

Optimizing Protocols for DNA Metabarcoding of Plankton in the Guana Tolomato Matanzas National Estuarine Research Reserve

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BACKGROUND

Plankton are valuable indicators of ecosystem health, but traditional monitoring is time-consuming and requires expertly trained taxonomists. DNA metabarcoding is an efficient method to characterize plankton communities.

OBJECTIVE

Optimize an efficient and cost-effective protocol for monitoring plankton communities in the Guana Tolomato Matanzas (GTM) National Estuarine Research Reserve.

METHODS

Samples were collected at Ft. Matanzas (a low-turbidity site) to compare two major components of the metabarcoding protocol:

1. DNA Extraction Kits, which differ in lysis method, PCR inhibitor removal, and cost.
2. Metabarcoding Primer Selection, which differ in the targeted region of the genome.

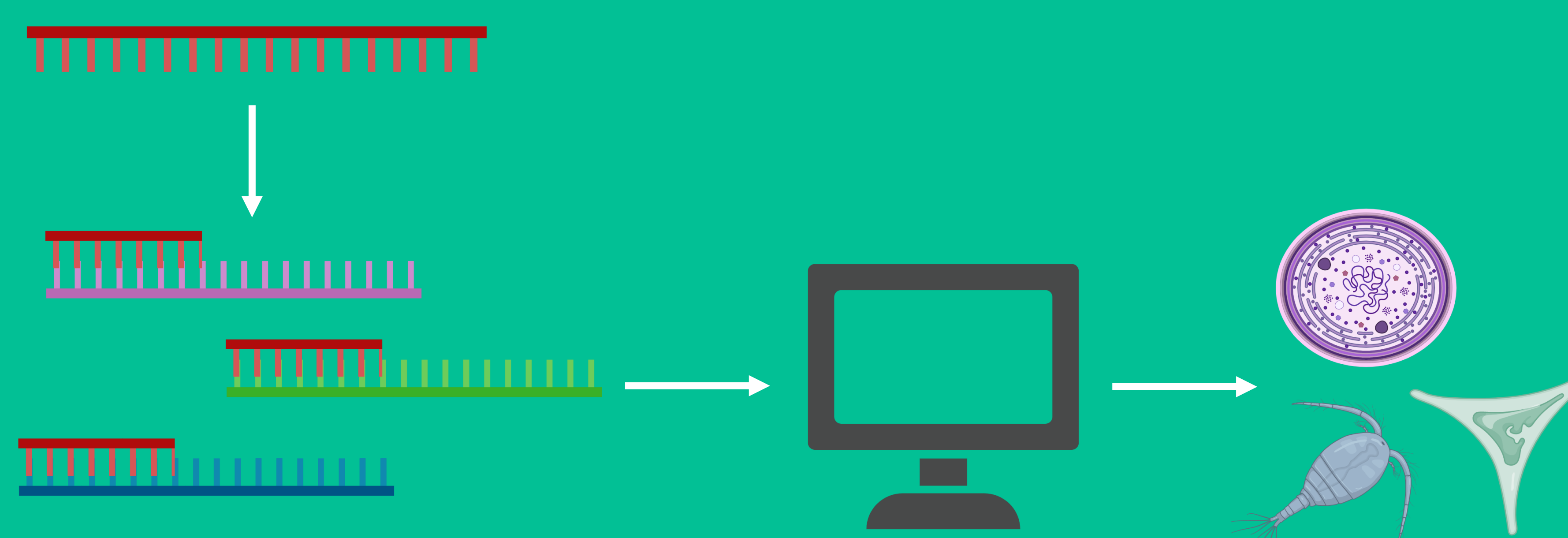
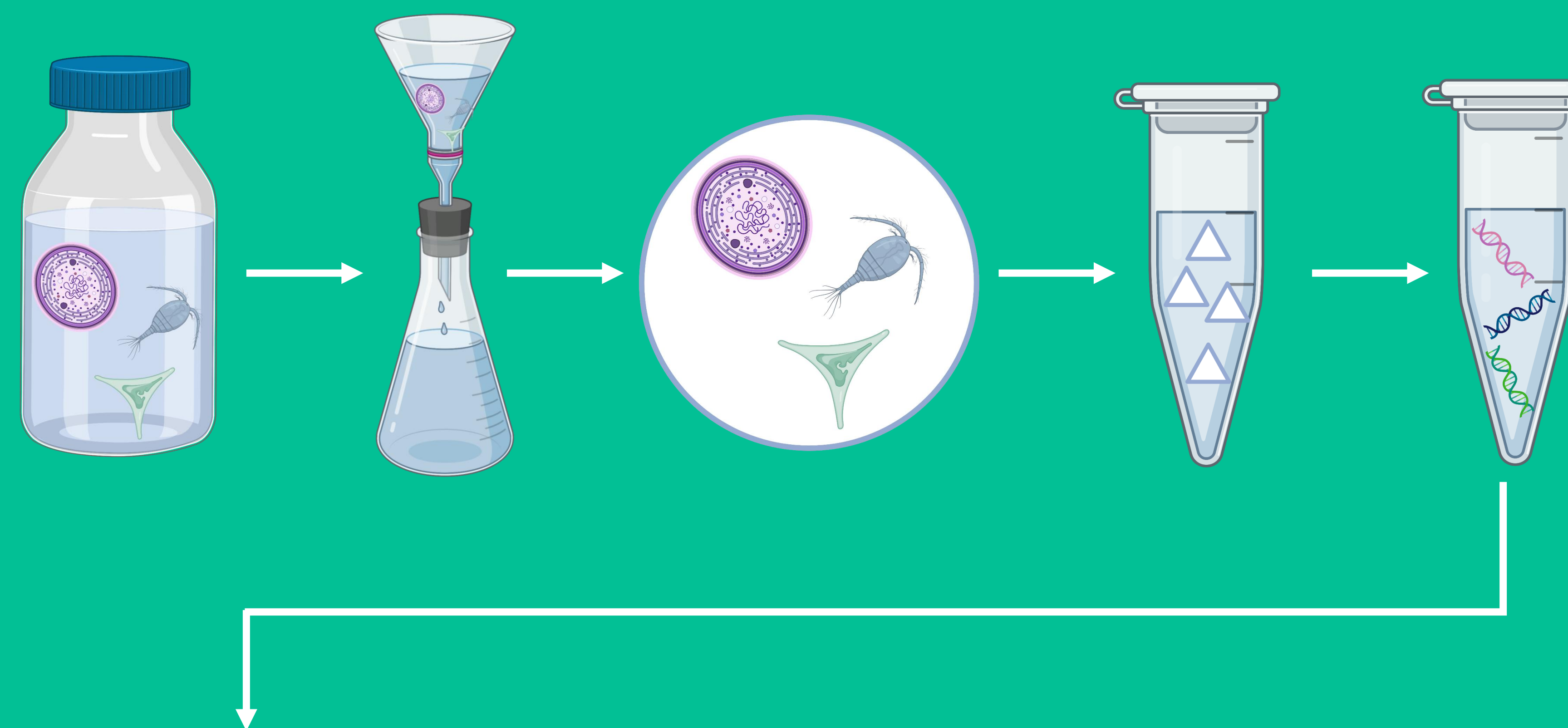
PRELIMINARY RESULTS

