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M613A46

(For Research Use Only) V4

1. Intended Use

TANBead® Nucleic Acid Extraction Kit (M613A46) is suitable for isolating nucleic acids from plant samples. Automated nucleic acids extraction can be performed by Maelstrom 8 series and Maelstrom 4800 series. Extracted nucleic acids can be analyzed by downstream applications, such as real-time PCR, next-generation sequencing.

2. Purpose

TANBead® Nucleic Acid Extraction Kit (M613A46) is suitable for a variety of samples, including plants, mushrooms, etc. This kit, with Maelstrom 8 series and Maelstrom 4800 series, simplifies nucleic acids extraction. With simple treatment of samples, it does not need repetitive centrifugations, reducing time for manual processing, and lowering the risk of cross contamination.

3. The basic principle

The silicon dioxide layer coated on the magnetic beads can adsorb the negatively charged molecules to purify nucleic acids from samples.

4. Specification

Starting Materials	50 – 100 mg plant sample
Elution Volume	90 - 130 μL
Typical DNA yield	Up to 5 μg
Typical A260 / A280	≥ 1.7

5. Component Supplied with the Kit ₹₉₆ Auto Plate Auto Plate with reagent buffers Lysis Buffer 90 mL x 1 Guanidine salt. Tris buffer. surfactants **Elution Buffer** Nuclease-Free Water 1.5 mL x 1 Spin tips Spin tip assembled box 96 tips Protocol Instruction guide for user

6. Auto Plate Content

Well	Buffer	Volume (μL)
1 / 7	-	-
2/8	Washing Buffer 1	800
3 / 9	Magnetic Beads	800
4 / 10	Washing Buffer 2	800
5 / 11	Washing Buffer 2	800
6 / 12	Elution Buffer	130

7. Kit Storage and Shelf Life

 Components under room temperature (15~35°C) can be stored until the expiration date labeled on the box.

8. Precautions

- 1) For research use only.
- 2) Avoid using expired reagents.
- 3) When the temperature is below 20°C, place the Auto Plates in an oven (preheated 42~60°C) for 5 to 10 minutes.
- Avoid vigorous shaking, in order to avoid excessive formation of foam
- 5) Carefully remove aluminum foil to avoid splashing.
- 6) Do not expose the opened reagents or Auto Plates to air. The evaporation would lead to pH change or effect on the extraction effectiveness.
- 7) Please check the integrity of the Auto Plates and remember to mount the spin tips into the appropriate position of the suitable instrument before operating them.
- 8) Please wear a mask and disposable gloves when handling.
- 9) Use sterile consumables to avoid nuclease contamination.
- Reagent solution contains guanidine salt, avoid using bleachcontaining detergent.
- Avoid eyes, skin, and clothing contact with reagents. In case of any contact, flush with flowing water.
- 12) If any serious incident occurs, please report to the manufacturer and the competent authority of the member state in which the user and/or the patient is established.

 Reagents are all colorless and transparent. Colored reagents indicate contamination, please replace a fresh plate before proceeding.

9. Materials required, Not Supplied

- TANBead[®] Nucleic Acid Extraction System Model: Maelstrom 8 series, Maelstrom 4800 series (non-sterile)
- 2) Disposable gloves
- 3) Scissors, utility knives
- 4) Micropipette, disposable tips (10 μ L / 200 μ L / 1000 μ L)
- 5) 1.5 mL microcentrifuge tube
- 6) 15 mL / 50 mL conical tube
- 7) IPA: Isopropanol for molecular biology
- CTAB buffer: 2% CTAB, 100 mM Tris pH8.0, 20 mM EDTA, 1.4 M NaCl
- 9) Liquid nitrogen (Optional)

10. Sample Collection, Transportation, and Storage

■ Sample collection and storage

- 1) Plant sample can be stored at
 - a. RT for 24 hours
 - b. 2 8°C up to 7 days

■ Sample transportation

Transportation of plant samples should follow specific plant transportation related law. Plant sample should be kept between 2 - 25°C during transportation.

11. Nucleic acids extraction protocol Sample preparation

- Add 800 µL Lysis Buffer to the plant sample and grind it by using the grinder or disposable pestle.
 - Note: If the sample is hard to grind, it could be ground with liquid nitrogen. Then add 800 µL Lysis Buffer and mix well.
- 2) Incubate at room temperature for 10 min.
- 3) Centrifuge at 5000 8000 RPM for 5 min.

Sample preparation (with high silicon content)

- Add appropriate volume of CTAB Buffer to the sample and then grind it by using the grinder or disposable pestle.
 - Note: The optimal volume of CTAB buffer may be varied according to different sample types. In general, use 4 mL CTAB buffer for 1g plant sample.
- Incubate at 65°C for 0.5 1 hour and then centrifuged at 4000 -6000 RPM for 5 minutes.
- Transfer the supernatant to a new tube and add ice-cold IPA (0.6-1x volume of the supernatant) and gently invert for 5-10 times
- 4) Centrifuge at 6000 10000 RPM for 5 minutes.
- 5) Discard the supernatant.
- 6) Add 800 µL Lysis Buffer and mix well.

