## Leaf Homogenization Using the Bullet Blender

RS18-0238B.HLEL

## **Materials**

- Bullet Blender® for 50 mL tubes
- Homogenization Buffer
- FoamBlocker (Optional)
- Lysis Beads
  - 4.8 mm Stainless Steel Beads in HIPPO tubes
- Sample up to 3500 mg

Table 1. Proper sample, bead and buffer volume ratios for 50 mL tubes.

| Bead Choices                 | Sample Volume | <b>Bead Volume</b> | <b>Buffer Volume</b> |
|------------------------------|---------------|--------------------|----------------------|
| 4.8 mm Stainless Steel Beads | Up to 3500 mg | 10 - 20 mL         | Up to 20 mL          |

## **Procedure**

- 1. Prepare a tube with the recommended volume of bead choices from the table above.
- 2. Add the appropriate volume of buffer according to the table above
- 3. Prepare the sample by cutting it into small thin pieces and then transfer it into the buffer-filled tubes.
- 4. (Optional) To avoid excess foaming, add FoamBlocker up to 1-2% of the total volume of the homogenization buffer.
- 5. Close the tubes tightly and place into the Bullet Blender sample chamber. If using the Gold or Gold<sup>+</sup> models, pre-cool the chamber before adding sample tubes.
- 6. Set the controls to speed 8, time 5 minutes then press Start.
- 7. After the run, remove the tubes from the instrument and visually inspect the samples. If homogenization is incomplete, homogenize for an additional 30 seconds, or repeat the homogenization step with a higher speed.
- 8. Using a pipette, transfer the homogenized samples into new tubes.
- 9. Proceed with downstream application.

## **Notes**

This protocol does not specify a particular buffer – choose a buffer that is most appropriate for the downstream application or use the lysis buffer provided in a  $\frac{PrecisionPak^{TM}}{PrecisionPak^{TM}}$ , a simplified workflow solution which also includes a bead lysis kit, supplemental reagents for high quality nucleic acids isolations, and an optimized protocol for specific samples.

The provided homogenization conditions serve as a general guideline. Homogenization times, speeds, or beads may need to be optimized based on sample characteristics and desired outcomes.

