

La diagnostica biomolecolare a supporto dei controlli ufficiali per le api regine d'importazione

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Sperimentale delle Regioni
Lazio e Toscana

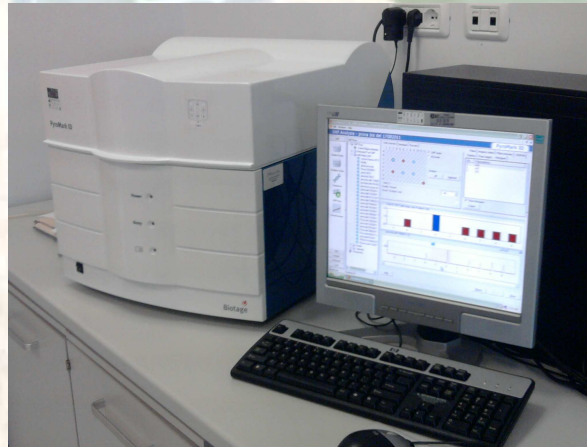
PREMESSA

La disponibilità di “importanti” apparecchiature di laboratorio, come i sequenziatori di DNA, unitamente alla crescente diffusione di strumenti informatici per la condivisione ed il confronto dei dati analitici con essi prodotti, ha contribuito in modo fondamentale allo sviluppo di nuovi approcci d'indagine laboratoristica. Un esempio pratico, che coinvolge il nostro Istituto ed il settore dell'apicoltura, è relativo all'identificazione di un importante parassita degli alveari, lo scarabeo *Aethina tumida*. Nella presentazione, verrà illustrato l'approccio biomolecolare sviluppato per il riconoscimento, soprattutto negli stadi larvali, di questo insetto

Biotecnologie IZSLT

Strumentazione ad elevato contenuto tecnologico:

- Un sequenziatore di DNA, monocapillare
- Un pirosequenziatore di DNA
- Due amplificatori per PCR “Real Time”
- Pacchetti *software* di bioinformatica e, in fase di acquisizione
- Un sequenziatore di DNA, 8 capillari



Biotecnologie IZSLT

PRINCIPALI ATTIVITA':

- Centro di Referenza Nazionale per la ricerca di OGM
- Caratterizzazioni genetiche (in specie animali, batteriche, virali)
- Sviluppo e produzione di ibridomi, cellule staminali e proteine ricombinanti
- Isolamenti virali
- Diagnostica molecolare
- Promozione e partecipazione ad attività di ricerca
- “Identificazione molecolare” di specie animali
- Supporto ad altre strutture dell'Istituto, soprattutto per lo sviluppo di protocolli diagnostici.....

Attività a sostegno dell'unità operativa “Apicoltura”

Attivazione di protocolli di “*Polymerase Chain Reaction*” (PCR, sia “end point” che “Real Time”) per il rilevamento dei seguenti patogeni:

- ABPV (Acute Bee Paralysis Virus)
- CBPV (Chronic Bee Paralysis Virus)
- DWV (Deformed Wing Virus)
- SBV (Sacbrood Virus)
- KBV (Kashmir Bee Virus)
- IAPV (Israeli Acute Paralysis Virus)
- BQCV (Black Queen Cell Virus)
- Nosema ceranae*
- Nosema apis*

....e, relativamente ai **controlli ufficiali sulle api regine d'importazione**, l'attivazione di un protocollo di “PCR- sequenziamento del DNA” per l'identificazione del coleottero *Aethina tumida*.

Necessità di una diagnosi differenziale negli stadi adulti e/o larvali

Aethina tumida



*Cryptophagus
hexagonalis*



Cychramus luteus



Galleria mellonella



Approcci possibili

- Morfologico
- Anatomico
- Etologico
- Biochimico
- Biomolecolare
- Multidisciplinare

Approccio biomolecolare: la scelta per *Aethina tumida*

Si è optato per lo sviluppo di un metodo di *PCR* classico (*end point*), seguito dal sequenziamento del prodotto di amplificazione e dal confronto di questo con le sequenze depositate in banche dati pubbliche.

In particolare, la strumentazione di laboratorio ed i supporti informatici (commerciali e/o pubblici) a disposizione hanno contribuito a.....

Approccio biomolecolare: la scelta per *Aethina tumida*

- individuare la regione bersaglio della PCR e a definire una coppia di primer in grado di rilevarla (applicazione *WEB pubblica primerBLAST-NCBI*).
- definire le condizioni ottimali per l'esecuzione del metodo di PCR (*software commerciale Oligo 6, MBI, USA*).
- applicare e verificare la bontà del saggio, su larve del coleottero.
- sequenziare (ed analizzare) il prodotto di amplificazione, (sequenziatore automatico monocapillare *ABI310, Applied Biosystems*).
- confrontare le sequenze ottenute con quelle depositate in banche dati pubbliche (applicazioni *WEB pubbliche: nBLAST-NCBI e BOLD Identification System-BOLD*)

Approccio biomolecolare: quale “regione bersaglio”?