Automatic process

- 1) Carefully remove the aluminum foil from the Auto Plates.
- Use micropipette to load 800 μL lysate into wells of column #1/ #7 of Auto Plate.
- 3) Set up spin tip:

Maelstrom 8 series: Hand to mount tips and make sure there is no gap between the neck of the spin tips and the spin shaft. **Maelstrom 4800 series:** Go to Tip page and mount tips region by

- region.

 Push Auto Plates completely to the bottom of the plate rack. Make sure that the chamfer of Auto plate is at the lower left.
- 5) Close the door panel.
- 6) Select the program:

Maelstrom 8 series: Press "613-1" or "613-7" for input samples at wells of column #1 or column #7, respectively.

Maelstrom 4800 series: Press "613".

The parameters are given in following section.

- Once the program has ended, buzzer shall alarm. Take out Auto Plate carefully.
- Use micropipette to transfer the purified nucleic acids from wells of column #6/ #12 to a clean tube.

9) Discard used Auto Plate and spin tips into the waste recovery bin.

12. Program

■ Maelstrom 8 series

Program Name: 613-1/7						
Well	1/7	2/8	3/9	4 / 10	5/11	6 / 12
Volume	800 (μL)	150 (μL)				

Step	Well	Action	RPM	Time (Second)	CW/CCW (Second)	Temp.	Temp. Control
1	3/9	Mixing	3000	60	0	55	YES
2	3/9	Collection	0	30	0	55	YES
3	2/8	Mixing	3000	60	0	55	YES
4	2/8	Collection	0	30	0	55	YES
5	1/7	Mixing	3000	600	0	55	YES
6	1/7	Collection	0	30	0	55	YES
7	2/8	Mixing	3000	120	0	45	YES
8	2/8	Collection	0	30	0	45	YES
9	3/9	Mixing	3000	120	0	45	YES
10	3/9	Collection	0	30	0	45	YES
11	4/10	Mixing	3000	120	0	45	YES
12	4/10	Collection	0	30	0	45	YES
13	5/11	Mixing	3000	120	0	45	YES
14	5/11	Collection	0	30	0	45	YES
15	5/11	Vapor	0	300	0	45	YES
16	6/12	Mixing	2700	600	0	45	YES
17	6/12	Collection	0	60	0	45	YES
18	6/12	Collection	0	60	0	45	YES
19	5/11	Mixing	3000	60	0	0	NO

■ Maelstrom 4800 series

Program Name: 613		Model: Maelstrom 4800 series					
Temp1	Temp2						
45	40						
Well	Name	Volume	Action	Mixing	Collect		
1/7	LB	800	For.	Low	Low		
2/8	WB1	800	For.	Low	Low		
3/9	MB	800	For.	Low	Low		
4 / 10	WB2	800	For.	Low	Low		
5 / 11	WB2	800	For.	Low	Low		
6 / 12	EB	150	For.	Low	Low		
Step	Well	Temp (°C)	Mixing (M)	Mixing Speed (RPM)	Collect (M)	Vapor (M)	Pause
1	3		0.5	2500	0.5	0	Off
2	2		0.5	2500	0.5	0	Off
3	1	55	10	3000	0.5	0	Off
4	2		2	2500	0.5	0	Off
5	3		1	2500	0.5	0	Off
6	4		1	2500	0.5	0	Off
7	5		1	2500	0.5	10	Off
8	6	45	5	2500	1	0	Off
9	3		0.5	2500	0	0	Off

13. Reagent performance

■ Repeatability

Under repeatability conditions where nucleic acids are extracted with the same reagent kit on the same source samples by the same operator. The coefficient of variation of nucleic acids extraction concentration is less than 5%.

Reproducibility

A five-day reproducibility test was carried out with the same source samples for 5 consecutive days with the same reagent kit by different operators. The coefficient of variation of nucleic acids extraction concentration is less than 5%.

■ The stability of extracted DNA

Storage Conditions	DNA stability
-80°C	Over 90 days
-20°C	28 days
4°C	14 days
25°C	2 days
Freeze-thaw	10 times

14. Explanation of Symbols

	Manufacturer	[]i	Consult instructions for use
15°C-	Temperature limit	\sum	Contains sufficient for test
REF	Catalogue number	\triangle	Caution
LOT	Batch code	NON	Non-sterile
8	Do not re-use	漆	Keep away from sunlight
سا	Date of manufacture	₽	Use-by date
RUO	For research use only		