



NextGenerationSequencing

AmpSeq

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Eating behaviour of grasshoppers



Amplicon sequencing

Pitteloud, unpublished



Metabarcoding

1) Composition known from field observation

Option: literature, metagenomic approach, pilots

2) Primers design-What can be detected?

3) Establish databases based on Sanger Sequencing

Option: literature, ncbi

4) Long Illumina paired-end reads e.g. Miseq for all samples

Option: PacBio

Similar to RNAseq have replicates



- Using qRT-PCR to validate some of your candidates