- CITOCROMO-C OSSIDASI subunità I (“COI”)
- rDNA 16s
- CITOCROMO b (“Cyt b”)
- ITS-1
- rbcL & matK
-

“COI” come bersaglio d’elezione

- Sufficientemente stabile a livello intraspecifico
- Sufficientemente variabile a livello interspecifico
- Consente lo sviluppo di protocolli di PCR “trasversali”, in grado cioè di essere applicati, potenzialmente, su gruppi tassonomici distanti (es: mammiferi ed echinodermi)

Riassumendo: la “COI” possiede le caratteristiche ideali per assumere il ruolo di *marker* genetico d’elezione nell’identificazione “biomolecolare” di specie.

Sequenziamento con il metodo *CHAIN TERMINATION* (o metodo di *Sanger*)

E' una PCR asimmetrica condotta in presenza di una opportuna miscela di dNTP/ddNTP-fluorescenti

L'incorporazione di un ddNTP-fluorescente, nel filamento di DNA in estensione, determina sia l'interruzione della sintesi di quest'ultimo, sia la sua marcatura. Le condizioni di reazione sono tali per cui, statisticamente, si ottiene una popolazione di filamenti marcati, ciascuno dei quali interrotto in una posizione specifica: nel loro insieme, queste interruzioni, interessano tutta (entro certi limiti) la regione da sequenziare. La successiva separazione e caratterizzazione (della fluorescenza) dei filamenti, mediante elettroforesi (capillare o gel), consente di determinare la sequenza del DNA oggetto dello studio

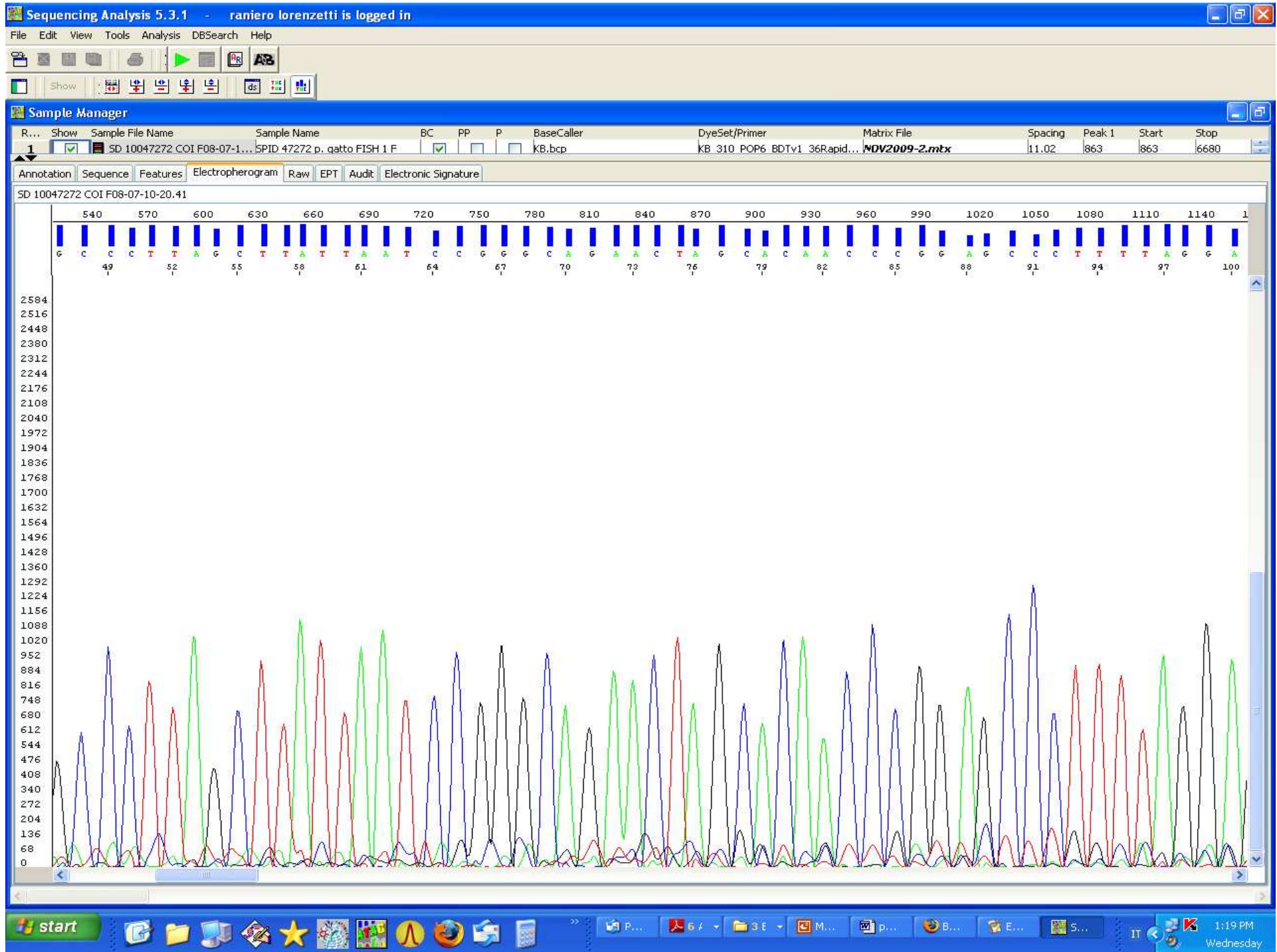
Gel:



