OUR GENOTYPING-BY-SEQUENCING (GBS) SERVICES...

...provide solutions for every phase of your project, from discovery, to validation, to screening. Our Agrigenomics specialists can advise on the best strategy to reach your breeding goals.

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Genomics

FROM COMPLEXITY TO CLARITY

> Accelerating Selective Breeding with Genotyping-by-Sequencing

THE DNA UNIVERSE

1 Targeted GBS (Amplicon-based)

Method: Multiplex PCR amplicons target SNP regions and sequenced at high coverage
Benefit: Highly cost-effective for genotyping <5,000 SNPs

Key Applications in Agrigenomics:

- **Marker-Assisted Breeding (MAB):** Identify and track specific genetic variations associated with desirable traits in crops and livestock.
- **Quantitative Trait Locus (QTL) Analysis:** Study the genetic basis of complex traits, such as yield, disease resistance, and stress tolerance.
- **Parentage Verification:** Confirm parent-offspring relationships to improve breeding program accuracy.
- **Diversity Analysis:** Assess genetic diversity within a population for conservation and breeding purposes.

2 Low-Pass Sequencing with Imputation

Method: Sequence genome at <2X coverage
Benefit: Cost effective method for obtaining very high density, genome-wide variant analysis (10s of millions of SNPs) without full genome resequencing

Key Applications in Agrigenomics:

- **Genome-Wide Association Studies (GWAS):** Identify genetic variants associated with important agronomic traits.
- **Genomic Selection:** Predict the breeding value of individuals based on genomic data, accelerating the breeding process.
- **Population Genetics:** Study the genetic structure and demographic history of plant, animal and aquatic populations.

3 Reduced representation sequencing: Gras-Di

Method: Random, genome-wide amplicons sequenced at high coverage
Benefit: More cost effective for genotyping genome-wide SNPs than WGS

Key Applications in Agrigenomics:

- **High-Density Genotyping:** Obtain a comprehensive set of genetic markers for genomic analysis.
- **Genomic Diversity Analysis:** Assess genetic diversity at a large scale for germplasm characterization and conservation.
- **Comparative Genomics:** Identify genetic differences between different varieties or breeds.
- **Marker Development:** Facilitate SNP marker discovery for species with limited genomic resources.

COMPARISON TABLE

Method	Targeted GBS	Low-Pass Sequencing with Imputation	Reduced Representation Library Sequencing (GRAS-Di)
SNP Marker Range	Medium (hundreds to thousands)	High (tens of thousands to millions)	High (tens of thousands to millions)
SNP Discovery	Limited to SNP flanking regions	Yes	Yes
Reference Genome Needed	Yes	Yes	Optional
Comparative Costs	Low	Medium	Medium
Sample Throughput	High	High	Medium