

The European Commission's science and knowledge service

Joint Research Centre

MetScan

Novel nuclear barcode regions for the identification of flatfish species

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Knowledge for Health and Consumer Safety Unit
JRC Directorate F - Health, Consumers and Reference Materials





DG Joint Research Centre



Established in
1957



3000 staff
Almost 75% are scientists and researchers.



10
Directorates



>1000
Publications per year



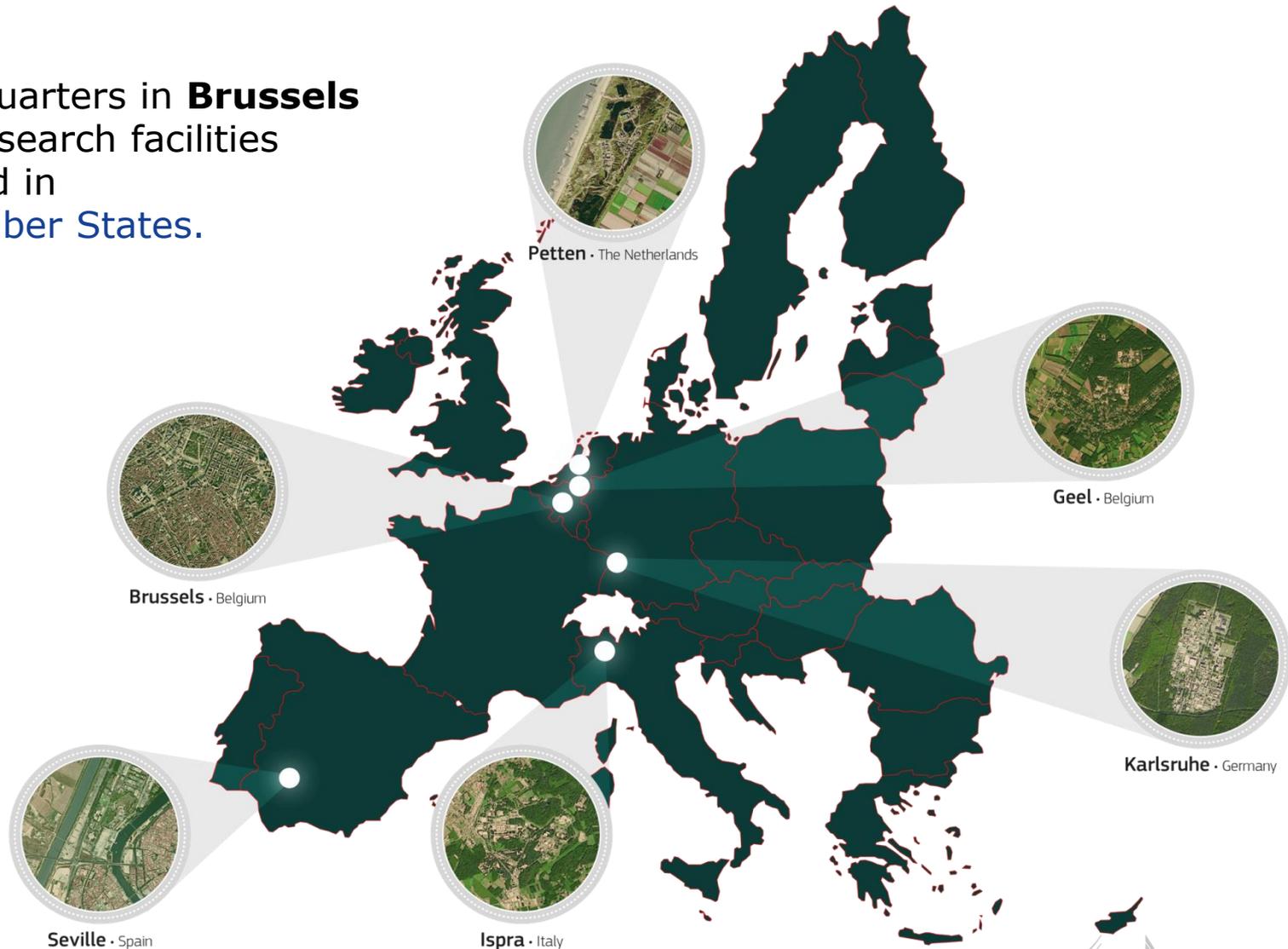
6
Locations in 5 Member States



42
Large scale facilities

The Joint Research Centre at a glance

Headquarters in **Brussels**
and research facilities
located in
5 Member States.





