

INSTITUTE
OF PLANT
SCIENCES



Sant'Anna
School of Advanced Studies – Pisa

Microsatellite DNA



07/05/2025

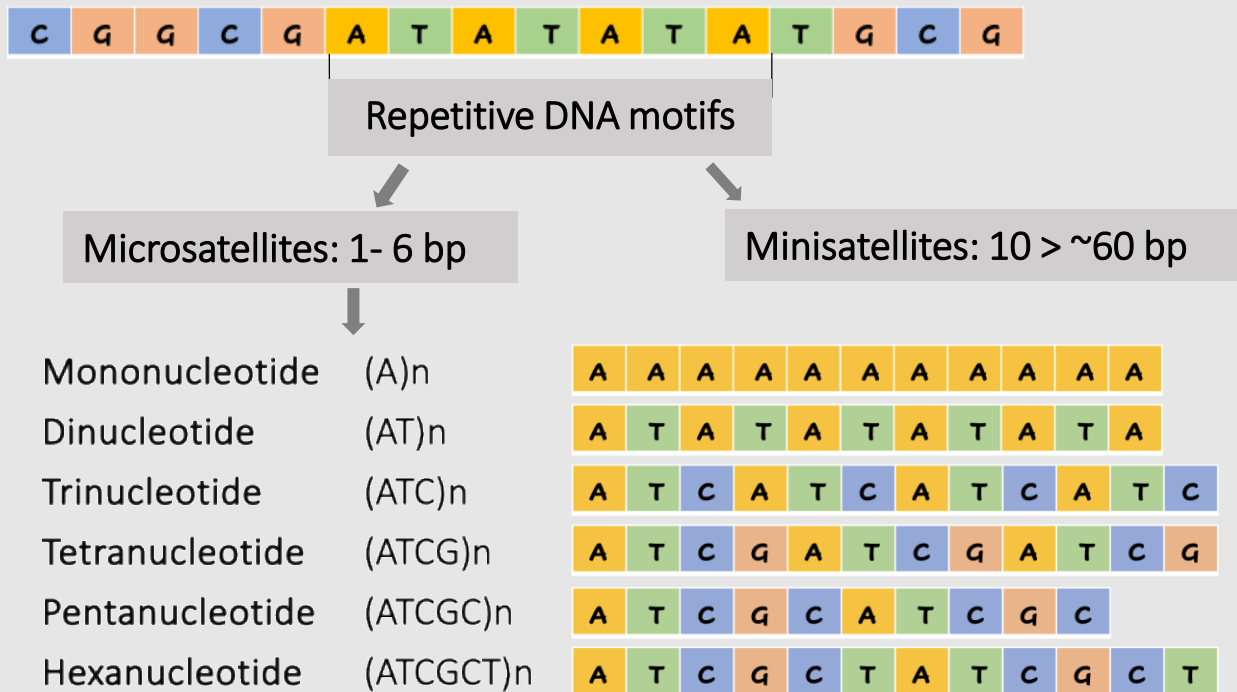
BREEDTECH project: Students' Training Workshop

Prepared by Racheal Gwokyalya



BRIEF INTRODUCTION

Short Tandem Repeats (STRs)/Simple Sequence Repeats (SSRs)



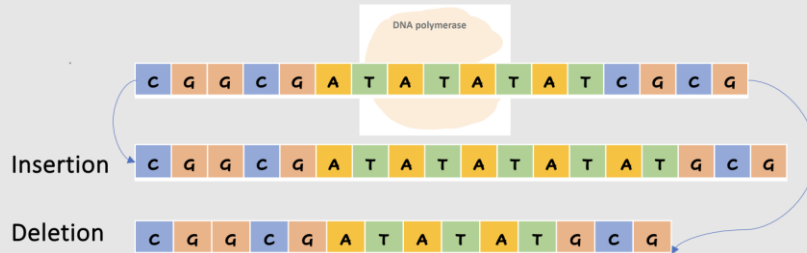
POLYMORPHISM

The variation in the number of repetitive motifs at a specific locus of the genome.

- Can vary between individuals, populations, or species.
- polymorphism is highly useful for genetic diversity studies, population genetics and marker-assisted selection.

