

QUESTIONNAIRE FOR DEVELOPMENT OF SPECIES GENOYTPING

1. For what species do you want to develop? _____.
2. Number of samples: _____.
3. What type of population do you wish to genotype? _____.
Individuals in the population are expected to be:
 Fully homozygous (e.g. RIL) _____.
 Heterozygous _____.
Ploidy: _____.
 Haploid _____.
 Diploid: _____.
 Other (please specify): _____.

4. Number of polymorphic loci desired? _____.

Why do we ask? The number of polymorphic loci needed is dependent on the application desired by the collaborator. For example, genetic mapping for quantitative trait loci (QTL) analysis typically requires a few thousand markers. Other applications, such as genome-wide selection, may require tens of thousands of markers. The number of markers needed defines, in part, the primers to be used for amplification.

5. Is there a reference genome available? _____ If not, can you specify what genomic resource is available? (e.g. EST data, short read sequences)

6. What is the estimated nucleotide diversity (i.e. average number of polymorphic sites between any two random samples) in your population? _____

Why do we ask? The nucleotide diversity defines the likelihood of sequencing loci that are polymorphic among samples in a population. If the nucleotide diversity is low (e.g. 1/1,000 nucleotides), then a greater number of loci need to be sequenced to identify a sufficient set of polymorphic ones. With high nucleotide diversity (e.g. 1/50 nucleotides), most sequenced loci are expected to be polymorphic.

The estimated nucleotide diversity, in combination with the information about the number of polymorphic loci desired, are used to identify the primers to be used for amplification.