DG JRC's Vision:

"To play a central role in creating, managing and making sense of the collective scientific knowledge for better EU policy."

DG JRC's Mission:

"As the science and knowledge service of the Commission our mission is to support EU policies with independent evidence throughout the whole policy cycle."



DG JRC Role

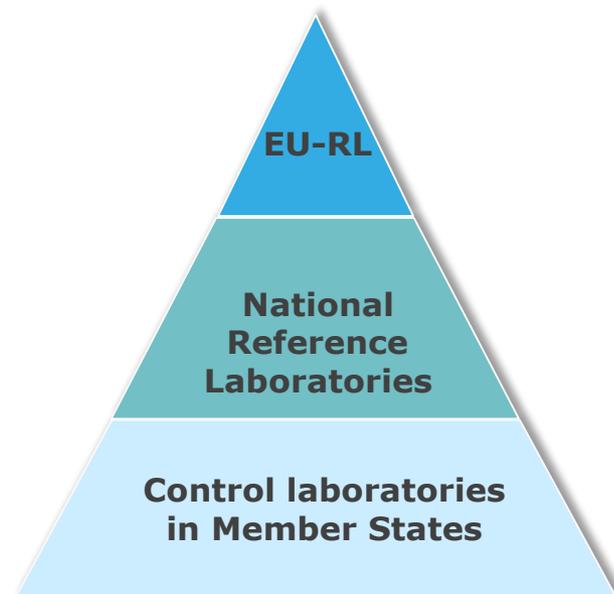
- **Independent** of private, commercial or national interests
- **Policy neutral**: has no policy agenda of its own
- *Transversal service - cuts across policy silos*
- **30%** of activities in **policy preparation**, **70%** in **implementation**
- **Expertise in a wide range of areas** from economics and financial analysis to energy and transport, health, environment and nuclear safeguards



The context

European Reference Laboratories hosted by the JRC

- Feed additives
- Food contact materials
- **GMOs**
- Heavy metals in feed and food
- Mycotoxins
- Polycyclic aromatic hydrocarbons and process contaminants





MetScan

In support to EU legislation on Genetically Modified Organisms (GMOs)

Under Directive 2001/18/EC and Regulation (EC) No 1829/2003

- Bioinformatics analyses of submitted DNA sequences in the GMO approval process
- Ad-hoc bioinformatics analyses to specific requests on GMO sequence data



MetScan

Is a Bioinformatics Pipeline to support EURL GMFF for in-silico analysis of GMO detection methods

Submission



The screenshot shows the MetScan web interface. At the top, there is a header with the European Union flag and the text 'JOINT RESEARCH CENTRE European Union Reference Laboratory for GM Food and Feed'. Below this is a navigation bar with 'MetScanUI', 'Application', 'Requests', and a 'log out (partial)' button. The main content area is titled 'New MetScan Request' and contains three input fields: 'Name', 'Comments', and 'Primer1'.

