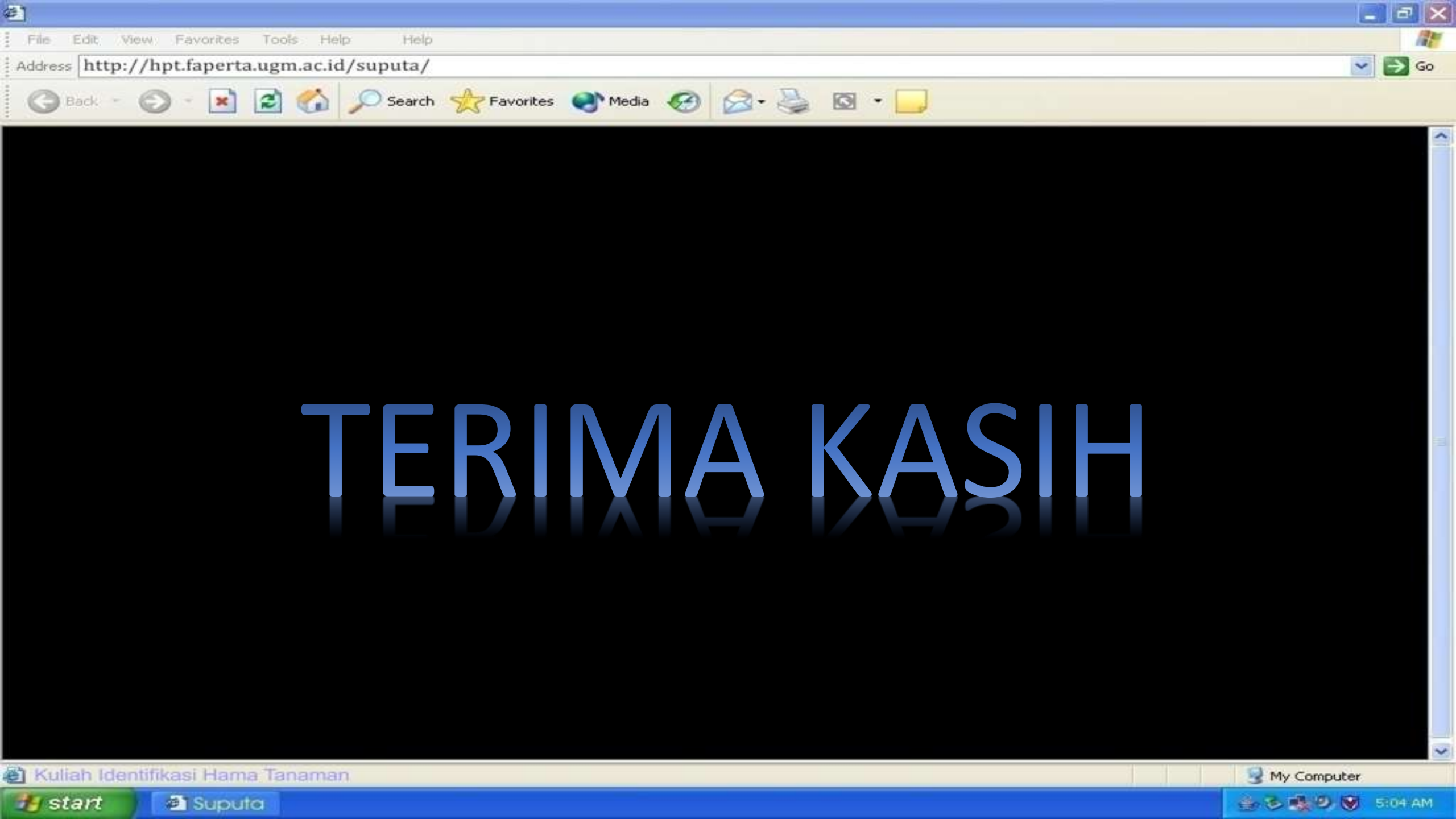
Nucleotide collection (nr/nt)

Organism: Enter organism name or id - completions will be suggested

Exclude:  Models (MXP)  Uncultured/environmental sample sequences

Entrez Query: Enter an Entrez query to limit search

Windows taskbar: start, Suputa, 000\_SP\_FT, 516CANON, Modem AC2726..., Nucleotide BLA..., Corel PHOTO-P..., BioEdit Sequenc..., My Computer, 5:04 AM



TERIMA KASIH

Kuliah Identifikasi Hama Tanaman

start Suputa

My Computer

5:04 AM