Mechanism of mutation & variability

- Major cause; **Replication Slippage** -DNA polymerase dissociates

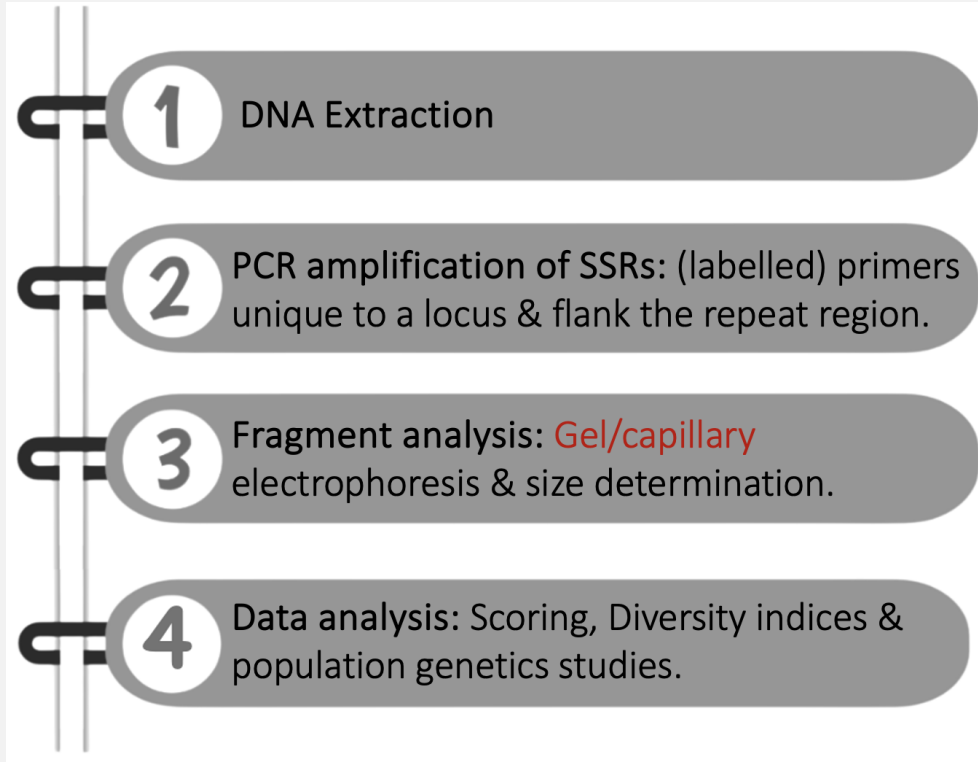


- Leading to high mutation rates and genetic diversity.

MICROSATELLITES



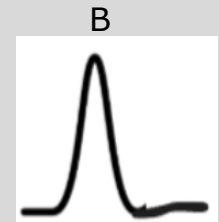
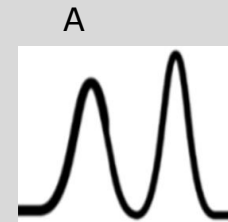
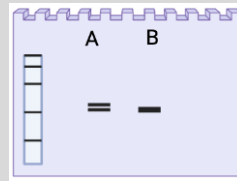
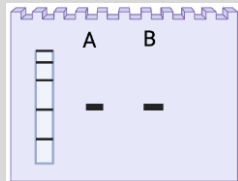
ASSAY WORKFLOW



FRAGMENT ANALYSIS

Agarose	Polyacrylamide Gel (PAGE)	Capillary Electrophoresis
Resolution 5–10 bp	1–2 bp	1 bp
Advantages <ul style="list-style-type: none"> • Simple • Inexpensive 	<ul style="list-style-type: none"> • Higher resolution • Moderately inexpensive 	<ul style="list-style-type: none"> • Highest resolution • Automated, Multiplexing
Disadvantages <ul style="list-style-type: none"> • Low resolution • Cannot resolve 1- 6 bp differences 	<ul style="list-style-type: none"> • Time-consuming, • Toxic reagents 	<ul style="list-style-type: none"> • Expensive • Specialized equipment

Sample (Diploid)	Allele 1 (bp)	Allele 2 (bp)
A (Heterozygous)	200	210
B (Homozygous)	200	200



APPLICATIONS

- **Genetic Diversity Analysis:** genetic variation within and between populations, aiding breeding programs.
- **Conservation Genetics:** evaluating genetic bottlenecks and inbreeding in endangered species .
- **Genetic Mapping:** genetic linkage maps essential for identifying genes associated with specific traits.
- **Forensic & Paternity Testing:** the unique allelic profiles are essential for individual identification and kinship testing.



ADVANCES IN GENETIC MARKER TECHNOLOGY

SSRs to Single Nucleotide Polymorphisms (SNPs) in modern genotyping

- A **SNP** is variation at a single nucleotide position in the genome.

Reference sequence:



Variant sequence:

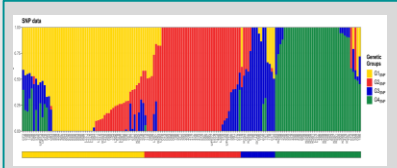


- Occur every 100 - 300 base pairs in genomes.
- SNPs, the **gold standard** in genotyping now.



KEY BENEFITS OF SNPs

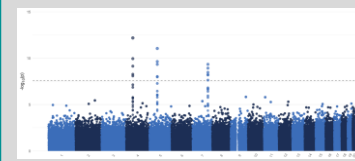
Why are SNPs replacing SSRs?



Denser genetic maps for improved resolution.



High-throughput:
SNP arrays and NGS enable large-scale, automated genotyping vs SSR (PCR + gel electrophoresis)



Standardized, reliable data, enhancing GWAS studies vs SSR (Parentage testing, diversity studies)

Lower mutation rate → **Higher Stability:** More stable over generations, making them reliable for long-term studies.

SNP genotyping is cheaper per marker for large datasets.



THE FUTURE OF GENETIC MARKERS

- SSRs remain useful in specific applications like:
 - Forensic & Parentage testing (high polymorphism per locus).
 - Studies on recent evolution and genetic drift.
 - Low-cost genotyping for small-scale studies.
- Advances in NGS and AI-driven genomics will further enhance SNP-based studies.



Thank you