DNA stampo

.....ACGCAGGTGTTGCGATGTCCAC
Primer →
GCGAATGCGTCCACACGCTACAGGTG
GCGAATGCGTCCACACGCTACAGGT
GCGAATGCGTCCACACGCTACAGG
GCGAATGCGTCCACACGCTACAG
GCGAATGCGTCCACACGCTACAG
GCGAATGCGTCCACACGCTAC
GCGAATGCGTCCACACGCTA
GCGAATGCGTCCACACGCT
GCGAATGCGTCCACACGCT
GCGAATGCGTCCACACG
GCGAATGCGTCCACAC
GCGAATGCGTCCACAA
GCGAATGCGTCCACA
GCGAATGCGTCCAC
GCGAATGCGTCC
GCGAATGCGTC
GCGAATGCGT
GCGAATGCG
GCGAATGC
GCGAATG
GCGAAT

.....T G C GTCCA C A..



STANDARD DI RIFERIMENTO PER L'APPROCCIO BIOMOLECOLARE

Sono le sequenze di DNA bersaglio, ottenute dalle specie d'interesse, raccolte in basi dati proprie e/o pubbliche e utilizzate per il confronto (mediante applicazione WEB o software di laboratorio) con le sequenze ottenute nel corso delle analisi.

GenBank - Celebrates 25 Years of Service - Mozilla Firefox

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http://www.tech-res.com/genbank25/ genbank

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- Monday, April 7, 2008
- Tuesday, April 8, 2008

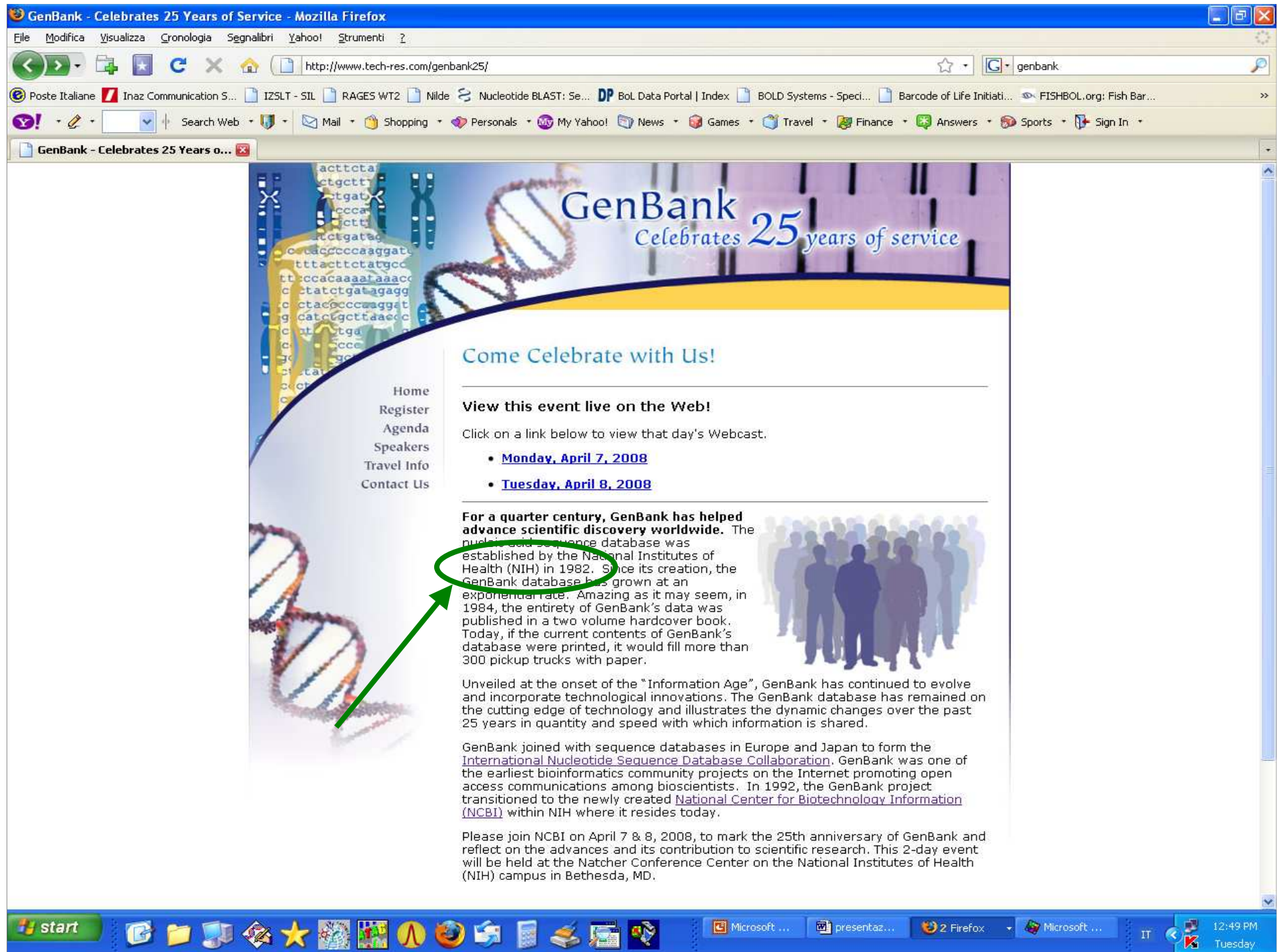
For a quarter century, GenBank has helped advance scientific discovery worldwide. The public DNA sequence database was established by the National Institutes of Health (NIH) in 1982. Since its creation, the GenBank database has grown at an exponential rate. Amazing as it may seem, in 1984, the entirety of GenBank's data was published in a two volume hardcover book. Today, if the current contents of GenBank's database were printed, it would fill more than 300 pickup trucks with paper.