Processing



Report

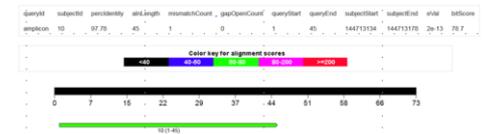
Dossier (EURL-VL-04-17) provided by Syngenta (2 x primer2)

Analyses results

Plant genomes BLAST

hits found:

Zea_mays.AGPv3.27.dna.toplevel



MetScan *Submission*



JOINT RESEARCH CENTRE

European Union Reference Laboratory for GM Food and Feed

MetScanUI

Application ▾

Requests ▾

log out puertao

New MetScan Request

* Name

Comments

* Primer1

* Primer2

Probe

* Amplicon

Test all primer combinations

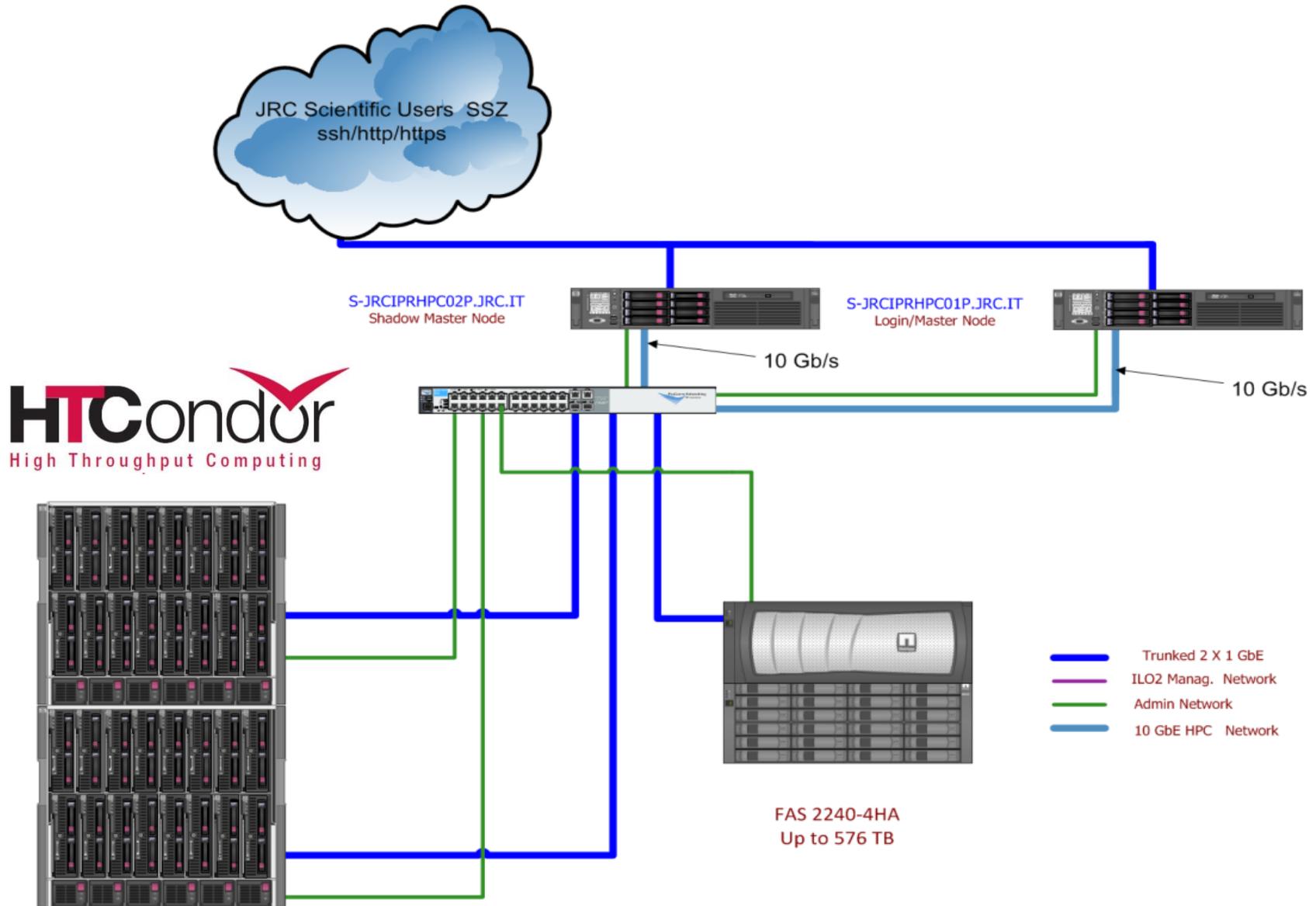
Cancel

Create Met scan request



European
Commission

MetScan Processing HTCondor



MetScan Report

 **JOINT RESEARCH CENTRE**
European Union Reference Laboratory for GM Food and Feed

MetScanUI Application Requests log out puorba

Name: Verification of MZIR098 Maize (SYNØØØ98-3) with 5- and 3-prime flanking sequences based on the Dossier (EURL-VL-04-17) provided by Syngenta (2 x primer2)

