Promega

Product Application

Automated extraction of DNA from *Cannabis sativa*

Purify DNA from Cannabis sativa *tissue samples using the Maxwell® RSC System and Maxwell® RSC Plant DNA Kit.*

Kit: Maxwell® RSC Plant DNA Kit (Cat.# AS1490)

Sample Type(s): *Cannabis sativa* leaf, bud, flower, meristem tissue

Input: up to 30mg

Materials Required:

- Maxwell® RSC Instrument (Cat.# AS4500)
- Maxwell® RSC Plant DNA Kit (Cat.# AS1490)
- Bead-beating device
- Centrifuge

This protocol was developed by Promega Applications Scientists and is intended for research use only.

Users are responsible for determining suitability of the protocol for their application.

For further information, contact Technical Services at: **techserv@promega.com**

Protocol:

1. Add 1-30mg of plant tissue sample.
2. Add 300µl Tail Lysis Buffer.
3. Add 10µl RNase A.
4. Homogenize samples.
    a. Depending on homogenization technique, disruption may be more effective before buffers are added.
    b. Inefficient homogenization will lead to excessive variability in DNA yields.
5. Centrifuge the samples at maximum speed for 2 minutes.
    a. Centrifuge time may need to be increased to separate oils from aqueous layer.
6. Prepare the Maxwell® RSC cartridge rack.
7. Transfer sample into well 1 of the Maxwell® RSC cartridge.
8. Add 50µl Elution buffer to all elution tubes.
9. Run the Maxwell® RSC Plant DNA method on the Maxwell® RSC instrument.
10. Remove the elution tubes for downstream analysis and dispose of the spent Maxwell® RSC cartridges.

Results:

DNA was successfully extracted from *Cannabis sativa* leaf, flower, bud, and meristem tissues using this protocol. 1-30mg samples were purified and quantitated using both spectrophotometric (data not shown) and dye-based (Figure 1) techniques. All samples were amplified in a gender testing qPCR assay, Figure 2. The variability in DNA yield was due to poor sample homogenization as these samples were homogenized using bead beating tubes on a vortexer.

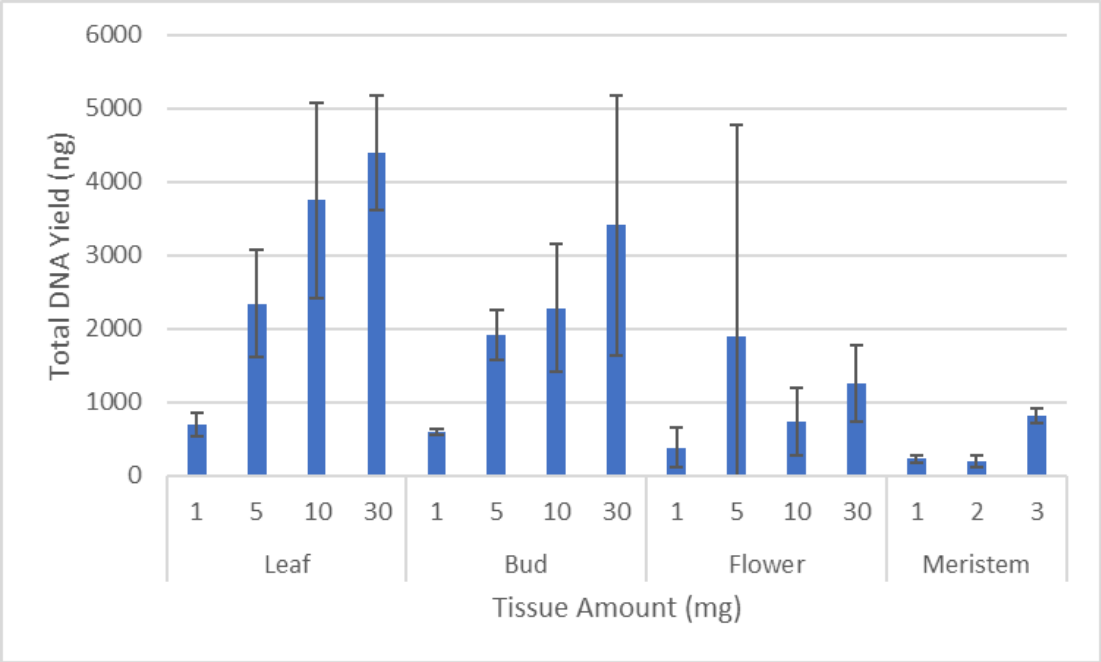

Figure 1. QuantiFluor® ONE dsDNA quantitation. 1µl of eluate was assayed using the QuantiFluor® ONE dsDNA System. Data are shown as Avg ± StDev of N=3 replicates. Meristem samples are N=2.

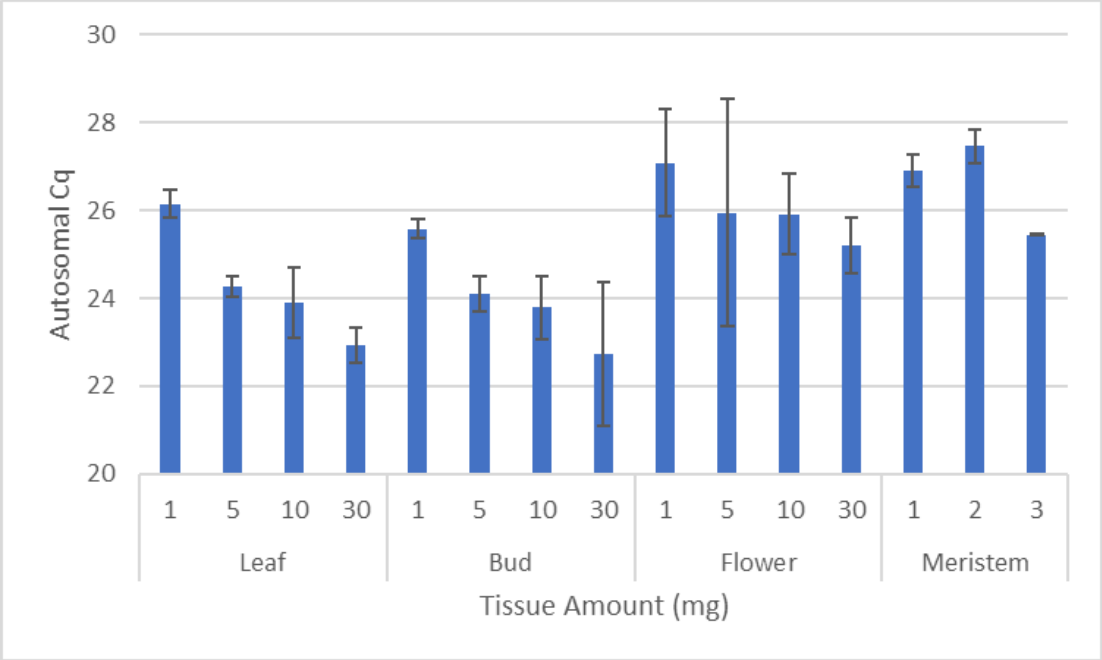

Figure 2. qPCR *Cannabis* Gender Assay. The autosomal target from a Cannabis specific gender assay was used to assess sample amplifiability. Data are shown as Avg ± StDev of N=3 replicates. Meristem samples are N=2.