

*Scienze Forensi e criminalistica: nuove tecniche di  
analisi e applicazioni pratiche*

# **Le nuove frontiere dell'analisi del DNA a scopo forense**

A large, faint, light-gray watermark of the University of Florence logo is visible in the bottom left corner of the slide.

*Bologna, 22 novembre 2014*

*Dott.ssa Elena Pilli*

**1975**

Sanger, Maxam e Gilbert  
sviluppano il metodo di  
sequenziamento del DNA

**1953**

Watson e Crick  
scoprono il DNA

**1986**

Prima volta che il  
DNA viene usato in  
UK in un caso  
forense di doppio  
omicidio

**1991**

Vengono utilizzati  
per la prima volta  
gli STR

**1992**

Gli YSTR vengono descritti  
per la prima volta ed  
utilizzati in Germania in una  
violenza sessuale

**1992**

Sviluppo del 1° kit  
STR forense

**1993**

Primo caso di  
mass disaster

**1958**

Meselson e Stahl  
dimostrano come si  
replica il DNA

**1985**

Mullis inventa  
la PCR

**1988**

Primo kit commerciale  
forense basato sull'analisi  
degli SNPs del locus  
polimorfico HLA-DQA1

**1992**

Utilizzo dell'mtDNA  
per la prima volta in  
UK in un casework

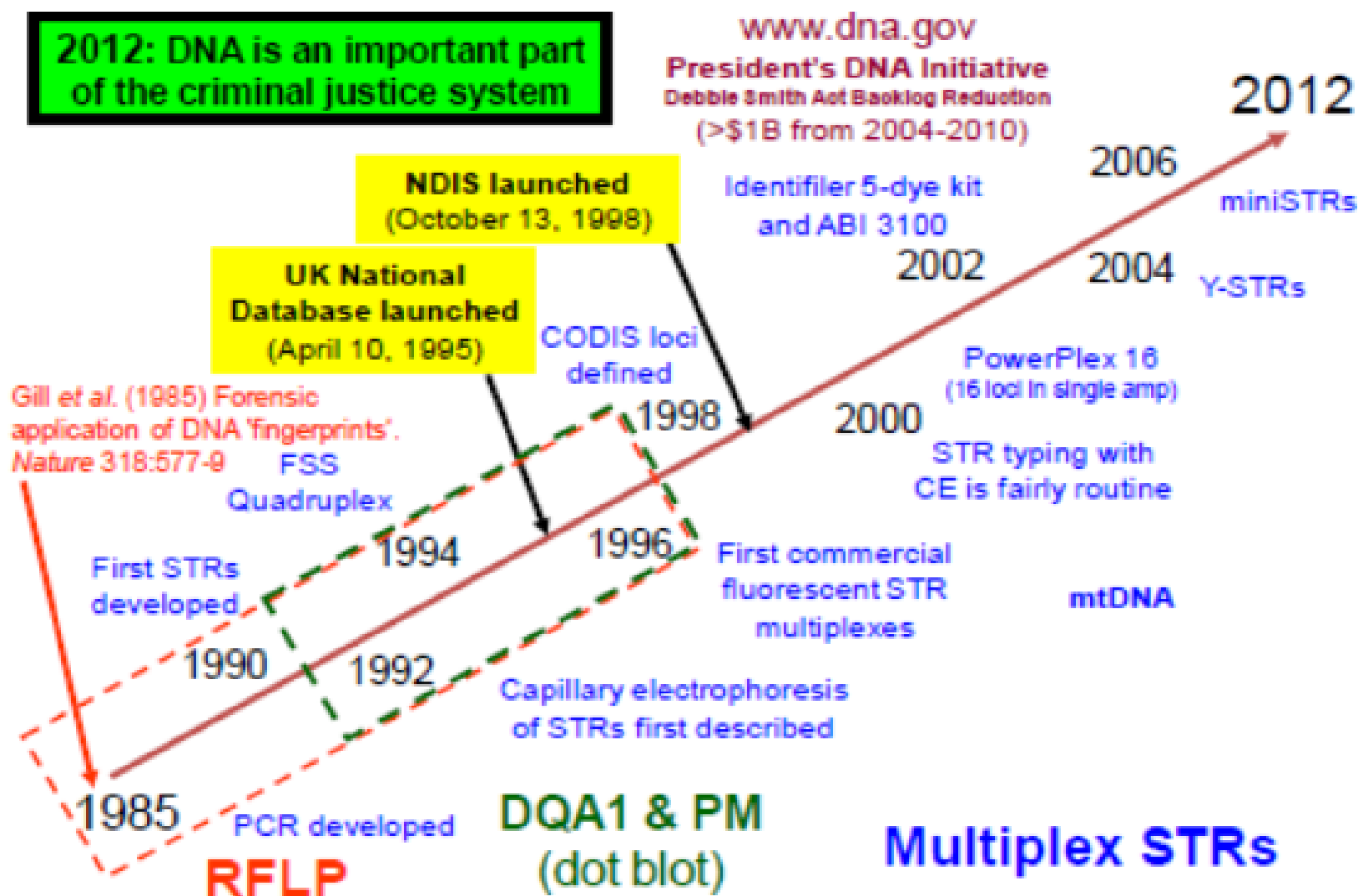
**Anni '80**

Jeffrey descrive la tecnica  
del DNA Typing



# L'evoluzione delle metodiche analitiche in genetica forense

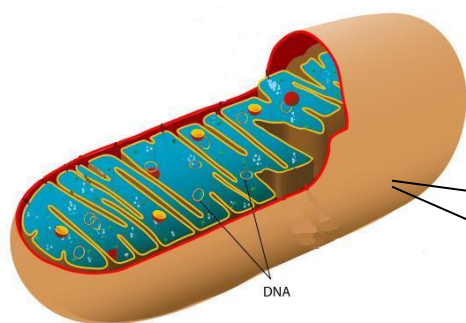
**2012: DNA is an important part of the criminal justice system**



# L'analisi tradizionale forense

- Il **genoma di ogni individuo è unico** (con l'eccezione dei gemelli omozigoti) e viene ereditato da ciascun genitore
- **Utilizzo dei marcatori** in grado di discriminare fra individui diversi
- La tipizzazione del DNA deve essere effettuata con **sistemi validati ed in maniera riproducibile**
- I test utilizzati, ad oggi, di routine in ambito forense, **non danno informazioni sui geni e poca o nessuna indicazione circa l'origine geografica, la predisposizione alle malattie e le caratteristiche fenotipiche**

# Genoma umano presente in una cellula

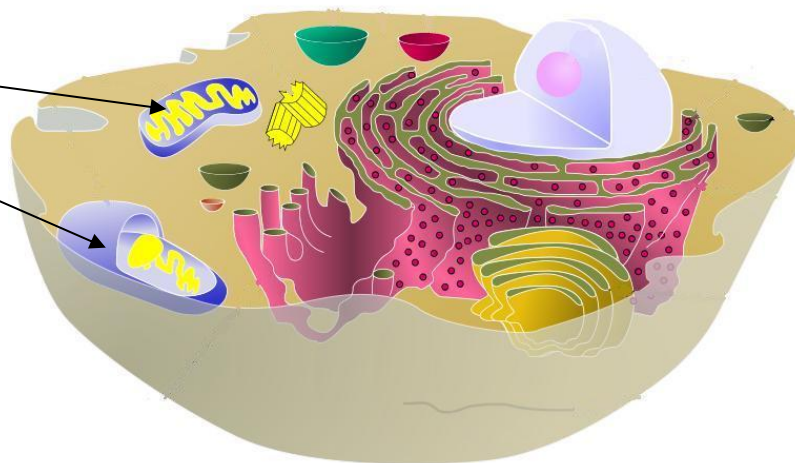


**Il mitocondrio contiene il  
DNA mitocondriale,  
centinaia copie per cellula**

**DNA Mitocondriale**  
(16,569 bp)

**Si eredita per linea  
materna**

**Nucleo contiene il dNA  
nucleare una copia per  
cellula**



**DNA nucleare**  
(3.2 miliardi bp)

**Si eredità per metà dalla  
madre e per metà dal padre**

# Tecnologia HID standardizzata

Estrazione  
DNA

Quantificazione  
RT-PCR

Amplificazione  
STR

Tipizzazione  
CE



# Marcatori genetici utilizzati in ambito forense

- *Short Tandem Repeats (STRs)*

*Sequenze ripetute di DNA non codificante che variano in lunghezza da individuo ad individuo*