Comments:
Event-specific system for MZIR098 Maize

Token: msf6ORjD9Vq4uJF-B1qAkTcg

Primer1: ACACCGTTAGGCTAGTGCCAGT

Primer2: ACACCGTTAGGCTAGTGCCAGT

Probe: CAAGTGACAGCGAACGGAGCTGGTTT

Amplicon:
ATCTCAGACACCAACCGAGATCCAAGTGACAGCGAACGGAGCTGGTTTAACTGGCACTAGCCTAACGGTGT

Bioinformatics report for request: Verification of MZIR098 Maize (SYNØØØ98-3) with 5- and 3-prime flanking sequences based on the Dossier (EURL-VL-04-17) provided by Syngenta (2 x primer2)

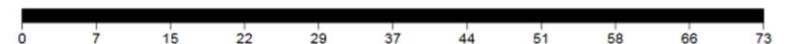
Analyses results

Plant genomes BLAST

hits found:

Zea_mays.AGPv3.27.dna.toplevel

queryId	subjectId	percIdentity	alnLength	mismatchCount	gapOpenCount	queryStart	queryEnd	subjectStart	subjectEnd	eVal	bitScore
amplicon	10	97.78	45	1	0	1	45	144713134	144713178	2e-13	78.7



DNA metabarcoding

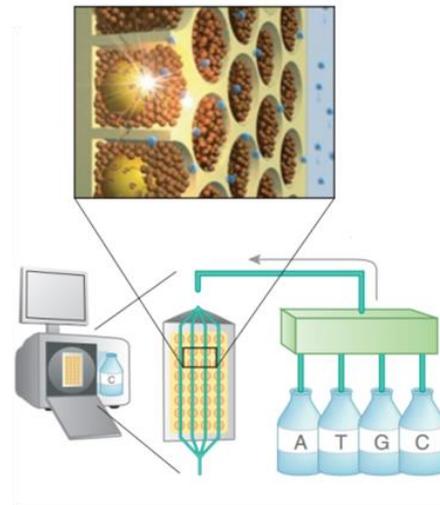


- Monitoring of the food chain to fight fraud and protect consumer health
- The difficulty in assessing highly processed food products consisting of a mixture of species in unknown quantities
- DNA barcoding involves the amplification, followed by sequencing, of specific DNA sequences

