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Supplementary information

Rapid (30-second), equipment-free purification of nucleic acids using easy-to-make dipsticks

In the format provided by the authors and unedited

Supplementary method 1. Dipstick-based purification of DNA from *Pseudomonas syringae.*

CRITICAL

1. Add 1, 5, 10, or 50 µl of a *Pseudomonas syringae* pv. tomato str. DC3000 overnight culture to 500 µl of extraction buffer and briefly mix by inversion. One sample of each dilution (n=1) was prepared from the same overnight culture.
2. Using a dipstick with a 2x6 mm nucleic acid binding zone, capture nucleic acids by dipping the dipstick in the samples, remove the contaminating components from the dipstick by dipping in to dipstick wash buffer and finally elute the nucleic acids (as described in Steps 19-22) directly into a 25 µl qPCR reaction (described in Reagent Setup).
3. Perform repeated nucleic acid purifications in quadruplicate on the same set of samples using individual dipsticks and amplify extracted DNA on a real-time thermocycler. Perform qPCRs on the MyGo mini qPCR system using the following parameters: 1 cycle at 95^{o}C for 2 minutes, 45 cycles of 92^{o}C for 10 seconds, 60^{o}C for 10 seconds, 72^{o}C for 20 seconds, followed by a 60^{o}C to 92^{o}C melt curve analysis with a 0.1^{o}C/second increment.
4. Measure the initial concentration of the double stranded DNA in each sample in triplicate using the Promega QuantiFluor ONE dsDNA quantification system as per manufacturer's instructions
5. To determine the amount of DNA purified from each sample, perform a second set of five repeated dipstick purifications on each sample and elute into 25 µl 1x PCR buffer (20 mM Tris, 10 mM $(NH_4)_2SO4$, 10 mM KCl, 2 mM MgSO4, 0.1% (v/v) Triton-X-

100, pH 8.8). Calculate the total amount of purified DNA from the fluorometerically determined DNA concentrations of the elutions.

The raw data for this experiment is included as Supplementary Data 1. A correlation analysis was performed on the datasets assuming a Gaussian distribution using a two-tailed Pearson correlation and a $p = 0.05$ significance threshold in Graphpad Prism.