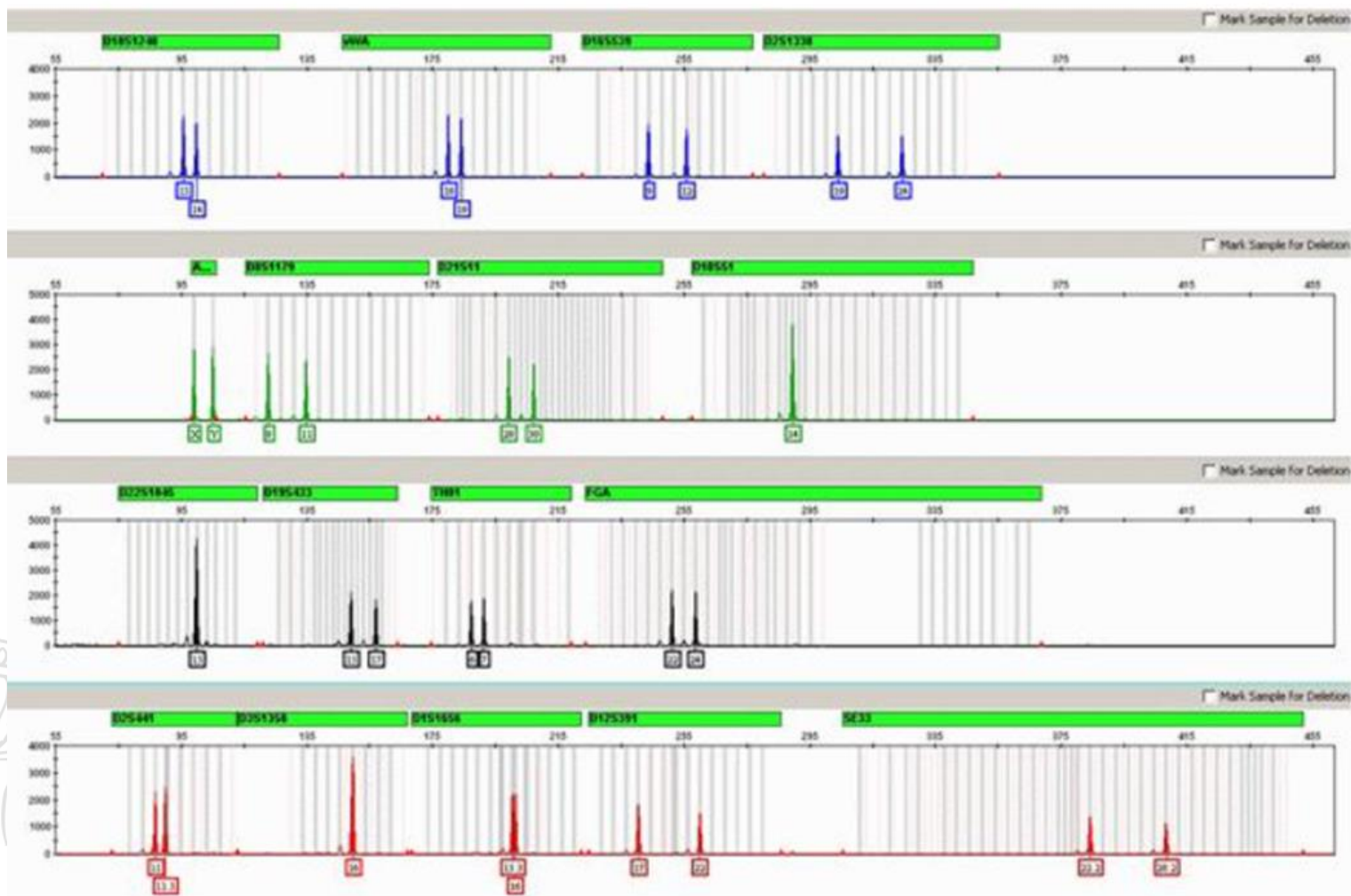
-----**(AATG)**(AATG)(AATG)-----

*3 repeats*

-----**(AATG)**(AATG)-----

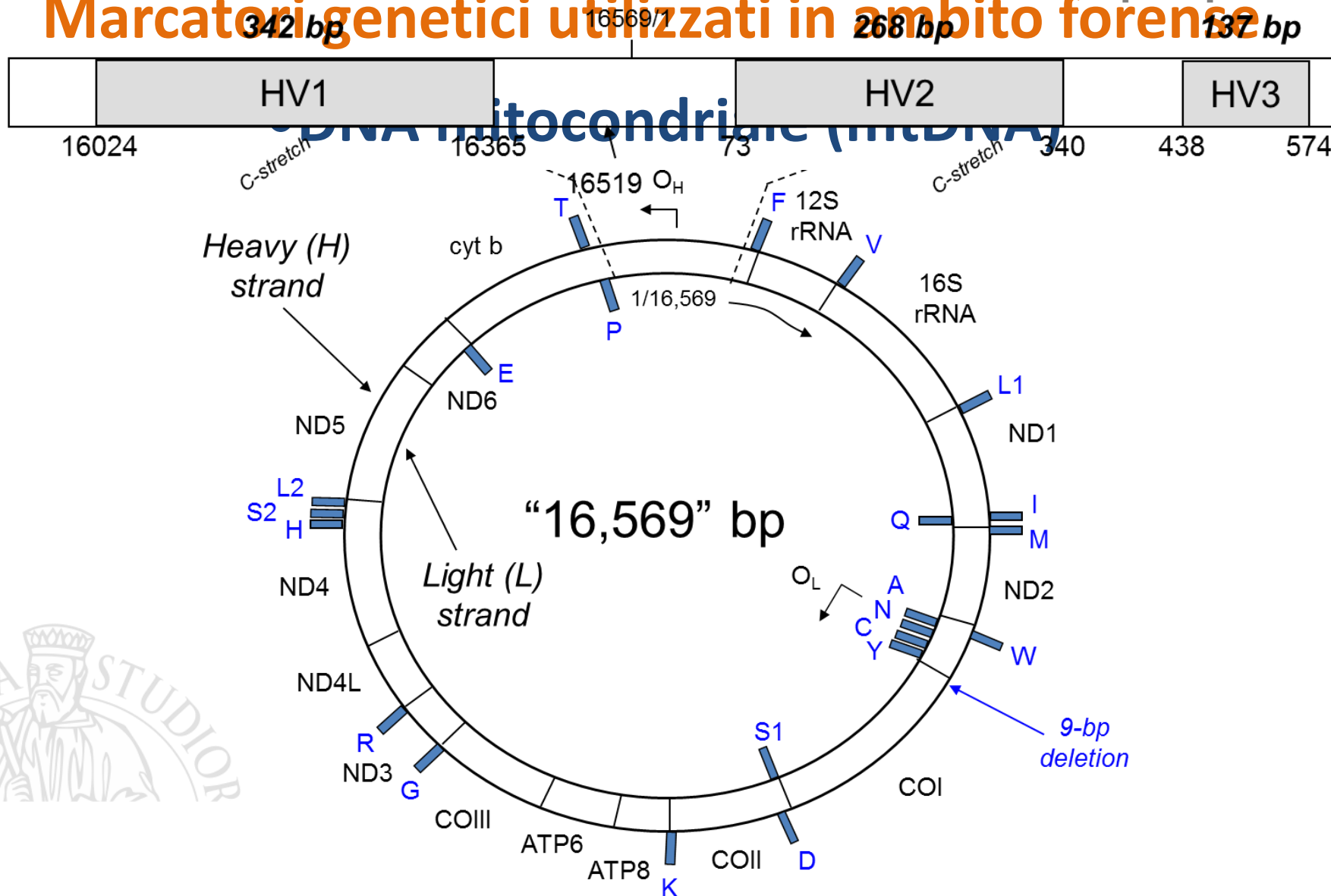
*2 repeats*







# Marcatori genetici utilizzati in ambito forense





Forensic Science International: Genetics 3 (2009) 149–153



ELSEVIER

Contents lists available at [ScienceDirect](http://www.sciencedirect.com)

