“Despite the cost of detection remaining high, [STR] markers had pervaded all areas of plant molecular genetics and breeding in late 90s and the beginning of the 21st century. However, during the last five years, the hegemony of medium-throughput [STRs] was eventually broken with SNP markers.”

<table>
<thead>
<tr>
<th>Short Tandem Repeat (STR) AKA Simple Sequence Repeat (SSR)</th>
<th>vs</th>
<th>Single-Nucleotide Polymorphism (SNP)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>ACTGTccgccccgCT</strong></td>
<td><strong>TCGTTGCTATGGTAGT</strong></td>
<td></td>
</tr>
<tr>
<td><strong>ACTGTccgccccgCT</strong></td>
<td><strong>TCGTTGCTATGGTAGT</strong></td>
<td></td>
</tr>
<tr>
<td><strong>ACTGTccgccccgCT</strong></td>
<td><strong>ACCTGCAAGTACACAGT</strong></td>
<td></td>
</tr>
<tr>
<td><strong>ACTGTccgccccgCT</strong></td>
<td><strong>ACCTGCAAGTACACAGT</strong></td>
<td></td>
</tr>
<tr>
<td>3 4 5 6</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

- Less abundant – 1 STR/15,000 bp
- Prone to mutation via slipped-strand mispairing.
- Requires intact DNA
- Medium throughput
- Prone to stutter products

- More abundant – 1 SNP/1,000 bp
- Greater mapping resolution
- Lower error rate
- Works with degraded DNA
- High throughput

**Experimental Complexity / Validation Complexity**

**STR**
- Complex multiplex design
- Need to avoid:
  - Primer dimer interaction,
  - Fluorophore overlap,
  - Imbalanced dye pooling,
  - Data variations from lab to lab due to interpretations, and low reproducibility

**SNP**
- Simple singleplex design
- Easy to score
- No lab to lab variation
- Low primer interaction
- Good reproducibility

**Novel Panel Time to Data**

<table>
<thead>
<tr>
<th>5000 Samples</th>
<th>32 STRs</th>
<th>90+ DAYS</th>
</tr>
</thead>
<tbody>
<tr>
<td>5000 Samples</td>
<td>96 SNPs</td>
<td>21 DAYS</td>
</tr>
</tbody>
</table>

"...collection of microsatellite data for the present study took 3 months, while SNP data were collected in a week." (400 samples, 11 microsatellites, 80 SNPs)

**Interpretation - What Do You See?**

**STR**
- High mutation rate leading to call errors
- Difficult to score
  - Microvariants
  - Stutter products
  - > 40 possible genotypes/assay

**SNP**
- Low mutation rate
- Easy to score
  - 3 possible genotypes/assay

**SNPs are:**
- Faster
- Cheaper
- Easy To Score
- Simpler
- Higher Resolution