

Stronger Science for Plant Testing

Quantabio supports advances in plant testing research by providing robust and highly sensitive amplification tools. Our PCR & qPCR ToughMix chemistries along with sparQ NGS solutions are used in the field and plant laboratories around the world to help genotype various plants, seeds and crops along with detection of multiple bacterial and viral plant pathogens.



PATHOGEN DETECTION



ToughMixes overcome challenging samples and inhibitors to help rapidly identify and detect pathogens in seeds and plant tissues. These mixes are validated and recommended in several protocols created by institutions like the International Seed Foundation (ISF) and the European and Mediterranean Plant Protection Organization (EPPO).

PLANT AND MICROBIOMICS SEQUENCING

Specialized ToughMix reagents and sparQ kits enable reliable plant genomics and metagenomics workflows. Optimized for tough plant samples and complex microbial communities, delivering accurate, consistent results.

PLANT & SEED GENOTYPING

Efficiently and correctly identify plant genotypes with the aid of ToughMix amplification chemistries to assist in breeding programs, crop production, GMO testing as well as QA/QC identity of plant varieties.

[Learn More](#)



ToughMix. Experience the Amplification Difference!

ToughMix chemistry is the trade secret difference to our mastermix formulations. For more than 20 years, it has helped scientists amplify and analyze challenging samples by overcoming common PCR inhibitors. ToughMix formulations can be used directly from crude lysates as well as from purified, extracted samples.

What can ToughMix do?

- Work directly with crude lysates
- Avoid expensive and time-consuming purification steps
- Compatible with a wide range of probe designs and detection chemistries
- High quality *Taq* polymerase – free of residual host DNA
- Neutralize problem causing inhibitors present in crude samples

Inhibitor	Common sources	Reagent performance	
		Competitor	ToughMix
Polyphenols	Plant extracts	—	✓
Humic acids	Soil Plant tissues	—	✓
Polysaccharides	Feces Plant tissues	—	✓

Sample Types

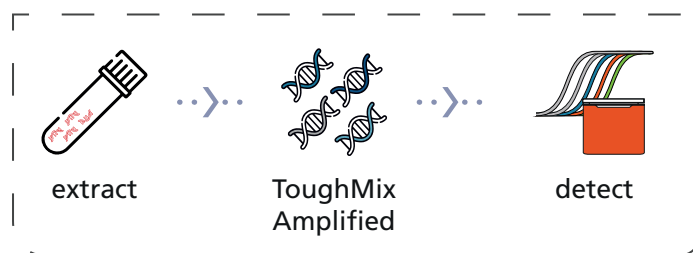


Seeds

Soil

Plant

WORKFLOW



Discover the Right Product by Application

	Product	Pathogen Detection	Genotyping	Gene Expression Analysis	GMO Screening/ Detection	Environmental DNA (eDNA) Detection and Analysis	16S/18S/ITS Amplicon Sequencing	Whole Genome and Mitogenome Sequencing
RT-qPCR	UltraPlex 1-Step ToughMix	X		X				
	eQo 1-Step ToughMix	X		X				
	qScript XLT 1-Step ToughMix	X		X				
qPCR	PerfeCt qPCR ToughMix/ Multiplex ToughMix	X	X	X	X	X		
	AccuStart Genotyping ToughMix		X					
PCR	repliQa HiFi ToughMix		X			X	X	
	AccuStart II PCR ToughMix		X			X	X	
	sparQ HiFi PCR MasterMix						X	
NGS	sparQ DNA Library Prep							X
	sparQ DNA Frag and Library Prep							X

ToughMix.

Designed for Diverse Plant PCR & qPCR Applications.

PATHOGEN DETECTION: VALIDATED STANDARDIZED PROTOCOLS

The high performance of ToughMix formulations have led to their inclusion in validated protocols from highly respected internationally recognized regulatory, governmental and non-governmental organizations, such as those from the International Seed Federation (ISF).



Virus detection: UltraPlex 1-Step ToughMix

- *Pepino mosaic virus (PepMV)* in tomato
- *Tomato brown rugose fruit virus (ToBRFV)* in tomato and pepper seeds

Bacteria detection: PerfeCta qPCR ToughMix

- *Clavibacter michiganensis subsp. michiganensis* in tomato seed
- *Xanthomonas hortorum pv. carotae* in carrot

"ISHI-Veg is a standard setting body under the International Seed Federation (ISF) and ISHI-Veg methods are developed using the collective expertise and experience of its members. The validation of the ISHI-Veg protocol was performed for detection of ToBRFV in tomato and pepper seeds, and currently the ISHI-Veg protocol is further validated and compared to other serological and molecular tests in an interlaboratory test performance study under the European Valitest project."