## Forensic Science International: Genetics

journal homepage: [www.elsevier.com/locate/fsig](http://www.elsevier.com/locate/fsig)

## Mini-midi-mito: Adapting the amplification and sequencing strategy of mtDNA to the degradation state of crime scene samples

Cordula Berger, Walther Parson\*

*Institute of Legal Medicine, Innsbruck Medical University, Müllerstrasse 44, 6020 Innsbruck, Austria*

Int J Legal Med (2008) 122:385–388

DOI 10.1007/s00414-008-0227-5

## ORIGINAL ARTICLE

**‘Mitominis’: multiplex PCR analysis of reduced size amplicons for compound sequence analysis of the entire mtDNA control region in highly degraded samples**

Cordula Eichmann • Walther Parson

Pilli et al. *Investigative Genetics* 2014, **5**:7  
<http://www.investigativegenetics.com/content/5/1/7>



***Investigative  
Genetics***

**RESEARCH**

**Open Access**

# Pet fur or fake fur? A forensic approach

Elena Pilli<sup>1\*</sup>, Rosario Casamassima<sup>2</sup>, Stefania Vai<sup>1</sup>, Antonino Virgili<sup>3</sup>, Filippo Barni<sup>4</sup>, Giancarlo D'Errico<sup>4</sup>, Andrea Berti<sup>4</sup>, Giampietro Lago<sup>5</sup> and David Caramelli<sup>1</sup>

# Marcatori genetici utilizzati in ambito forense

- Single Nucleotide Polymorphisms (SNPs)

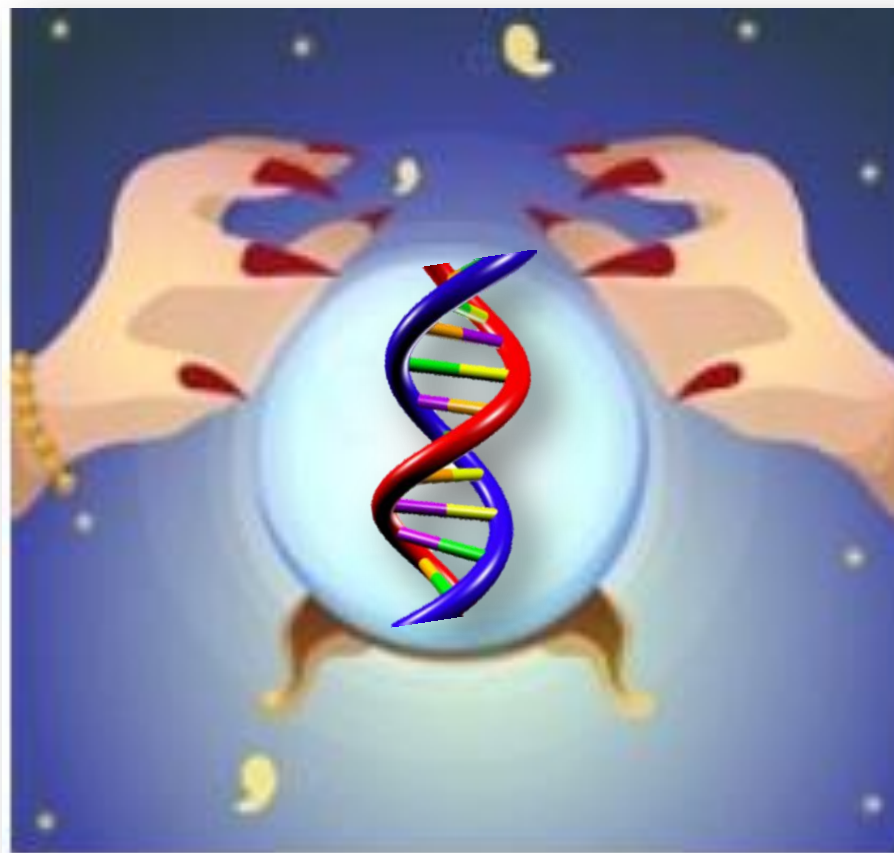
*Polimorfismi di sequenza*

-----AGACCTAGACATT-----  
-----AGATTTAGGCATT-----





# Le nuove frontiere del DNA a scopo forense



## Review

*Nature Reviews Genetics* **12**, 179-192 (March 2011) | doi:10.1038/nrg2952

[Corrected](#) online: 29 August 2012

There is a [Corrigendum \(1 October 2012\)](#) associated with this article.

### **Improving human forensics through advances in genetics, genomics and molecular biology**

Manfred Kayser<sup>1</sup> & Peter de Knijff<sup>2</sup> [About the authors](#)

top ↑

Forensic DNA profiling currently allows the identification of persons already known to investigating authorities. Recent advances have produced new types of genetic markers with the potential to overcome some important limitations of current DNA profiling methods. Moreover, other developments are enabling completely new kinds of forensically relevant information to be extracted from biological samples. These include new molecular approaches for finding individuals previously unknown to investigators, and new molecular methods to support links between forensic sample donors and criminal acts. Such advances in genetics, genomics and molecular biology are likely to improve human forensic case work in the near future.

# DNA altamente degradato

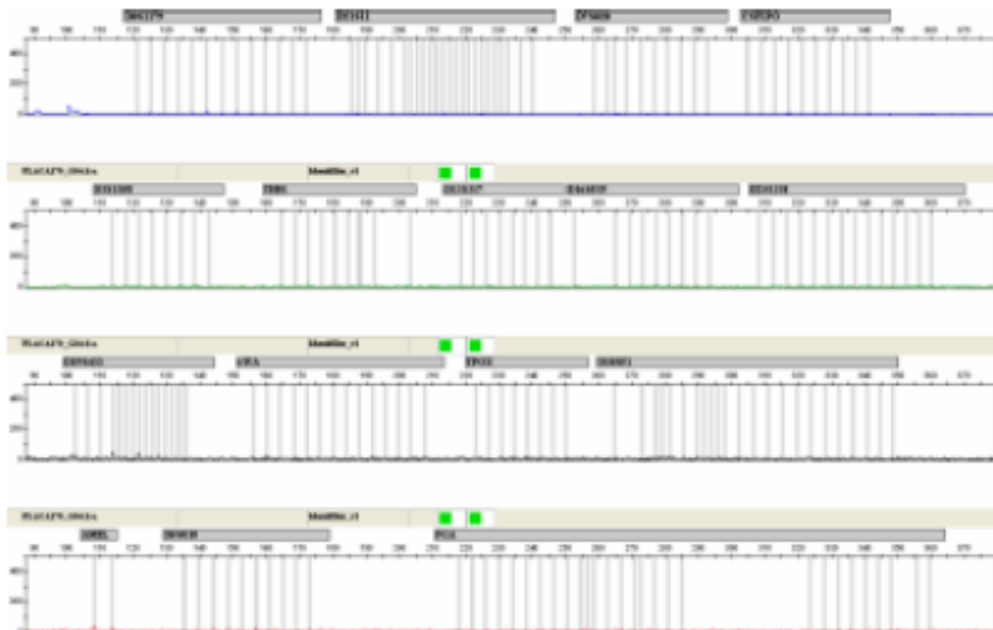


## SNP genotyping in an extreme degradation case

Corpse half buried in a forest for ten years

- Uncovered by a forest fire
- Calcinated remains

Identifiler success 0%









## Forensic Science International: Genetics

Volume 6, Issue 3, May 2012, Pages 341–349



### A new SNP assay for identification of highly degraded human DNA

A. Freire-Aradas<sup>a</sup>, M. Fondevila<sup>a</sup>, A.-K. Kriegel<sup>b</sup>, C. Phillips<sup>a</sup>  , P. Gill<sup>c, d</sup>, L. Prieto<sup>e</sup>, P.M. Schneider<sup>b</sup>,  
Á. Carracedo<sup>a</sup>, M.V. Lareu<sup>a</sup>

























## Forensic Science International: Genetics

Volume 6, Issue 4, July 2012, Pages 469–476



### Typing short amplicon binary polymorphisms: Supplementary SNP and Indel genetic information in the analysis of highly degraded skeletal remains

