Technical Brief: RAD Sequencing

HIGH THROUGHPUT GENOMIC MARKER DISCOVERY AND GENOTYPING

Restriction site Associated DNA sequencing (RAD-Seq) is a fractional sequencing strategy, designed to interrogate from 0.1% to 10% of a selected genome.

By focusing next-generation DNA sequencing (NGS) technologies on this subset of the genome, thousands to tens of thousands of genetic markers can be quickly and cost effectively identified or genotyped in large populations.

RAD-Seq works by first fragmenting the target genome using a restriction enzyme. After digestion, a series of molecular processing steps transform the DNA into a fragment library suitable for sequencing on a NGS platform (Figure 1).

RAD-SEQ WITH FLORAGENEX

- No oligonucleotide or reagent set up costs: just send in your samples
- Develop and genotype hundreds of thousands of markers as needed
- Flexible project architectures: sequence from two to two thousand samples
- Integrated with industry leading NGS platforms
- Streamlined bioinformatics and analysis
- Economical pricing competitive with leading array genotyping systems

Sequence data is then analyzed to identify and score genetic variations in the samples or population of interest. To date, multiple studies analyzing upwards of 100,000 genetic markers using RAD-Seq have been published.

Visit www.floragenex.com for more information, current publications and example RAD-Seq efforts.