Unveiled at the onset of the "Information Age", GenBank has continued to evolve and incorporate technological innovations. The GenBank database has remained on the cutting edge of technology and illustrates the dynamic changes over the past 25 years in quantity and speed with which information is shared.

GenBank joined with sequence databases in Europe and Japan to form the [International Nucleotide Sequence Database Collaboration](#). GenBank was one of the earliest bioinformatics community projects on the Internet promoting open access communications among bioscientists. In 1992, the GenBank project transitioned to the newly created [National Center for Biotechnology Information \(NCBI\)](#) within NIH where it resides today.

Please join NCBI on April 7 & 8, 2008, to mark the 25th anniversary of GenBank and reflect on the advances and its contribution to scientific research. This 2-day event will be held at the Natcher Conference Center on the National Institutes of Health (NIH) campus in Bethesda, MD.

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GenBank - Wikipedia, the free encyclopedia - Mozilla Firefox

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http://en.wikipedia.org/wiki/GenBank#Growth

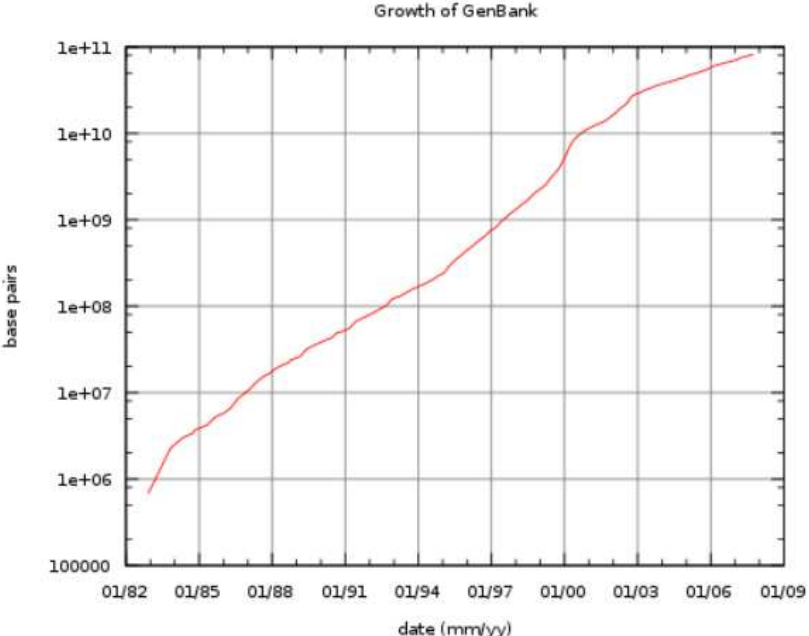
the growth of sequences in genbank

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the growth of sequences in ge SEARCH 36% f eBY

Growth [edit]

The GenBank [release notes](#) for release 162.0 (October 2007) state that "from 1982 to the present, the number of bases in GenBank has doubled approximately every 18 months".^[7] The following plot clearly shows the [exponential growth](#) (on a [semi-log scale](#) such as this, a straight line represents an exponential change).



base pairs

1e+11
1e+10
1e+09
1e+08
1e+07
1e+06
100000

01/82 01/85 01/88 01/91 01/94 01/97 01/00 01/03 01/06 01/09

date (mm/yy)

As of 15 October 2011, GenBank release 186.0 has 144,458,648 loci, 132,067,413,372 bases, from 144,458,648 reported sequences.^[7]

The GenBank database includes additional data sets which are constructed mechanically from the main sequence data collection, and therefore are excluded from this count.

See also [edit]

- Ensembl
- HPRD
- Sequence analysis
- Sequence profiling tool
- Sequence motif

start C:\Docu... La diagn... Posta in ... breve a... GenBank... IT 9:39 AM Friday

BLAST: Basic Local Alignment Search Tool - Mozilla Firefox

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http://blast.ncbi.nlm.nih.gov/Blast.cgi

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NCBI BLAST Home

BLAST finds regions of similarity between biological sequences. [more...](#)

New Aligning Multiple Protein Sequences? Try the **COBALT Multiple Alignment Tool**. [Go](#)

BLAST Assembled RefSeq Genomes

Choose a species genome to search, or [list all genomic BLAST databases](#).