C. Romanini<sup>a</sup>  , M.L. Catelli<sup>a</sup>  , A. Borosky<sup>b</sup>  , R. Pereira<sup>d</sup>  , M. Romero<sup>a</sup>  , M. Salado Puerto<sup>c</sup>  ,  
 , C. Phillips<sup>e</sup>  , M. Fondevila<sup>e</sup>  , A. Freire<sup>e</sup>  , C. Santos<sup>e</sup>  , A. Carracedo<sup>e</sup>  , M.V. Lareu<sup>e</sup>  , L.  
Gusmao<sup>d</sup>, C.M. Vullo<sup>a, b</sup>  

# Predizione dell'origine geografica





## Forensic Science International: Genetics

Volume 7, Issue 1, January 2013, Pages 63–74



## Forensic Science International: Genetics

Volume 11, July 2014, Pages 13–25



### Revision of the SNPforID 34-plex forensic ancestry test: Assay enhancements, standard reference sample genotypes and extended population studies

M. Fondevila<sup>a</sup>, C. Phillips<sup>a</sup>, , , C. Santos<sup>a</sup>, A. Freire Aradas<sup>a</sup>, P.M. Vallone<sup>b</sup>, J.M. Butler<sup>b</sup>, M.V. Lareu<sup>a</sup>, Á. Carracedo<sup>a</sup>

### Building a forensic ancestry panel from the ground up: The EUROFORGEN Global AIM-SNP set

C. Phillips<sup>a</sup>, , , W. Parson<sup>b,c</sup>, B. Lundsberg<sup>d</sup>, C. Santos<sup>a</sup>, A. Freire-Aradas<sup>a</sup>, M. Torres<sup>e</sup>, M. Eduardoff<sup>b</sup>, C. Børsting<sup>d</sup>, P. Johansen<sup>d</sup>, M. Fondevila<sup>a</sup>, N. Morling<sup>d</sup>, P. Schneider<sup>f</sup>, the EUROFORGEN NoE Consortium, Á. Carracedo<sup>a,e,g</sup>, M.V. Lareu<sup>a</sup>



BMC Genomics. 2014; 15(1): 543.

Published online Jun 30, 2014. doi: [10.1186/1471-2164-15-543](https://doi.org/10.1186/1471-2164-15-543)

PMCID

### Evaluating the accuracy of AIM panels at quantifying genome ancestry

Jacobo Pardo-Seco<sup>✉</sup>, Federico Martín-Torres, and Antonio Salas<sup>✉</sup>

[Author information](#) [Article notes](#) [Copyright and License information](#)

# ELECTROPHORESIS

## Research Article

### Development of a novel forensic STR multiplex for ancestry analysis and extended identity testing

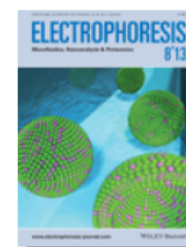
Chris Phillips<sup>1,†,\*</sup>, Luis Fernandez-Formoso<sup>1,†</sup>, Miguel Gelabert-Besada<sup>1</sup>, Manuel Garcia-Magariños<sup>2</sup>, Carla Santos<sup>1</sup>, Manuel Fondevila<sup>1</sup>, Ángel Carracedo<sup>1,3</sup> and Maria Victoria Lareu<sup>1</sup>

Article first published online: 18 MAR 2013

DOI: 10.1002/elps.201200621

© 2013 WILEY-VCH Verlag GmbH & Co. KGaA, Weinheim

## Issue



**ELECTROPHORESIS**  
Volume 34, Issue 8, p  
1151–1162, April 2013

# Predizione delle caratteristiche fenotipiche

Irisplex



Hirisplex



# Classificazione degli SNPs

Table 2

Categories for SNP markers classified by Ken Kidd

---

*Individual Identification SNPs (IISNPs)*: SNPs that collectively give very low probabilities of two individuals having the same multi-locus genotype

*Ancestry Informative SNPs (AISNPs)*: SNPs that collectively give a high probability of an individual's ancestry being from one part of the world or being derived from two or more areas of the world

*Lineage Informative SNPs (LISNPs)*: Sets of tightly linked SNPs that function as multi-allelic markers that can serve to identify relatives with higher probabilities than simple bi-allelic SNPs

*Phenotype Informative SNPs (PISNPs)*: SNPs that provide a high probability that the individual has particular phenotypes, such as a particular skin color, hair color, eye color, etc.

---





**Presente**

**Identificazione tramite campione di  
confronto**

**Futuro**

**«Identikit» genetico della traccia**



# **Next generation sequencing (NGS) or high-throughput sequencing**

**Rappresenta una nuova tecnica di sequenziamento che permette di analizzare in maniera massiva, in parallelo, un grande numero di ampliconi in una singola corsa con estrema accuratezza e altissima sensibilità.**



# Cosa si intende per multiplexing?

- Un metodo che permette di analizzare più campioni biologici in una singola corsa
- Ciascun campione viene «etichettato» con sequenze specifiche in modo da riconoscerlo rispetto agli altri
- Un volta aggiunta questa «etichettatura» può essere fatto un pool di diversi campioni
- I dati della corsa possono così essere analizzati e ricondotti a quello specifico campione





# Perché NGS in ambito forense?

- Ottenere dati utili all'identificazione in campioni low template (meno di 100 pg)
- Migliorare l'informazione che si può essere ottenuta da campioni complessi (es. misture/campioni degradati)
- Aumentare a quantità di informazione che posso ottenere da un campione ignoto



2009

# Primi approcci alla tecnologia NGS in forense

## 1. Introduction

The molecular analysis of blood or biological stains at crime scenes is an important tool in forensic science [1] and [2]. However, the quantity and quality of extractable nucleic acids are often too low to allow the necessary extensive analyses, e.g. species and/or individual identification, environmental composition of the stain, and DNA profiling [3]. The analysis of nuclear single copy genes and the detection of microsatellites usually require relatively large amounts of high quality DNA [4]. Under standard conditions (approximately 28-cycle PCR) at least 100–500 pg of DNA with fragment lengths of more than 150–200 bp have to be available. The application of post-PCR purification increases the sensitivity of low-template DNA down to approximately 20 pg of DNA [4] and [5]. A plethora of other sophisticated methods have been developed and used to increase the sensitivity and specificity of DNA and RNA analysis in forensic medicine [6] and [7]. Especially the recent development of miniaturized biological and chemical analytical devices has opened new possibilities in the analysis of minute amounts of templates [8] and [9]. An extremely important tool that has been introduced into forensic science recently, is the whole genome amplification (WGA) which reduces the requirement of template DNA to almost less than a single cell, i.e. 5

# 454-Roche



## A NEW ULTRADEEP LT (LOW TEMPLATE) DNA PROFILING APPROACH BASED ON AN EMULSION-BASED CLONAL AMPLIFICATION OF AN STRS MULTIPLEX PCR PRODUCT FOLLOWED BY MASSIVE PYROSEQUENCING