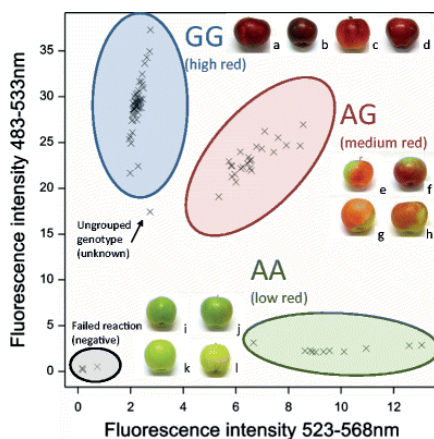


Figure 2 Allelic discrimination of SNP associated with apple coloration. AccuStart Genotyping ToughMix was used for highly specific stratification of different genotypes. Figure from Chagné et al. A functional genetic marker for apple red skin coloration across different environments, 2016.

GENOTYPING

Genotyping is used extensively for new crop development or GMO detection/certification. Plants can be genotyped to detect and select for environmental hardiness, pathogen or plant pest resistance, or even for attractive phenotypes for commercial sales.

Chagné et al. used AccuStart Genotyping ToughMix to assess a SNP marker for accurate prediction of apple skin coloration, a desirable commercial trait (Figure 2).

sparQ.

Designed for Diverse Plant Sequencing Applications.

The increasing availability and decreased cost of sequencing has unlocked a wider range of applications for agricultural testing.

WHOLE GENOME SEQUENCING

Quantabio's sparQ kits have been used for genomic analysis and better understanding of plant genomes as well as the pathogens that impact them. Barrett et al. (2023) utilized the sparQ DNA Frag & Library Prep for library preparation from both field collected plants and herbarium specimens dating back to the 1930s. Mitogenomic SNP analysis was utilized to generate a maximum likelihood phylogenetic tree for greater understanding of the dispersion and evolution of the invasive Japanese stiltgrass plant in the United States (Figure 3).

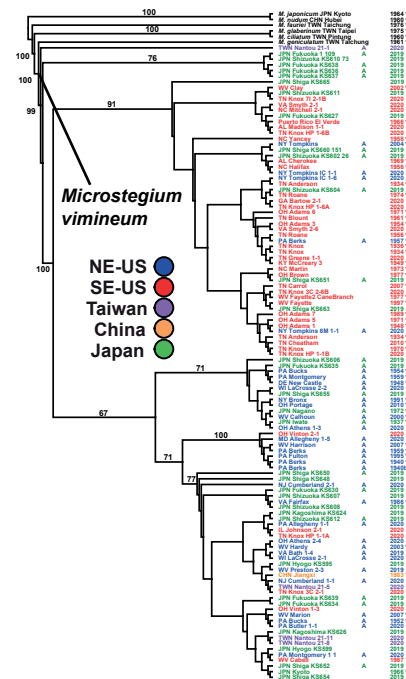


Figure 3 Maximum likelihood phylogenetic tree derived from mitogenome sequencing of *M. vimineum* samples. The sparQ DNA Frag & Library Prep Kit was used to generate sequencing libraries from 112 accession samples to characterize haploid SNPs in the mitogenome. Figure from Barrett et al. Mitochondrial genome sequencing and analysis of the invasive *Microstegium vimineum*: A resource for systematics, invasion history and management, 2023.

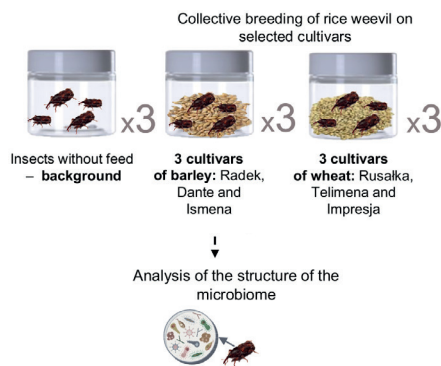


Figure 4 Experimental scheme for microbial analysis of rice weevil microbiome. repliQa HiFi ToughMix was used for 16S library preparation for Oxford Nanopore Sequencing. Figure modified from Kosewska et al. Effect of different chemical properties of cereal grains on the foraging and microbiome of the rice weevil (*Sitophilus oryzae* L.), 2024.

MICROBIOMICS AND 16S SEQUENCING

16S sequencing utilizes PCR for a cost-effective look at microbial communities. The use of end-point PCR products like repliQa HiFi ToughMix and AccuStart II PCR ToughMix allows for high yield and robust amplification from challenging sample sources like the soil and fecal microbiome.

A recent paper (Figure 4) investigated the impact of selected plant cultivars on the digestive symbiotic microbiome of the plant pest, rice weevil insects. repliQa HiFi ToughMix was used to generate 16S libraries utilizing the protocol in the Quantabio application note entitled "Rapid 16S Metagenomic Library Preparation for Oxford Nanopore Technologies (ONT) Platform".