

Seed and Grain

DNA Extraction Performance

High-throughput DNA extraction workflows for seed and grain matrices, designed to deliver consistent yield and DNA integrity for SNP genotyping and next-generation sequencing pipelines.

Note: Data on leaf performance can be found in the Plant and Crop Dataset

Performance Summary

METRIC	RESULT
SPECIES TESTED	Wheat, Barley, Lentil, Soybean, Rice, Maize, Sunflower, Mustard, Oat
SAMPLE TYPES TESTED	Seeds, grain, leaf
TYPICAL YIELD	5ng/μL – 200ng/μL (dsDNA, fluorescence-based quant – Qubit)
INPUT MASS	5-200mg
FRAGMENT SIZE	10-55kb
FORMAT	Magnetic Bead
AUTOMATION COMPATIBILITY	KingFisher, Hamilton, Tecan

Large-scale seed and grain genotyping programs require DNA extraction workflows that deliver consistent DNA yield and fragment integrity at high throughput while maintaining low per-sample costs.

Grain and seed matrices present specific challenges due to their heterogeneous structure (endosperm, embryo, and seed coat) and high concentrations of polysaccharides, starches, proteins, and secondary metabolites, all of which can impact DNA recovery and downstream assay performance. High sample input mass can also create challenges for DNA extraction workflows.

Azora Biosciences has developed extraction workflows specifically optimised for seed and grain samples across cereals, oilseeds, and legumes. These workflows incorporate customised reagent formulations tailored to individual laboratory requirements, enabling robust performance across varying sample types, input masses, and automation platforms. This supports high-volume genotyping pipelines used in breeding programs, seed testing, trait screening, and agricultural diagnostics.

Core DNA Extraction Technology

Samples are lysed using proprietary buffer systems incorporating surfactants and polymer-based additives to efficiently disrupt seed and grain matrices, including endosperm and other starch-rich tissues, while mitigating the effects of polysaccharides, proteins, and secondary metabolites. The initial lysis phase can be optimized for higher input masses and pooled grain samples to support high-throughput and composite testing workflows. An optional RNA depletion step can be incorporated during lysis to reduce RNA carryover where required. DNA is subsequently captured via alcohol-mediated binding to solid phases, using carboxyl-functionalized magnetic beads. Multiple wash steps are applied to remove residual inhibitors, followed by elution in a customized buffer system designed for compatibility with downstream genotyping and sequencing workflows.

Fluorescence-quantified dsDNA Yields

Species	Sample Type	Binding Technique	Yield (dsDNA, Qubit, ng/μL)	Fragment Size Peak
Barley	200mg, grain	Magnetic Beads (-COOH)	76.2	Not available
Wheat	200mg, grain	Magnetic Beads (-COOH)	90.2	Not available
Lentil	200mg, seed	Magnetic Beads (-COOH)	190.3	53.0kb
Wheat	5mg, grain	Magnetic Beads (-COOH)	5.3	16.1kb
Barley	5mg, grain	Magnetic Beads (-COOH)	6.3	Not available
Soybean	5mg, seed	Magnetic Beads (-COOH)	11.0	Not available
Sunflower	5mg, seed	Magnetic Beads (-COOH)	8.7	14.9kb
Mustard	5mg, seed	Magnetic Beads (-COOH)	7.0	Not available
Maize	5mg, kernel fragment	Magnetic Beads (-COOH)	9.8	Not available
Rice	25mg, grain	Magnetic Beads (-COOH)	9.9	13.3kb
Oat	70mg, grain	Magnetic Beads (-COOH)	15.4	Not available
Barley*	20mg fresh leaf*	Magnetic Beads (-COOH)	20.2	16.6kb

Note: DNA yields are quantified using fluorescence-based dsDNA assays (Qubit), which measure only double-stranded DNA. Spectrophotometric methods (A260) commonly used in competitor specifications may overestimate DNA yield due to co-quantification of RNA and other contaminants

***for additional data on leaf performance, please see the Plant and Crop Dataset**

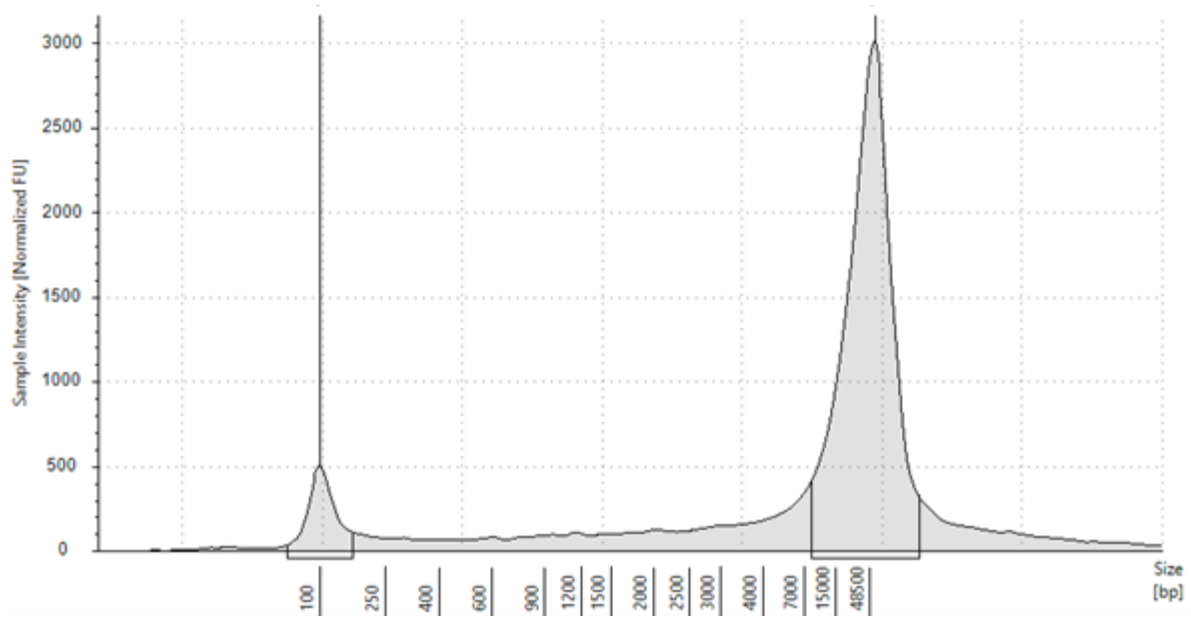


Figure 1. Fragment size distribution of Lentil seed extracted using Azora workflow.

Downstream Genotyping Compatibility

- SNP Genotyping Microarrays (Infinium, Axiom)
- Sequence-Based Genotyping inc. WGS, genotyping-by-sequencing (GBS), and targeted NGS
- PCR-based SNP genotyping (KASP, PACE, TaqMan, HRM)

Use Cases

- Plant breeding and seed production programs
- Marker-assisted selection (MAS) and genomic selection
- Variety identification, hybrid verification, and seed purity testing
- Trait screening and validation
- Agricultural and crop diagnostics