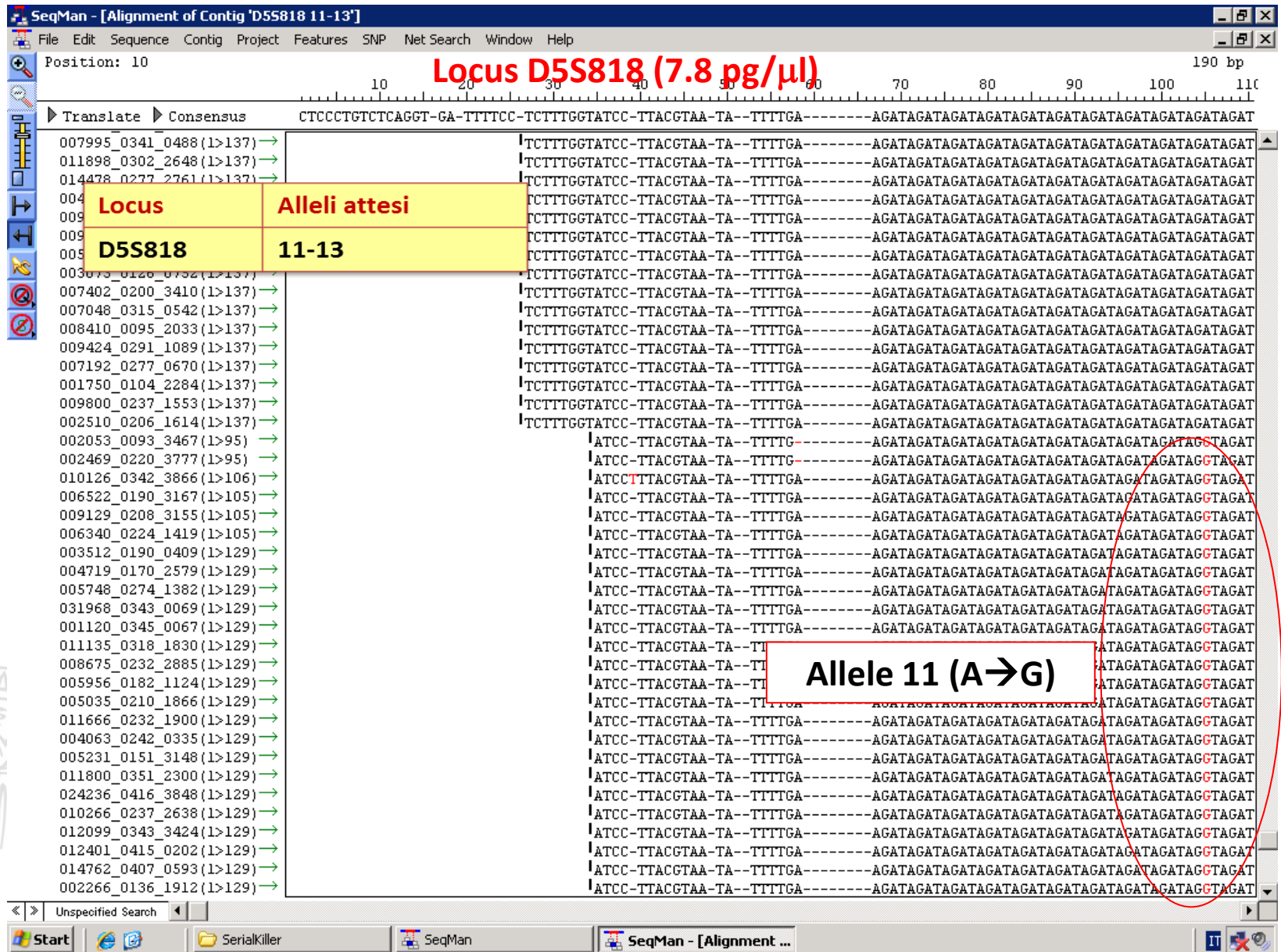
Berti, A.<sup>1</sup>, Barni, F.<sup>1</sup>, Pilli, E.<sup>2</sup>, Rizzi, E.<sup>3</sup>, Pianese, A.<sup>1</sup>, Corti, G.<sup>3</sup>, De Bellis, G.<sup>3</sup>, Caramelli, D.<sup>2</sup>

<sup>1</sup> Reparto Carabinieri Investigazioni Scientifiche di Roma, Sezione di Biologia, Rome, Italy

<sup>2</sup> Dipartimento di Biologia Evoluzionistica, Laboratori di Antropologia, Università di Firenze, Via del Proconsolo 12, 50122 Florence, Italy

<sup>3</sup> Istituto di Tecnologie Biomediche (ITB), Consiglio Nazionale delle Ricerche (CNR), Via F.lli Cervi 93, 20090 Segrate, Milan, Italy

Due to an insufficient quantity and quality of the template DNA and often to the presence of PCR inhibitory compounds, frequently, evidentiary items collected at the crime scene do not allow to obtain complete or even partial DNA interpretable profiles using standard forensic STRs DNA analyses. This has led to introduce several modifications to the traditional STRs genotyping methodologies known as LT DNA profiling which often allow to recover all the genetic information even from a trace containing DNA at or beneath the stochastic threshold. Nonetheless LT DNA profiling suffers of several disadvantages known as stochastic sampling effects (exaggerated stutter, relevant peak height imbalance, allelic drop-out and allelic drop-in).



# Tecnologie disponibili

life  
technologies



**Ion Personal Genome Machine® (PGM™)  
System**

illumina®



**MiSeq Desktop Sequencer**

# Applicazioni disponibili



ANALYZE  
HIGHLY DEGRADED  
OR TRACE DNA

.....

Identity-informative  
solution



GENERATE  
MORE INVESTIGATIVE  
LEADS

.....

Ancestry-informative  
solution





# Altre applicazioni forensi



ANALYZE  
HIGHLY DEGRADED  
OR TRACE DNA

.....  
Identity-informative  
solution



GENERATE  
MORE INVESTIGATIVE  
LEADS

.....  
Ancestry-informative  
solution



ANALYZE  
FAMILIAL AND  
KINSHIP CASES

.....  
Lineage-informative  
solution



ANALYZE  
REMAINS OR  
MISSING PERSONS

.....  
Mitochondrial  
solution



ANALYZE DNA  
MIXTURES MORE  
EFFICIENTLY

.....  
Next-generation  
technology



Human Identification Solutions (HIDS): Innovations and Perspectives Conference - Find out more >

## HID-Ion AmpliSeq™ Identity Panel

◀ PGM for Forensics

HID-Ion AmpliSeq™ Ancestry  
Panel

HID-Ion AmpliSeq™ Identity  
Panel

Analyze highly degraded  
or trace DNA



The HID-Ion AmpliSeq™ Identity Panel is a ready-to-use panel that includes 124 autosomal markers, and provides discrimination of individuals similar to STR genotype match probabilities used by forensic analysts (between  $1 \times 10^{-31}$  and  $6 \times 10^{-35}$ ). It's the newer version of our previous HID-Ion AmpliSeq™ Identity Community Panel.



## Single nucleotide polymorphism typing with massively parallel sequencing for human identification

Seung Bum Seo • Jonathan L. King •  
David H. Warshauer • Carey P. Davis • Jianye Ge •  
Bruce Budowle

Received: 5 April 2013 / Accepted: 21 May  
© Springer-Verlag Berlin Heidelberg 2013

Forensic Science International: Genetics 14 (2015) 50–60



ELSEVIER

Contents lists available at ScienceDirect

Forensic Science International: Genetics

journal homepage: [www.elsevier.com/locate/fsig](http://www.elsevier.com/locate/fsig)



### A SNaPshot of next generation sequencing for forensic SNP analysis

R. Daniel <sup>a,\*</sup>, C. Santos <sup>b</sup>, C. Phillips <sup>b</sup>, M. Fondevila <sup>b</sup>, R.A.H. van Oorschot <sup>a</sup>, Á. Carracedo <sup>b,c,d</sup>,  
M.V. Lareu <sup>b</sup>, D. McNevin <sup>e</sup>

<sup>a</sup> Office of the Chief Forensic Scientist, Forensic Services Department, Victoria Police, Australia

<sup>b</sup> Forensic Genetics Unit, Institute of Forensic Science "Luis Concheiro", University of Santiago de Compostela, Spain

<sup>c</sup> CIBERER, Genomic Medicine Group, University of Santiago de Compostela, Spain

<sup>d</sup> Center of Excellence in Genomic Medicine Research, King Abdulaziz University, Jeddah, Saudi Arabia

<sup>e</sup> National Centre for Forensic Studies, University of Canberra, Australia