DNA metabarcoding



DNA extraction and
Barcode amplification



Next Generation
sequencing



Analysis

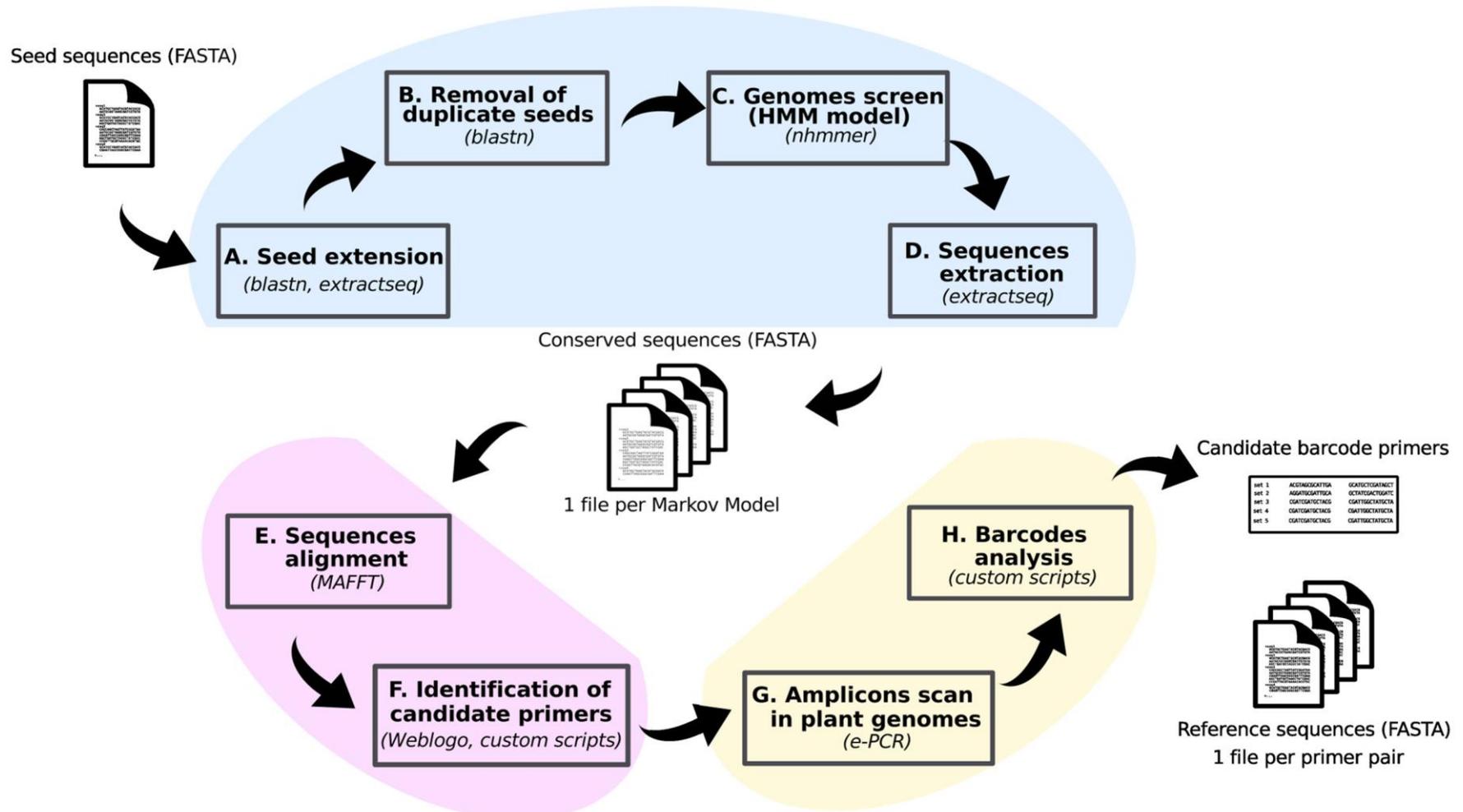


DNA metabarcoding allows the simultaneous analysis of mixtures of DNA barcodes and is currently mostly used for the analysis of microbiomes

Applied to food mixes, it would allow analyses of complex samples (e.g. mixes)

DNA metabarcoding Pipeline

A complex **pipeline** has been developed for detecting the nuclear barcode regions



DNA metabarcoding *Processing*

Seed sequences (FASTA)



A. Seed extension
(*blastn*, *extractseq*)



B. Removal of duplicate seeds
(*blastn*)



C. Genomes screen (HMM model)
(*nhmmer*)



D. Sequences extraction
(*extractseq*)

Conserved sequences (FASTA)

HTCCondor
High Throughput Computing



CERN Commodity File System

DNA metabarcoding

The pipeline has been published as proof of concept on plants



RESEARCH ARTICLE

Towards Plant Species Identification in Complex Samples: A Bioinformatics Pipeline for the Identification of Novel Nuclear Barcode Candidates

Alexandre Angers-Loustau^{*✉}, Mauro Petrillo[✉], Valentina Paracchini, Dafni M. Kagkli, Patricia E. Rischitor, Antonio Puertas Gallardo, Alex Patak, Maddalena Querci, Joachim Kreysa