- Mean DNA concentration per sample varied between extraction kits (2.2-6.19 ng/ μ L).
- The Qiagen Power Soil Kit resulted in a significantly higher ($p < 0.05$; LM) average DNA concentration of 6.19 ng/ μ L.
- PCR inhibition was detected only in the Qiagen Blood & Tissue kit.

NEXT STEPS

- Test kits on turbid water samples from Guana Lake.
- Sequence samples to determine community composition resolved by each kit.

Creating a metabarcoding toolkit for the study of plankton communities.



Figures created with BioRender.com



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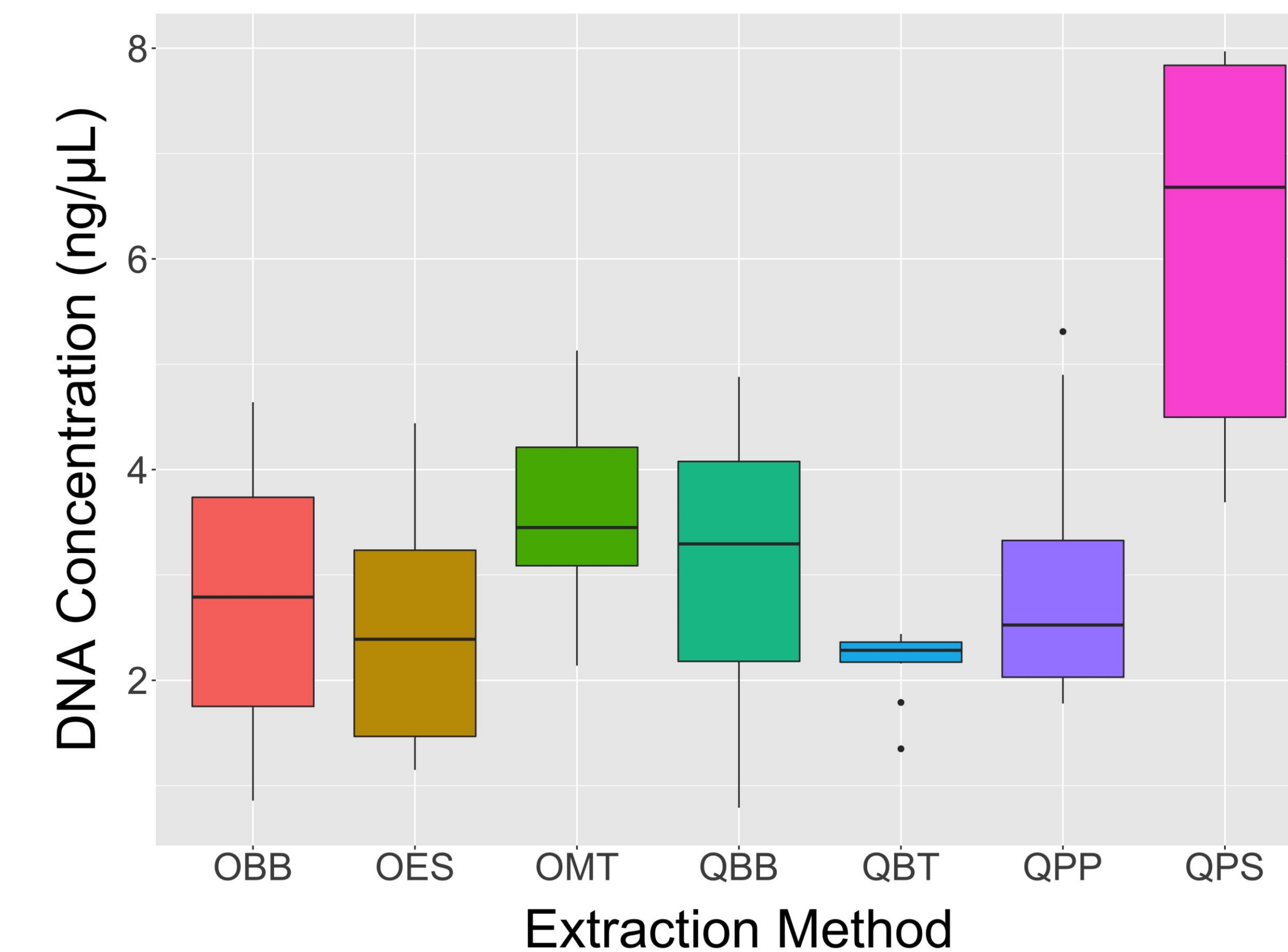


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LEGEND

ABBREVIATION	KIT TYPE	\$ PER SAMPLE
OBB	Omega Tissue + Beads	\$2.39
OES	Omega EZNA Soil	\$3.56
OMT	Omega Tissue	\$1.44
QBB	Qiagen Blood & Tissue + Beads	\$3.99
QBT	Qiagen Blood & Tissue	\$3.04
QPP	Qiagen Plant Pro	\$5.11
QPS	Qiagen Power Soil	\$6.65

DNA CONCENTRATION



qPCR Cq VALUES