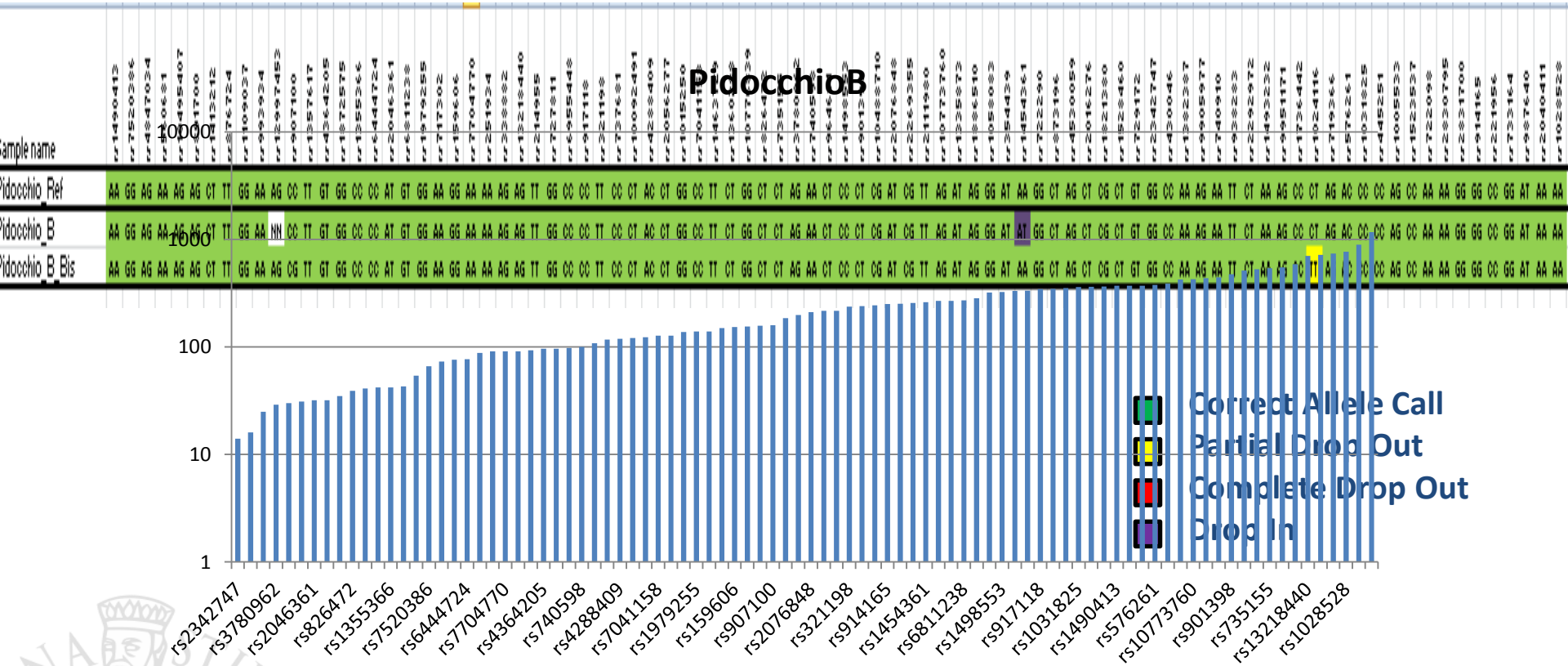


# Entomogenetica



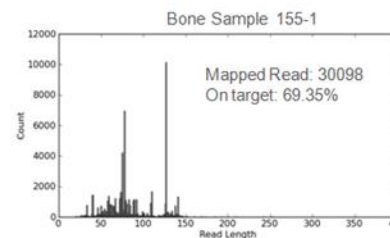
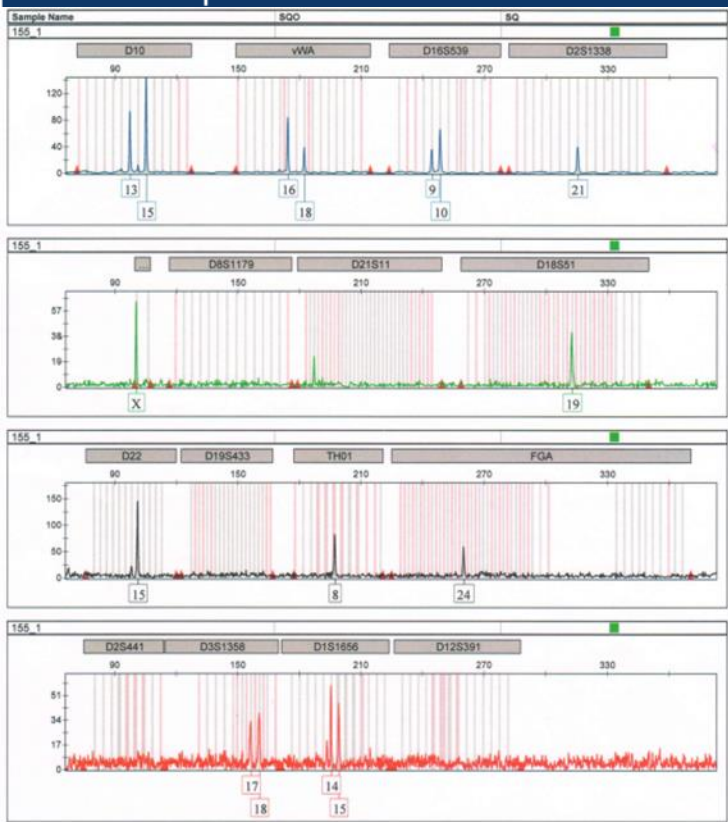
Well	Sample	Target	Task	Quantity	Quantity (Mean)	Quantity (Std Dev)	C <sub>T</sub>	C <sub>T</sub> (Mean)	C <sub>T</sub> (Std Dev)
A3	Pidocchio_	T.IPC	Unk				26.8092	27.11	0.43
A3	Pidocchio_	T.Large Autosomal	Unk	0.0069	0.01	0.00	31.9014	31.87	0.04
A3	Pidocchio_	T.Small Autosomal	Unk	0.0128	0.01	0.00	33.3061	33.69	0.54
A3	Pidocchio_	T.Y	Unk				Undetermined		
B3	Pidocchio_	T.IPC	Unk				27.4106	27.11	0.43
B3	Pidocchio_	T.Large Autosomal	Unk	0.0072	0.01	0.00	31.8478	31.87	0.04
B3	Pidocchio_	T.Small Autosomal	Unk	0.0073	0.01	0.00	34.0688	33.69	0.54
B3	Pidocchio_	T.Y	Unk				Undetermined		





Sample Name	Target Name	Ct Mean	Quantity Mean	Conc pg/ul	Degradation Index Mean	Vol Library	Q library(pg)
Ardeatine 155	T.Small Autosomal	35,80	0,0031	3,11	4,36	6	18,66
Ardeatine 155-1	T.Small Autosomal	35,67	0,0033	3,34	39,84	6	20,06
Ardeatine 264	T.Small Autosomal	35,58	0,0036	3,56	4,89	6	21,38
Ardeatine 264-1	T.Small Autosomal	38,03	0,0007	0,67	4,88	6	4,03
Ardeatine 98	T.Small Autosomal	34,76	0,0063	6,31	78,67	6	37,87
Ardeatine 98-1	T.Small Autosomal	36,70	0,0016	1,64	2,56	6	9,86
Sangue 1	T.Small Autosomal	34,95	0,0056	5,59	12,85	6	33,56
Sangue 3	T.Small Autosomal	39,24	0,0003	0,30		6	1,80
Dente 1	T.Small Autosomal	28,02	0,7137	713,65	1,44	1	700,00
Dente 2	T.Small Autosomal	37,60	0,0009	0,95	3,99	6	5,69

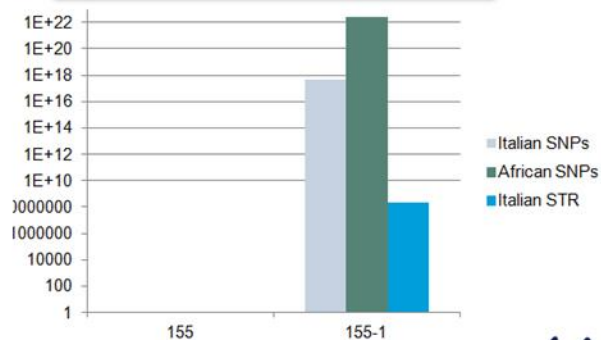




66 SNPs Extraction 1 Replicate 1  
71 SNPs Extraction 1 Replicate 2

0 SNPs Extraction 2 Replicate 1  
0 SNPs Extraction 2 Replicate 2

46 consensus SNPs



Sample name	Barcode	...
Ardestina_155	...	...
Ardestina_155-1	...	...
Ardestina_264	...	...
Ardestina_264-1	...	...
Ardestina_90	...	...
Ardestina_90-1	...	...
Dante_1	...	...
Dante_2	...	...
Sanqueto Traccia_1	...	...
Sanqueto Traccia_2	...	...



## HID-Ion AmpliSeq™ Ancestry Panel

◀ PGM for Forensics

**HID-Ion AmpliSeq™  
Ancestry Panel**

HID-Ion AmpliSeq™ Identity  
Panel

Generate more  
investigative leads



The HID-Ion AmpliSeq™ Ancestry Panel is a ready-to-use panel that includes 165 autosomal markers. Used with multiplex PCR and next-generation sequencing technologies, it can provide biogeographic ancestry information to help guide your investigation process.

