MARKER SELECTION IN FORENSIC GENETICS

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INTRODUCTION AND HISTORICAL OVERVIEW

Forensic genetics is the branch of biology that uses genetic techniques in order to help out legal authorities in solving cases.

Early 20th century — First marker discovery (Landsteiner)

→ **1985** — DNA fingerprinting, VNTR (Alec Jeffreys)

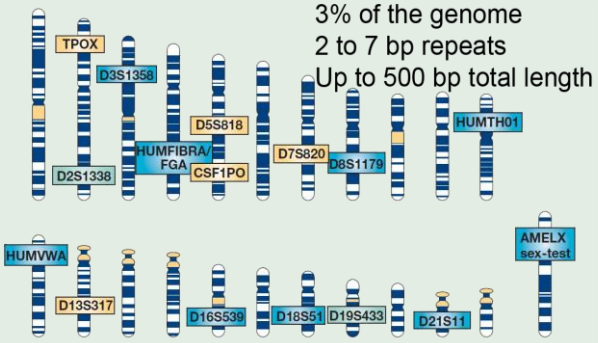
→ **1986** — First criminal case (Colin Pitchfork)

→ **1988** — PCR invention (Kary Mullis)

→ **Early 90's decade** — Application of STR, mtDNA

MARKERS

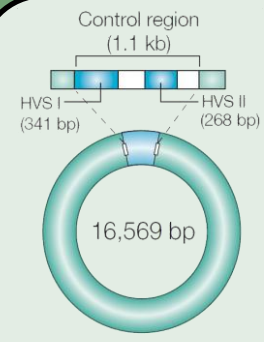
STR



(Jobling, Gill. 2004. Nature Reviews Genetics)

Advantages	Disadvantages
Smaller than VNTR	Less alleles than VNTR
Higher quantity than VNTR	Less heterocigosity
Can be amplified from degraded samples	PCR contamination risk
Fast and easy to apply technique (PCR)	Wrong genotyping risk in big amplicons
Reaction can be multiplexed	Highly degraded samples can lead to wrong results
High statistical power	

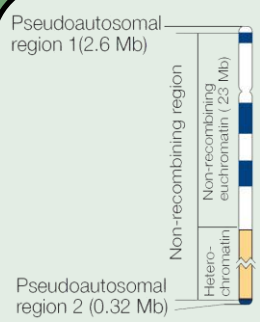
mtDNA



(Jobling, Gill. 2004. Nature Reviews Genetics)

Advantages	Disadvantages
Haploid genome	Heteroplasmy
High number of mitochondrion per cell	Absence of recombination leads to less variability
Maternal inheritance	
Slower degradation than nuclear DNA	

Y-STR



(Jobling, Gill. 2004. Nature Reviews Genetics)

Advantages	Disadvantages
Paternal inheritance	Absence of recombination
Highly conserved in lineages	Less discriminating power than nuclear STR
Variable between populations	Low mutation rate
Samples can be recovered even with victim material excess	

DISCUSSION

-STR are the most commonly used markers.
-mtDNA and Y-STR are mainly used in lineage construction and sex discrimination.
-STR research is advancing with the discovery of new markers and the development of smaller amplicons (miniSTR).
-New types of markers are emerging (X chromosome markers, indel polimorphisms, methylation patterns).
-The future of forensic genetics might be markers with high genotypic – phenotypic correlation (i.e. eye color).
-SNP marker use is not yet extended due to its limitations (mostly biallelic).
-Forensic genetics highly relies on the use of databases to obtain and compare significant results.

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