Molecular Biology and Genomic Unit, Institute for Health and Consumer Protection, Joint Research Center, European Commission, Ispra, Italy

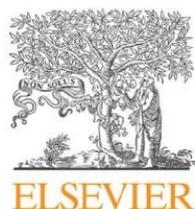
PLOS ONE | DOI:10.1371/journal.pone.0147692



Novel nuclear barcode regions for the identification of flatfish species

The steady increase of fish consumption makes necessary development of an efficient seafood traceability

Food Control 79 (2017) 297–308



Contents lists available at [ScienceDirect](#)

Food Control

journal homepage: www.elsevier.com/locate/foodcont



Novel nuclear barcode regions for the identification of flatfish species



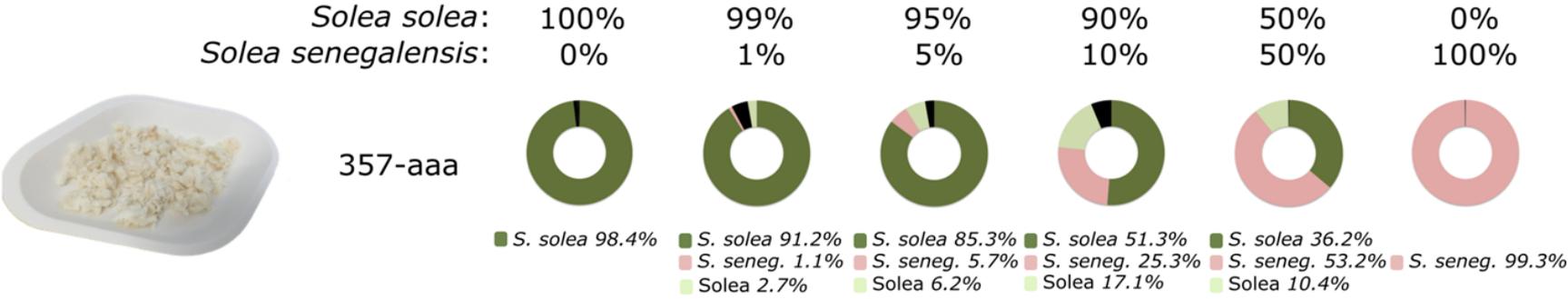
Valentina Paracchini ^a, Mauro Petrillo ^a, Antoon Lievens ^a, Antonio Puertas Gallardo ^a,
Jann Thorsten Martinsohn ^a, Johann Hofherr ^a, Alain Maquet ^b, Ana Paula Barbosa Silva ^b,
Dafni Maria Kagkli ^a, Maddalena Querci ^a, Alex Patak ^a, Alexandre Angers-Loustau ^{a,*}

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<https://doi.org/10.1016/j.foodcont.2017.04.009>

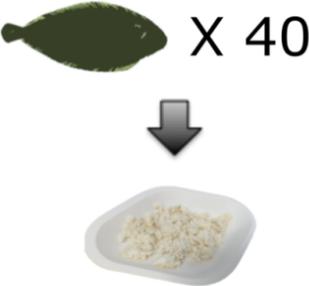


Flat fishes sample analysis

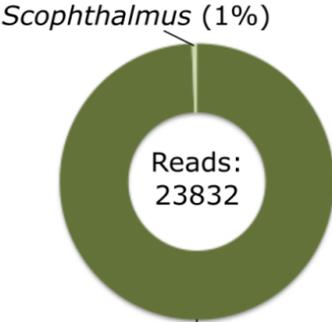


40 x *Solea solea*

40 x *Scophthalmus maximus*



357-aaa



357-aaa



19-aaa

Conclusions

HTCondor is at the core of the EU regulation for GMO authorizations.

HTCondor is giving support to EFSA.

HTCondor is a key player at the JRC research to fight against food fraud and species identification.



Thank you for your attention!



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