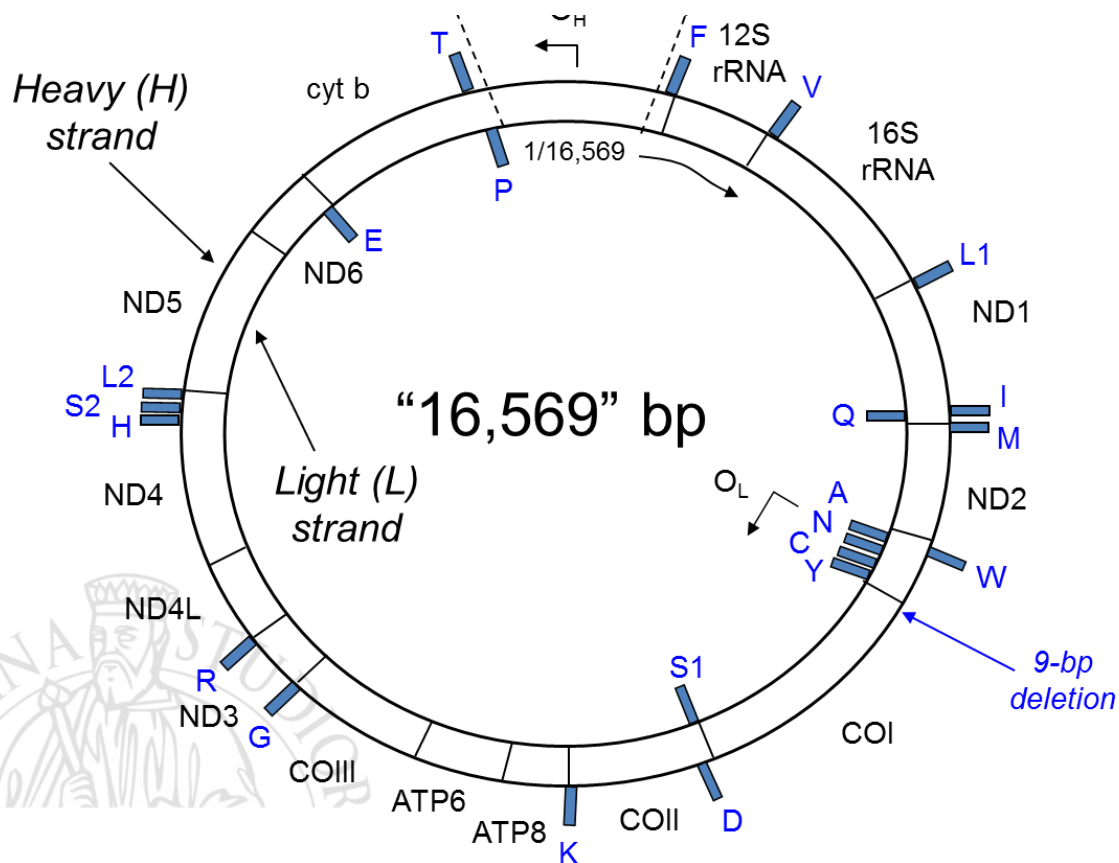
# Informazioni sull'origine geografica

## Casi forensi di routine



## Casi di sicurezza nazionale

# Marcatore mitocondriale





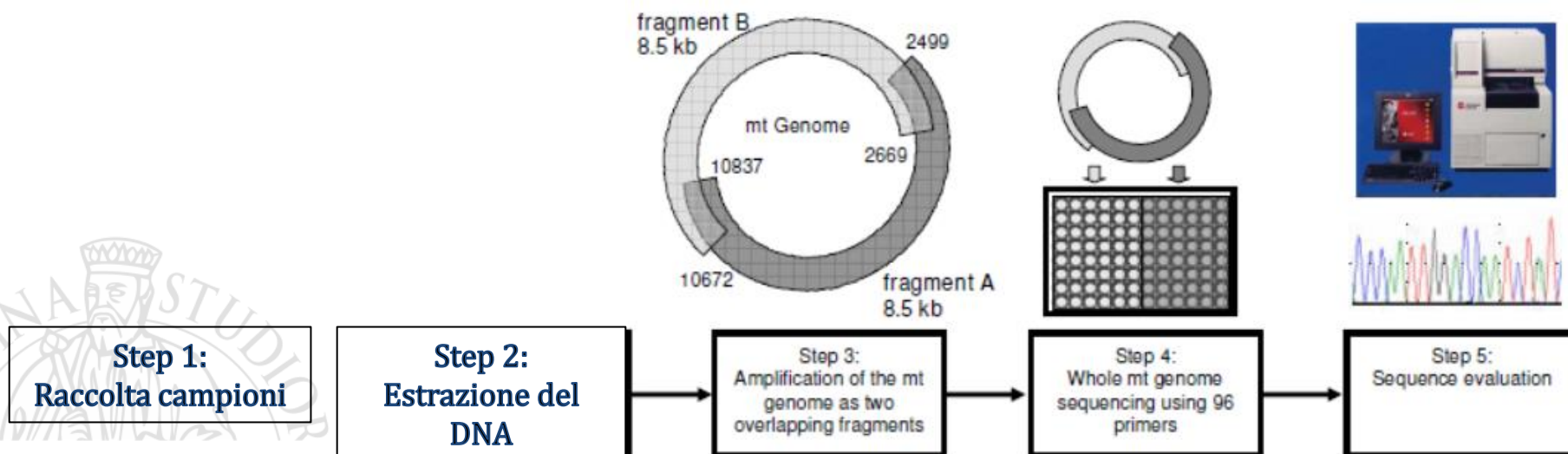
# BMC Genomics

Methodology article

**Open Access**

## Sequencing strategy for the whole mitochondrial genome resulting in high quality sequences

Liane Fendt<sup>1</sup>, Bettina Zimmermann<sup>1</sup>, Martin Daniaux<sup>2</sup> and Walther Parson<sup>\*1</sup>



# Altre applicazioni *non-human DNA*



## 1. Introduction

The molecular analysis of blood or biological stains at crime scenes is an important tool in forensic science [1] and [2]. However, the quantity and quality of extractable nucleic acids are often too low to allow the necessary extensive analyses, e.g. species and/or individual identification, environmental composition of the stain, and DNA profiling [3]. The analysis of nuclear single copy genes and the detection of microsatellites usually require relatively large amounts of high quality DNA [4]. Under standard conditions (approximately 28-cycle PCR) at least 100–500 pg of DNA with fragment lengths of more than 150–200 bp have to be available. The application of post-PCR purification increases the sensitivity of low-template



ELSEVIER

Contents lists available at ScienceDirect

## Forensic Science International

journal homepage: [www.elsevier.com/locate/forsciint](http://www.elsevier.com/locate/forsciint)



### The environmental biological signature: NGS profiling for forensic comparison of soils



S. Giampaoli<sup>a</sup>, A. Berti<sup>b</sup>, R.M. Di Maggio<sup>c</sup>, E. Pilli<sup>d</sup>, A. Valentini<sup>e</sup>, F. Valeriani<sup>a</sup>,  
G. Gianfranceschi<sup>a</sup>, F. Barni<sup>b</sup>, L. Ripani<sup>b</sup>, V. Romano Spica<sup>a,f,\*</sup>

<sup>a</sup> University of Rome "Foro Italico", Department of Movement, Human and Health Sciences, Public Health Unit, Piazza Lauro De Bosis, 6, 00135 Rome, Italy

