**ALA2.2 Comparison of Single Nucleotide Polymorphism (SNP) marker detection systems**

**Prerequisite**

Understanding of:

1. Importance of DNA sequence variation within species
2. SNP and INDEL markers basics
3. Basic applications of markers: fingerprinting and gene-tagging

**Purpose**

To provide an in depth understanding of selected SNP marker detection systems, and to identify which criteria are relevant for comparing different marker assay options

**Background**

During the past 10-20 years, a multitude of different SNP marker detection assays have been developed. None of these assays is optimal for all applications because all have strengths and weaknesses. It is thus important to understand the main characteristics of SNP marker assays, in order to make the best choice for any given application.

**Tasks**

This ALA depends on either access to the internet (preferable), or articles to be provided by the instructor.

1. Add the properties of SNP marker assays to the table below (one table per marker system). Fill out this table for a) Taqman assay, b) Sequenome assay, c) a SNP assay of your choice.

|  |  |
| --- | --- |
| Properties | Marker System |
| **Costs per Datapoint (DNA, 1 equipment available, no salary)** | In $ |
| 10 samples | For 1-10-100-1000-10000 markers |
| 96 samples | For 1-10-100-1000-10000 markers |
| 960 samples | For 1-10-100-1000-10000 markers |
| 9600 samples | For 1-10-100-1000-10000 markers |
| **Time per Datapoint (DNA, 1 equipment available, 1 person)** | In hours |
| 10 samples | For 1-10-100-1000-10000 markers |
| 96 samples | For 1-10-100-1000-10000 markers |
| 960 samples | For 1-10-100-1000-10000 markers |
| 9600 samples | For 1-10-100-1000-10000 markers |
| **Time per Datapoint post assay for preparing data matrix** |  |
| **Multiplex size** | No. of markers per multiplex |
| **Multiplexing flexibility** | Low to high |
| **Costs for special equipment** | In $ |
| **Service: costs per datapoint** | In $ |
| **Automatization capability** | Low to high |
| **Set-up costs (e.g., Affy.-Array)** | Yes or no |
| **Target sequence requirement** | No, 1 allele, 2 or more alleles |
| **Ease to use** | Low to high |
|  |  |
| **Reproducibility** | Low to high (or %, if available) |
| **Sensitivity** | Low to high |
| **Robustness** | Low to high |
| **DNA requirements** | Low to high quality; costs & time per DNA sample; DNA amount/assay |
|  |  |
| **Dominant / codominant system** | Dominant or codominant |
| **Number of alleles per marker** | 2, 4, multiple |
| **Detection of rare alleles** | Yes or no |
| **Underlying polymorphism** | SNP, INDEL, SSR, Restriction site |
| **Level of polymorphism** | Expected polymorphic information content / marker |
| **Stability (mutation)** | Low to high |
| **Species Transferability** | Low to high |
| **Gene / target specificity** | Yes or no |
| **Genome coverage** | Even – uneven; Low to high |
|  |  |
| **Ability to detect epigenetic changes** | Yes or no |
| **Ability to detect transcript variation** | Yes or no |

1. Describe strengths and weaknesses of the three marker systems that you are comparing.
2. Provide arguments as to which marker system is preferred for a marker-assisted backcrossing procedure for tracking the target gene(s), and which is preferred for fingerprinting to monitor the background genome composition.

**Tentative answers** (can differ, based on context / assumptions made)