**Supplementary file 4.** The MIAME Checklist

Experimental Design:

1. Type of experiment:
 - Comparison of untreated vs. OPDA-, JA-, and MeJA-treated Arabidopsis.
 - Comparison of control (no wounding) vs. wounded Arabidopsis.

2. Experimental factors:
 - Time course (0 min, 30 min and 180 min)
 - Treatment (OPDA, JA, MeJA, and wounding)

3. Number of hybridizations performed in the experiment: 16

4. Hybridization design:

| | Label | Strain | Condition | | Harvested | Tissue |
|---|---|---|---|---|---|---|
| | | | Growth | Treatment | | |
| 1 | C1 | wild-type | MS medium, 10 days | none | 0 min | whole plants |
| | OP11 | wild-type | MS medium, 10 days | OPDA | 30 min | whole plants |
| 2 | C2 | wild-type | MS medium, 10 days | none | 0 min | whole plants |
| | OP12 | wild-type | MS medium, 10 days | OPDA | 180 min | whole plants |
| 3 | C3 | wild-type | MS medium, 10 days | none | 0 min | whole plants |
| | OP21 | wild-type | MS medium, 10 days | OPDA | 30 min | whole plants |
| 4 | C4 | wild-type | MS medium, 10 days | none | 0 min | whole plants |
| | OP22 | wild-type | MS medium, 10 days | OPDA | 180 min | whole plants |
| 5 | C5 | wild-type | MS medium, 10 days | none | 0 min | whole plants |
| | JA11 | wild-type | MS medium, 10 days | JA | 30 min | whole plants |
| 6 | C6 | wild-type | MS medium, 10 days | none | 0 min | whole plants |
| | JA12 | wild-type | MS medium, 10 days | JA | 180 min | whole plants |
| 7 | C7 | wild-type | MS medium, 10 days | none | 0 min | whole plants |
| | JA21 | wild-type | MS medium, 10 days | JA | 30 min | whole plants |
| 8 | C8 | wild-type | MS medium, 10 days | none | 0 min | whole plants |
| | JA22 | wild-type | MS medium, 10 days | JA | 180 min | whole plants |
| 9 | C9 | wild-type | MS medium, 10 days | none | 0 min | whole plants |
| | MA11 | wild-type | MS medium, 10 days | MeJA | 30 min | whole plants |
| 10 | C10 | wild-type | MS medium, 10 days | none | 0 min | whole plants |
| | MJ12 | wild-type | MS medium, 10 days | MeJA | 180 min | whole plants |
| 11 | C11 | wild-type | MS medium, 10 days | none | 0 min | whole plants |
| | MJ21 | wild-type | MS medium, 10 days | MeJA | 30 min | whole plants |
| 12 | C12 | wild-type | MS medium, 10 days | none | 0 min | whole plants |
| | MJ22 | wild-type | MS medium, 10 days | MeJA | 180 min | whole plants |
| 13 | C13 | wild-type | MS medium, 21 days | none | 0 min | Rosette leaf |
| | WOD11 | wild-type | MS medium, 21 days | wounding | 30 min | Rosette leaf |
| 14 | C14 | wild-type | MS medium, 21 days | none | 0 min | Rosette leaf |
| | WOD12 | wild-type | MS medium, 21 days | wounding | 180 min | Rosette leaf |
| 15 | C15 | wild-type | MS medium, 21 days | none | 0 min | Rosette leaf |
| | WOD21 | wild-type | MS medium, 21 days | wounding | 30 min | Rosette leaf |
| 16 | C16 | wild-type | MS medium, 21 days | none | 0 min | Rosette leaf |
| | WOD22 | wild-type | MS medium, 21 days | wounding | 180 min | Rosette leaf |

5. Quality control steps taken: Confirmation of mRNA levels by RNA 6000 RNA Nano Assay (Agilent Technologies, Inc., U.S.A.)

Samples used, extract preparation and labeling:

1. The origin of the biological sample:
 - *Arabidopsis thaliana* ecotype Columbia

2. Manipulation of biological samples and protocols used:
 - *Arabidopsis thaliana* cultured in a growth chamber controlled at 22ºC
 - Continuous light
 - Sterile culture
 - MS medium (Murashige and Skoog, (1962) Physiol. Plant. 15, 493-497)

 For comparison of untreated vs. OPDA-, JA-, and MeJA-treated Arabidopsis, liquid medium was used. On the other hand, solid medium was applied to compare wounded Arabidopsis to the control (no wounding).

3. Protocols or preparation of the hybridization extract:
 - RNA extraction with the RNeasy Plant Mini Kit (Qiagen, Hilden, Germany)

4. Labeling Protocols:
 - Double-stranded cDNA synthesis using Low RNA Input Linear Amplification Kit (Agilent Technologies, Inc.)
 - Synthesis of Cy3-labeled (for treated sample) or Cy5-labeled (for untreated sample) cRNA by in vitro transcription using the Low RNA Input Linear Amplification Kit (Agilent Technologies, Inc.)
 - Purification of labeled cRNA with the RNeasy column (Qiagen)
 - Fragmentation of labeled cRNA: 60ºC, 30 min using the In Situ Hybridization Kit Plus (Agilent Technologies, Inc.)

Hybridization procedures and parameters:

1. Hybridization of fragmented cRNA to Arabidopsis 2 Microarray (Agilent Technologies, Inc.)
 - 60ºC, 17 hr hybridization in a hybridization oven (Agilent Technologies, Inc.)
 - Hybridization Cocktail

 1.0 µg fragmented cRNA labeled with Cy3 and Cy5

 Hybridization Buffer (Agilent Technologies, Inc.)

 Deposition Control (Operon Technologies, Inc., U.S.A.)

 Human Cot-1 DNA (Invitrogen Corporation, U.S.A.)

2. Washing
 - Wash Buffer 1

 6× SSPE (Agilent Technologies, Inc.)

0.005% N-lauroylsarcosine (Agilent Technologies, Inc.)

- Wash Buffer 2

0.06× SSPE

0.005% N-lauroylsarcosine

- Wash Buffer 3

Stabilization and Drying Solution (Agilent Technologies, Inc.)

- Wash Buffer 1, 1 min, room temperature
- Wash Buffer 2, 1 min, room temperature
- Wash Buffer 3, 30 sec, room temperature

Measurement data and specifications:

1. Scanning: DNA Microarray Scanner (Agilent Technologies, Inc.)

2. Image analysis: Agilent Feature Extraction software (Agilent Technologies, Inc.)

3. Fold expression of signal intensities (Relative Expression) were calculated from the following comparisons. Signal intensities of the probes and Relative Expression are presented in an Excel file (supplementary file 5).

| | |
|---|---|
| A | OP11 *vs.* C1 |
| B | OP12 *vs.* C2 |
| C | OP21 *vs.* C3 |
| D | OP22 *vs.* C4 |
| E | JA11 *vs.* C5 |
| F | JA12 *vs.* C6 |
| G | JA21 *vs.* C7 |
| H | JA22 *vs.* C8 |
| I | MJ11 *vs.* C9 |
| J | MJ12 *vs.* C10 |
| K | MJ21 *vs.* C11 |
| L | MJ22 *vs.* C12 |
| M | WOD11 *vs.* C13 |
| N | WOD12 *vs.* C14 |
| O | WOD21 *vs.* C15 |
| P | WOD22 *vs.* C16 |

Array Design:

Arabidopsis 2 oligo microarray (Agilent Technologies, Inc.)

The content of this microarray was derived from the ATH1 v. 3 database of The Institute for Genomic Research (TIGR) and represents 21,500 genes.