<input type="checkbox"/> Human	<input type="checkbox"/> Oryza sativa	<input type="checkbox"/> Gallus gallus
<input type="checkbox"/> Mouse	<input type="checkbox"/> Bos taurus	<input type="checkbox"/> Pan troglodytes
<input type="checkbox"/> Rat	<input type="checkbox"/> Danio rerio	<input type="checkbox"/> Microbes
<input type="checkbox"/> Arabidopsis thaliana	<input type="checkbox"/> Drosophila melanogaster	<input type="checkbox"/> Apis mellifera

Basic BLAST

Choose a BLAST program to run.

nucleotide blast	Search a nucleotide database using a nucleotide query <i>Algorithms:</i> blastn, megablast, discontinuous megablast
protein blast	Search protein database using a protein query <i>Algorithms:</i> blastp, psi-blast, phi-blast
blastx	Search protein database using a translated nucleotide query
tblastn	Search translated nucleotide database using a protein query
tblastx	Search translated nucleotide database using a translated nucleotide query

Specialized BLAST

Choose a type of specialized search (or database name in parentheses.)

- ☐ Make specific primers with [Primer-BLAST](#)
- ☐ Search [trace archives](#)
- ☐ Find [conserved domains](#) in your sequence (cds)
- ☐ Find sequences with similar [conserved domain architecture](#) (cdart)
- ☐ Search sequences that have [gene expression profiles](#) (GEO)
- ☐ Search [immunoglobulins](#) (IgBLAST)
- ☐ Search for [SNPs](#) (snp)
- ☐ Screen sequence for [vector contamination](#) (vecscreen)
- ☐ [Align](#) two (or more) sequences using BLAST (bl2seq)

start

Identificazione ... presentazione - ... BLAST: Basic Lo... IT 4:00 PM Tuesday

Nucleotide BLAST: Search nucleotide databases using a nucleotide query - Mozilla Firefox

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Nucleotide BLAST: Search nucleotide databa... +

http://www.ncbi.nlm.nih.gov/blast/Blast.cgi?PAGE=Nucleotides&PROGRAM=blastn&BLAST_PROGRAMS=megaBlast&PAGE_TYPE=BlastSea the source of blast

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NCBI/BLAST/blastn suite

blastn blastp blastx tblastn tblastx

Enter Query Sequence

BLASTn programs search nucleotide databases using a nucleotide query. more... Reset page Bookmark

Enter accession number(s), gi(s), or FASTA sequence(s) Clear Query subrange

tccttagcag gtattttctt tatttttaggt gcagtaaatt ttattactac
tgtaattaat atgcgacct caggcataac ctttgatcga atacctttat
ttgtttgagc tgtagtaatt acagctatcc ttcttctact ttcattacct
gtatttagcag gagctattac tatactacta acagatcgaa atctaaatac
tactttcttc gaccatcag gagggggtga tccaatccta taccacact
tattttgatt ctctcggtcac ccagaagttt atattttaat tctaccagga

From To

Or, upload file Sfoglia...

Job Title

Enter a descriptive title for your BLAST search

☐ Align two or more sequences

Choose Search Set

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

Nucleotide collection (nr/nt)

Organism Optional

Enter organism name or id—completions will be suggested ☐ Exclude +

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown.

Exclude Optional

☐ Models (XM/XP) ☐ Uncultured/environmental sample sequences

Entrez Query Optional

Enter an Entrez query to limit search

Program Selection

Optimize for

☒ Highly similar sequences (megablast)

☐ More dissimilar sequences (discontiguous megablast)

☐ Somewhat similar sequences (blastn)

Choose a BLAST algorithm

BLAST

Search database Nucleotide collection (nr/nt) using Megablast (Optimize for highly similar sequences)

☒ Show results in a new window

+ Algorithm parameters Note: Parameter values that differ from the default are highlighted in yellow and marked with + sign

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NCBI Blast:X59692:B.taurus mRNA for ubiquinol-cytochrome-c... - Mozilla Firefox

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Nucleotide BLAST: Search nucleotide dat... x NCBI Blast:X59692:B.taurus mRNA for u... x +

blast.ncbi.nlm.nih.gov/Blast.cgi

Legend for links to other resources: [GenBank](#) [EMBL](#) [Gene](#) [Structure](#) [Map](#) [Protein](#) [PubMed](#) [Ensembl](#)

Sequences producing significant alignments:

Accession	Description	Max score	Total score	Query coverage	E value	Max ident	Links
HM056079.1	Aethina tumida isolate Quebec1 cytochrome oxidase subunit I gene, i	1624	1624	100%	0.0	100%	
AF227646.1	Aethina tumida strain NthAm2 cytochrome oxidase I gene, partial cds	1620	1620	99%	0.0	100%	
AF522358.1	Aethina tumida strain ZimP9 cytochrome oxidase subunit I (CO1) gen	1605	1605	99%	0.0	99%	
AF522357.1	Aethina tumida strain ZimP12 cytochrome oxidase subunit I (CO1) ge	1605	1605	99%	0.0	99%	
AF522356.1	Aethina tumida strain ZimP15 cytochrome oxidase subunit I (CO1) ge	1605	1605	99%	0.0	99%	
AF227649.1	Aethina tumida strain SAJ5 cytochrome oxidase I gene, partial cds; n	1598	1598	99%	0.0	99%	
AF227652.1	Aethina tumida strain SAJ3 cytochrome oxidase I gene, partial cds; n	1592	1592	99%	0.0	99%	
AF227651.1	Aethina tumida strain SAD2 cytochrome oxidase I gene, partial cds; r	1592	1592	99%	0.0	99%	
AF227650.1	Aethina tumida strain SAA9 cytochrome oxidase I gene, partial cds; r	1592	1592	99%	0.0	99%	
AF227648.1	Aethina tumida strain SAJ7 cytochrome oxidase I gene, partial cds; n	1592	1592	99%	0.0	99%	
AF522354.1	Aethina tumida strain ZimP10 cytochrome oxidase subunit I (CO1) ge	1589	1589	99%	0.0	99%	
AF227645.1	Aethina tumida strain NthAm1 cytochrome oxidase I gene, partial cds	1587	1587	99%	0.0	99%	
AF227654.1	Aethina tumida strain SAF18 cytochrome oxidase I gene, partial cds;	1581	1581	99%	0.0	99%	
AF522355.1	Aethina tumida strain ZimP8 cytochrome oxidase subunit I (CO1) gen	1578	1578	99%	0.0	99%	
AF227653.1	Aethina tumida strain SAJ8 cytochrome oxidase I gene, partial cds; n	1578	1578	99%	0.0	98%	
AF227647.1	Aethina tumida strain SAJ2 cytochrome oxidase I gene, partial cds; n	1554	1554	99%	0.0	98%	
HM056064.1	Aethina tumida isolate AustHV1b cytochrome oxidase subunit I gene,	1530	1530	95%	0.0	99%	
HM056063.1	Aethina tumida isolate AustHV1a cytochrome oxidase subunit I gene,	1530	1530	95%	0.0	99%	
HM056078.1	Aethina tumida isolate CanCon2 cytochrome oxidase subunit I gene, i	1524	1524	95%	0.0	99%	
HM056077.1	Aethina tumida isolate CanAshv cytochrome oxidase subunit I gene, i	1524	1524	95%	0.0	99%	
HM056076.1	Aethina tumida isolate CanAlb3HP cytochrome oxidase subunit I gene	1524	1524	95%	0.0	99%	
HM056075.1	Aethina tumida isolate CanAlb1Vega cytochrome oxidase subunit I ge	1524	1524	95%	0.0	99%	
HM056073.1	Aethina tumida isolate AustHV5b cytochrome oxidase subunit I gene,	1524	1524	95%	0.0	99%	
HM056071.1	Aethina tumida isolate AustHV4c cytochrome oxidase subunit I gene,	1524	1524	95%	0.0	99%	
HM056070.1	Aethina tumida isolate AustHV4b cytochrome oxidase subunit I gene,	1524	1524	95%	0.0	99%	
HM056068.1	Aethina tumida isolate AustHV3b cytochrome oxidase subunit I gene,	1524	1524	95%	0.0	99%	

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GenBank

NCBI's GenBank database is a collection of publicly available annotated nucleotide sequences, including mRNA sequences with coding regions, segments of genomic DNA with a single gene or multiple genes, and ribosomal RNA gene clusters.

GenBank is specifically intended to be an archive of primary sequence data. Thus, to be included, the sequencing must have been conducted by the submitter. NCBI does some quality control checks and will notify a submitter if something appears amiss, but it does not curate the data; the author has the final say on the sequence and annotation placed in the GenBank record. Authors are encouraged to update their records with new sequence or annotation data, but in practice records are seldom updated.

BOLD Systems - Mozilla Firefox

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http://www.boldsystems.org/views/login.php#

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BOLD Systems

BARCODE OF LIFE DATA SYSTEMS v2.5

Advancing species identification and discovery through the analysis of short, standardized gene regions

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The Barcode of Life Data Systems (BOLD) is an online workbench that aids collection, management, analysis, and use of DNA barcodes. It consists of 3 components (MAS, IDS, and ECS) that each address the needs of various groups in the barcoding community.

MANAGEMENT & ANALYSIS

BOLD-MAS provides a repository for barcode records coupled with analytical tools. It serves as an online workbench for the DNA barcode community.

Username
Password
[Request a new user account](#)
[Forgot your username or password?](#)

IDENTIFICATION ENGINE

BOLD-IDS provides a species identification tool that accepts DNA sequences from the barcode region and returns a taxonomic assignment to the species level when possible.

EXTERNAL CONNECTIVITY

BOLD-ECS provides web developers and bioinformaticians the ability to build tools and workflows that can be integrated with the BOLD framework. BOLD-ECS supplies REST services that allows access to public sequence and specimen data. We welcome the addition of new analytical modules.