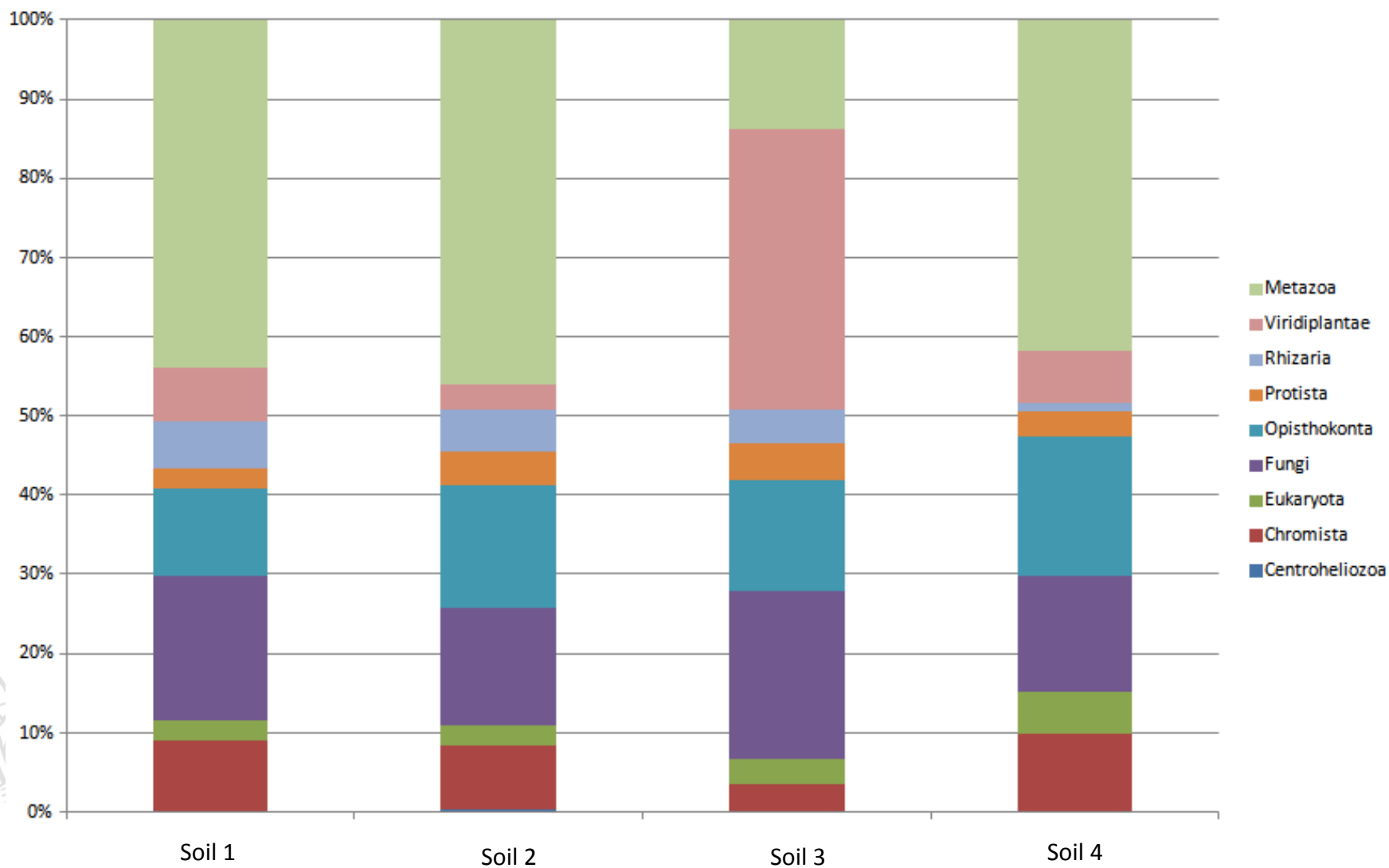
<sup>b</sup> Carabinieri, Reparto Investigazioni Scientifiche di Roma, Viale di Tor di Quinto, 119, 00191 Roma, Italy

<sup>c</sup> Geoscienze Forensi Italia<sup>®</sup>, Viale Mediterraneo 77, 00122 Rome, Italy

<sup>d</sup> Department of Biology, University of Florence, Via del Proconsolo 12, 50122 Florence, Italy

<sup>e</sup> Spygen, Savoie Technolac, Bâtiment Koala, 17, rue du Lac Saint-André, BP 274, 73375 Le Bourget-du-Lac Cedex, France

<sup>f</sup> MDD University Spin off, Viterbo, Italy





L'unica specie autoctona in Italia è *Heder helix*, rampicante sempreverde, tipica dei boschi freschi e umidi.



*Alnus* è un genere di piante della famiglia delle *Betulaceae* che comprende alcune specie comunemente note come ontani.



Il ceratofillo comune è una pianta acquatica



Quercia



Millefoglio d'acqua



Felci

Taxon	Rank	G	D	LAGO
Aizoaceae	family	44		
Chenopodium	genus		229	
Apiaceae	family		106	
Araliaceae	family	63		2124
Asteraceae	family	102	1385	
	genus	17	57	
	genus			2956
	species	178	96	
	family	53		
Pol	species	848		
Cer	species			601
	family	128	71	
	family	236	92	
Dryopteridaceae	family			825
Euphorbia maculata	species	10	69	
ativa	species		74	
ne	tribe		10	
a	genus	4347	34	
n	genus		10	
arcesum	species		13	
	genus	99	61	597
	genus		20	73240
	genus		15	
	familv		28	





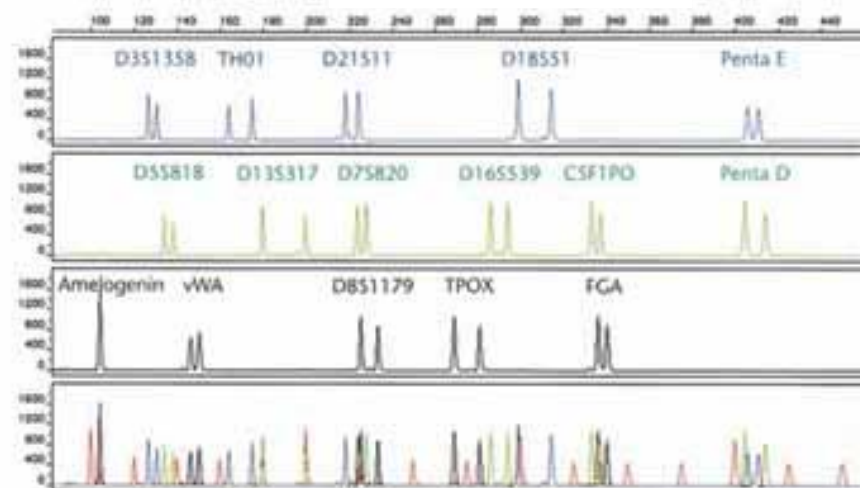
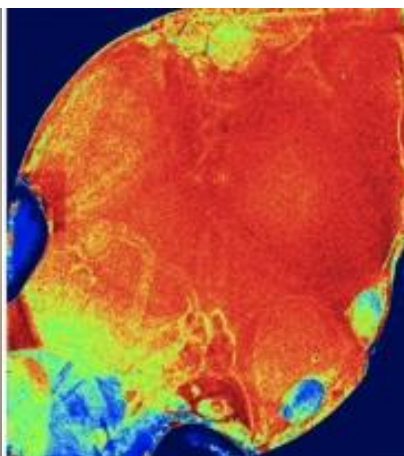


# Criticità nell'utilizzo della nuova tecnologia

- **Workflow innovativo**
- **Problematiche connesse con la gestione della mole di dati che può essere ottenuta da una singola traccia biologica**

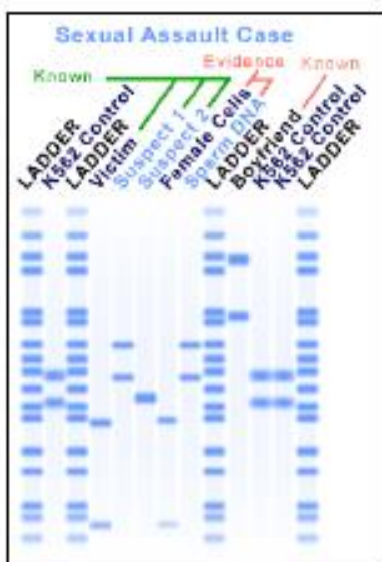


# Criticità nell'utilizzo della nuova tecnologia



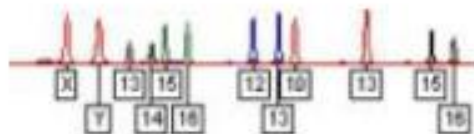
# The DNA Field Moves Forward...

## The Past



**RFLP**

## The Present



**STRs**

## The Future



**Dott.ssa Elena Pilli**  
mail: [elena.pilli@unifi.it](mailto:elena.pilli@unifi.it)