BARCODE COUNTS

Formally Described Species With Barcodes **79,151**

Total Barcode Records **1,008,300**

Source	Breakdown
GenBank	108,944
Canadian Centre	829,702
Others	69,654





BOLDSYSTEMS

BOLD 2.5 Release





Version 2.5, unveiled on Nov 11th 2009 at the Third International Barcoding of Life conference in Mexico City, provides new core functionality including support for multiple sequence markers per specimen and more complex workflows. Features include identification services for ITS, matK, and rbcL markers, comparative analytics, web services and a variety of convenience upgrades. A few are highlighted here:

- Accumulation curves** Explore diversity of species and sequences by site or higher level taxonomy.
- Multi-marker analysis** All analytical tools have been upgraded to support processing and visualization of all registered markers.
- Alignment browser** Quickly identify alignment errors and evaluate substitutions through the alignment browser which support visualization of amino translations of coding sequences.
- Web Services** A two phase data retrieval service based on Representational State Transfer (REST) is available at services.boldsystems.org to access and retrieve published data on BOLD in text, XML and JSON formats.


BARCODING CAMPAIGNS





   

BARCODING WEBSITES

Ratnasingham S, Hebert PDN (2007) **BOLD : The Barcode of Life Data System** Molecular Ecology Notes

 - Download PDF

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Identificazione ... presentazione - ... BOLD Systems - ... IT

3:49 PM Tuesday

BOLD Systems - Species Identification - Mozilla Firefox

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BOLD Systems - Species Identification

http://www.boldsystems.org/views/idrequest.php

aethina tumida

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aethina tumida SEARCH

BOLDSYSTEMS v2.5 Management & Analysis

BOLD - ID

Animal Identification [COI] Fungal Identification [ITS] Plant Identification [rbcL & matK]

The BOLD Identification System (IDS) for COI accepts sequences from the 5' region of the mitochondrial Cytochrome c oxidase subunit I gene and returns a species-level identification when one is possible. Further validation with independent genetic markers will be desirable in some forensic applications.

Historical Databases: [Jul-2011](#) [Jul-2010](#) [Jul-2009](#)

Search Databases:

- ☐ **All Barcode Records on BOLD (1,297,098 Sequences)**
Every COI barcode record on BOLD with a minimum sequence length of 500bp (warning: unvalidated library and includes records without species level identification). This includes many species represented by only one or two specimens as well as all species with interim taxonomy. This search only returns a list of the nearest matches and does not provide a probability of placement to a taxon.
- ☒ **Species Level Barcode Records (1,076,558 Sequences/102,856 Species/43,701 Interim Species)**
Every COI barcode record with a species level identification and a minimum sequence length of 500bp. This includes many species represented by only one or two specimens as well as all species with interim taxonomy.
- ☐ **Public Record Barcode Database (259,573 Sequences/34,884 Species/9,710 Interim Species)**
All published COI records from BOLD and GenBank with a minimum sequence length of 500bp. This library is a collection of records from the published projects section of BOLD.
- ☐ **Full Length Record Barcode Database (886,070 Sequences/93,151 Species/38,287 Interim Species)**
Subset of the Species library with a minimum sequence length of 640bp and containing both public and private records. This library is intended for short sequence identification as it provides maximum overlap with short reads from the barcode region of COI.

Enter sequence in fasta format:

```
tccttagcag gtatttcttc tatttttaggt gcagtaaatt ttattactac tgtaattaat
atgcgacct caggcataac ctttgatoga atacctttat ttgtttgagc tgtagtaatt
acagctatcc ttcttttact ttctattacct gtattagcag gagctattac tatactacta
acagatcgaa atctaatac tactttcttc gacctatcag gaggggggtga tccaatccta
taccacact tattttgatt cttgggtcac ccagaagttt atattttaat tctaccagga
tttgggtataa ttccacacat tattagacaa gaaagaggaa aaaaggaagc ctttggaact
ttaggaataa ttaacgcaat aatagcaatt ggtttattag gattttagt ttgagcacat
catatttta cagtaggaat agacgttgat actcgagcct atttcacttc tgcacaata
attattgctg ttcttactgg aattaaaatt tttagatgat tagctactct tcatggtaca
caaattactt acagccaggt aactctatga gcatttaggat ttgtattctt atttaccgta
ggtggattaa caggagtagt tctagctaac tcatctattg atattattct acatgatact
tactacgtag tagctcattt ccattatgta ttatctatag gagcagtatt tgcattata
gcgggatttg ttcaatgatt cccattaatt acaggattaa ctttaaatag aaattattta
aaaattcaat tctttgtaat atttattgga gtttaattaa cctttttccc acaacatttc
ttagggttaa gaggaatacc tcgacgatat tctgattac
```


BOLD Systems - Identification Result - Mozilla Firefox

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BOLD Systems - Identification Result x BOLD Systems - Taxonomy Browser x +

http://www.boldsystems.org/views/idsingleresult.php?display=99

MantisBT Inaz Communication S... RAGES WT2 Accedi a InfoView IZSLT - SIL Nilde Nucleotide BLAST: Se... Network Italiano per l... BOLD Systems - Speci... Barcode of Life Initiati... DP BoL Data Portal | Index >>

aethina concolor SEARCH

BOLDSYSTEMS v2.5 Management & Analysis

Specimen Identification Request

Search Request:
Type : COI SPECIES DATABASE

Search Result:
Identification Summary :

Taxonomic Level	Taxon Assignment	Probability of Placement (%)
phylum	Arthropoda	100
class	Insecta	100
order	Coleoptera	100
family	Nitidulidae	100
genus	Aethina	100
species	Aethina tumida murray	100

Distance Summary :

Similarity scores of the top 100 matches

A species level match could not be made, the queried specimen is likely to be one of the following :

- Aethina tumida murray
- Aethina tumida

Tree Based Identification

TOP 99 Matches :

Display option: default

Phylum	Class	Order	Family	Genus	Species	Specimen Similarity (%)
Arthropoda	Insecta	Coleoptera	Nitidulidae	Aethina	tumidamurray	100
Arthropoda	Insecta	Coleoptera	Nitidulidae	Aethina	tumida	99.24
Arthropoda	Insecta	Coleoptera	Nitidulidae	Aethina	tumida	99.24
Arthropoda	Insecta	Hymenoptera	Formicidae	Camponotus	MG062	91.11
Arthropoda	Insecta	Hymenoptera	Formicidae	Camponotus	MG047	90.91
Arthropoda	Insecta	Hymenoptera	Formicidae	Camponotus	DRQ03	90.91
Arthropoda	Insecta	Lepidoptera	Saturniidae	Hylesia	indurata	90.48
Arthropoda	Insecta	Lepidoptera	Praydidae	Prays	nephelomima	90.48
Arthropoda	Insecta	Lepidoptera	Depressariidae	Peritornenta	sp.ANIC4	90.48
Arthropoda	Insecta	Lepidoptera	Lymantriidae	Lymantria	monacha	89.74

Trova: Successivo Precedente Evidenzia: Maiuscole/minuscole

start 2 W 4 M... P... b... 2 S... M... IT 3:45 PM Thursday

Alcune identificazioni condotte presso l'IZSLT



EUROPA - Food Safety - Rapid Alert System for Food and Feed - (RASFF) - Introduction - Mozilla Firefox

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http://ec.europa.eu/food/food/rapidalert/index_en.htm

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cycle sequencing - Cerca con Google EUROPA - Food Safety - Rapid Ale... RASFF-portal RASFF-portal detail

RASFF

Rapid Alert System for Food and Feed

What's New?

RASFF annual report 2009 pdf

Press release: [RASFF - food safety remains a priority in the EU and beyond](#)

Frequently Asked Questions: [Rapid Alert System for Food and Feed: role and achievements](#)

1979-2009 RASFF celebrates its 30th anniversary.

Click [here](#) to read more about this event.

Press release: [The Rapid Alert System for Food and Feed more efficient than ever on its 30th birthday](#)

RASFF Portal database

On 16 July 2009, Commissioner for Health [Androulla Vassiliou](#) opened the RASFF Portal website and its new online searchable database of RASFF notifications. [This database replaces the weekly summary of notifications published on this web site](#). Users of the [RASFF Portal database](#) can now produce their own tables based on a multitude of criteria.

Welcome to the RASFF portal!

The Rapid Alert System for Food and Feed (RASFF) was put in place to provide food and feed control authorities with an effective tool to exchange information about measures taken responding to serious risks detected in relation to food or feed. This exchange of information helps Member States to act more rapidly and in a coordinated manner in response to a health threat caused by food or feed.

- [Read more about the legal basis of RASFF](#)
- [Who are the members of RASFF?](#)
- RASFF - Keeping an eye on your food - [Watch the video](#) en de fr
- International RASFF conference - 10 conclusions of Robert Madelin

Resources

- Press Releases
- Health & Consumer
- Voice Newsletter
- Publications

International Affairs

- Organisations
- Codex
- OIE
- WTO
- Import Conditions
- Pets and Animal Welfare
- Enlargement
- Agreements
- EU - Russia: SPS issues

FOOD AND FEED SAFETY

ANIMAL HEALTH AND WELFARE

PLANT HEALTH

FVO INSPECTIONS

start

4:06 PM Wednesday

RASFF-portal detail - Mozilla Firefox

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https://webgate.ec.europa.eu/rasff-window/portal/index.cfm?event=notificationDetail&NOTIF_REFERENCE=2009.0730

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Notification detail - 2009.0730

potentially toxic fish species (presence of *Lagocephalus* spp.) in frozen headless fish blocks from Spain

Reference : 2009.0730
Notification date : 09/06/2009
Last update : 16/06/2009
Notification type : food - alert - official control on the market
Action taken : product (to be) detained
Notification from : ITALY (IT)
Distribution status : distribution on the market (possible)
Product : frozen headless fish blocks
Product category : fish and fish products

Follow-up :

Reference	Follow-up from	Date	Follow-up type	Info
-----------	----------------	------	----------------	------

Hazards :

Substance / Hazard	Category	Analytical result	Units	Sampling date
potentially toxic fish species	biotoxins (other)	presence of <i>Lagocephalus</i> spp.		11/05/2009

Distributed to :

| ITALY |

Origin :

| SPAIN |

Close this window

start

4:04 PM Wednesday

Grazie per l'@ttenzione