

Natural variability in jasmonic acid signaling among maize parental NAM lines

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Introduction

The phytohormone jasmonic acid (JA) and its receptor-active derivative, jasmonoyl-L-isoleucine (JA-Ile), are key components in induced immunity against a variety of environmental stresses such as attack by insect herbivores, pathogens, and other forms of tissue damage. Induced immunity may be preferential to constitutive immunity due to its lower resource costs and potential for specialized response [1]. In a matter of hours after herbivory, the spike in JA-Ile levels is nearly completely metabolized into less active derivatives 12-OH-JA-Ile and 12-COOH-JA-Ile [2]. This targeted response allows plants to better balance growth-defense antagonism in order to optimize both growth and defense. Because JA is produced upon insect-induced damage, it is a key determinant in plant-insect interactions [3]. Our purpose was to quantify the natural variation in constitutive and herbivore-induced levels of JA and its derivatives among the founding maize Nested Associated Mapping (NAM) population lines [4].

Materials and methods

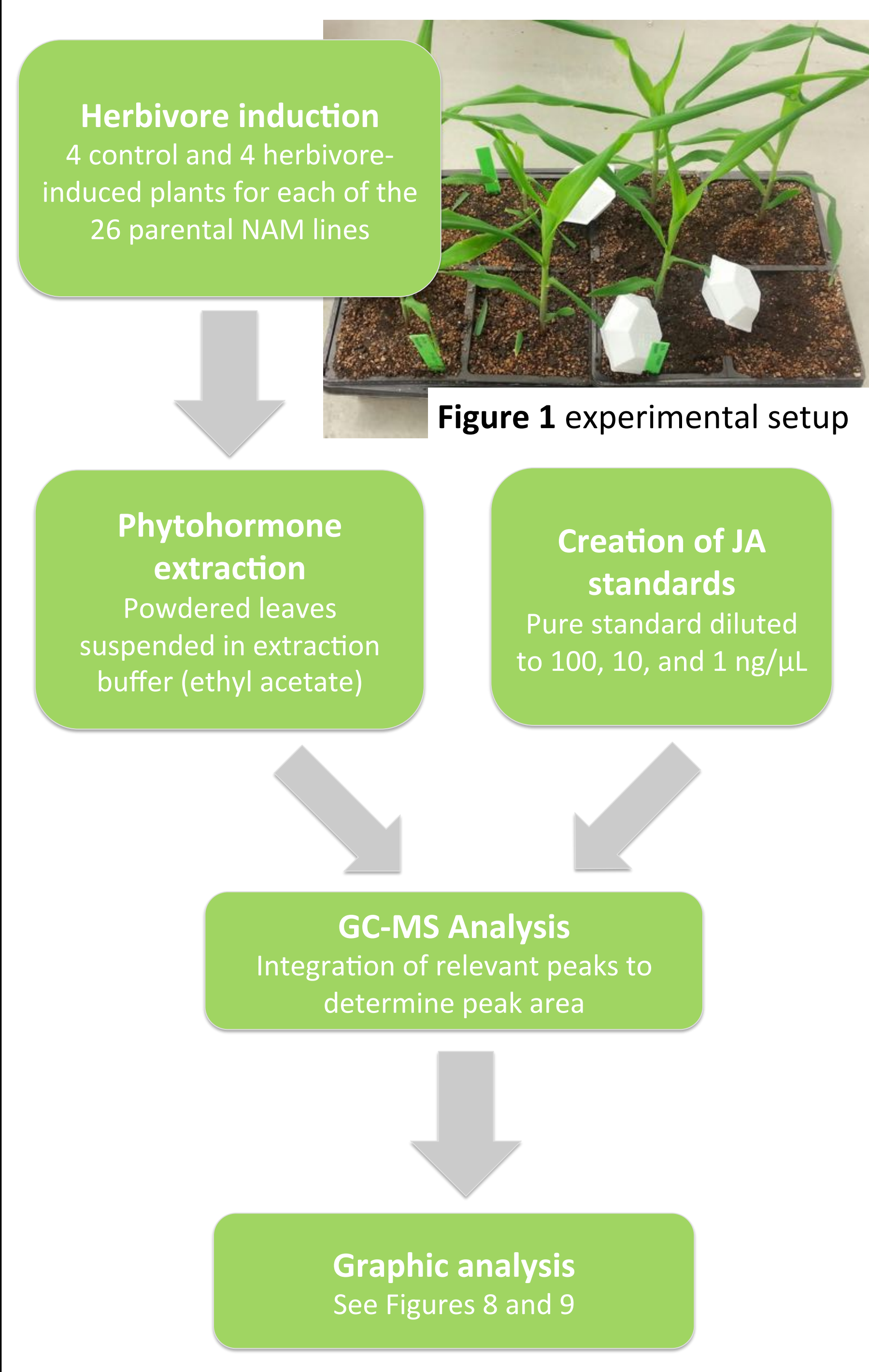
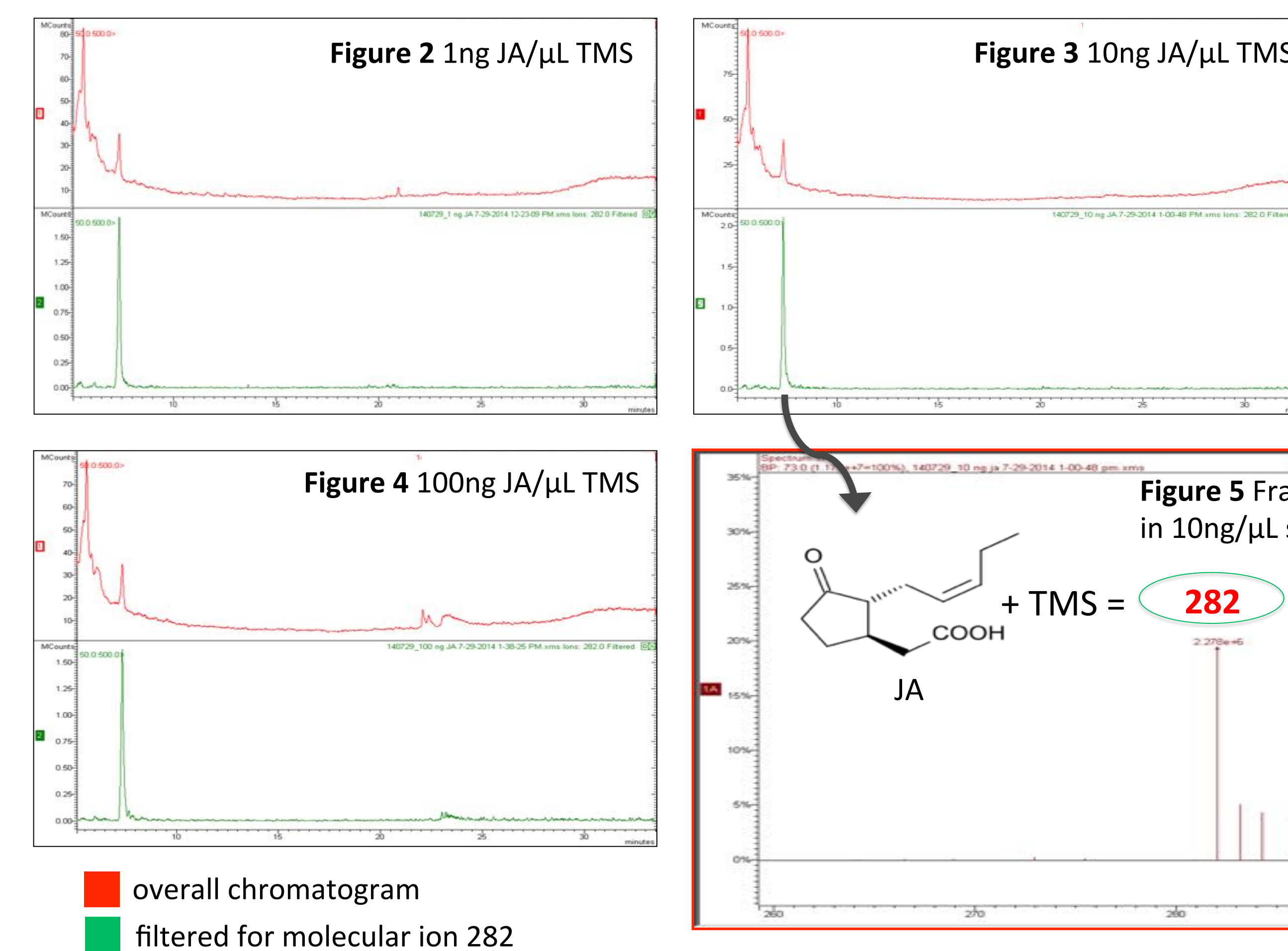
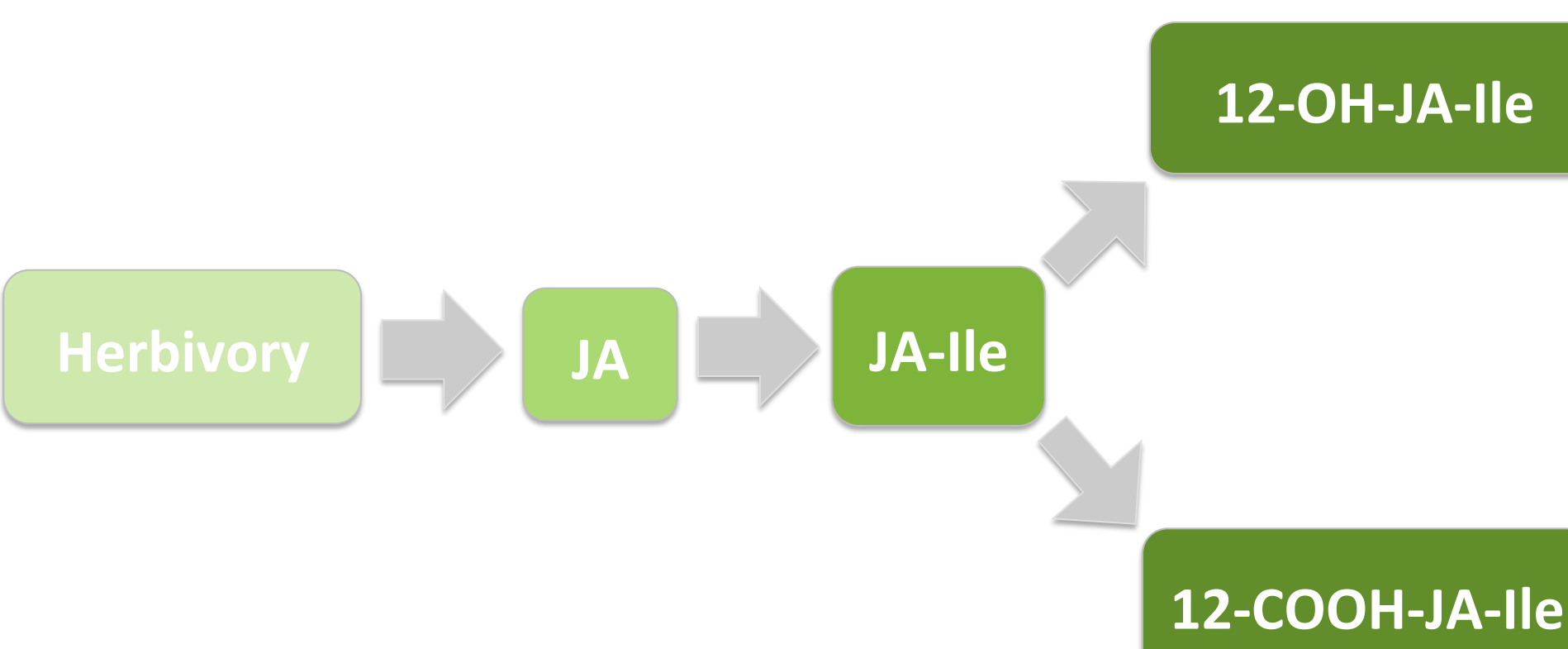
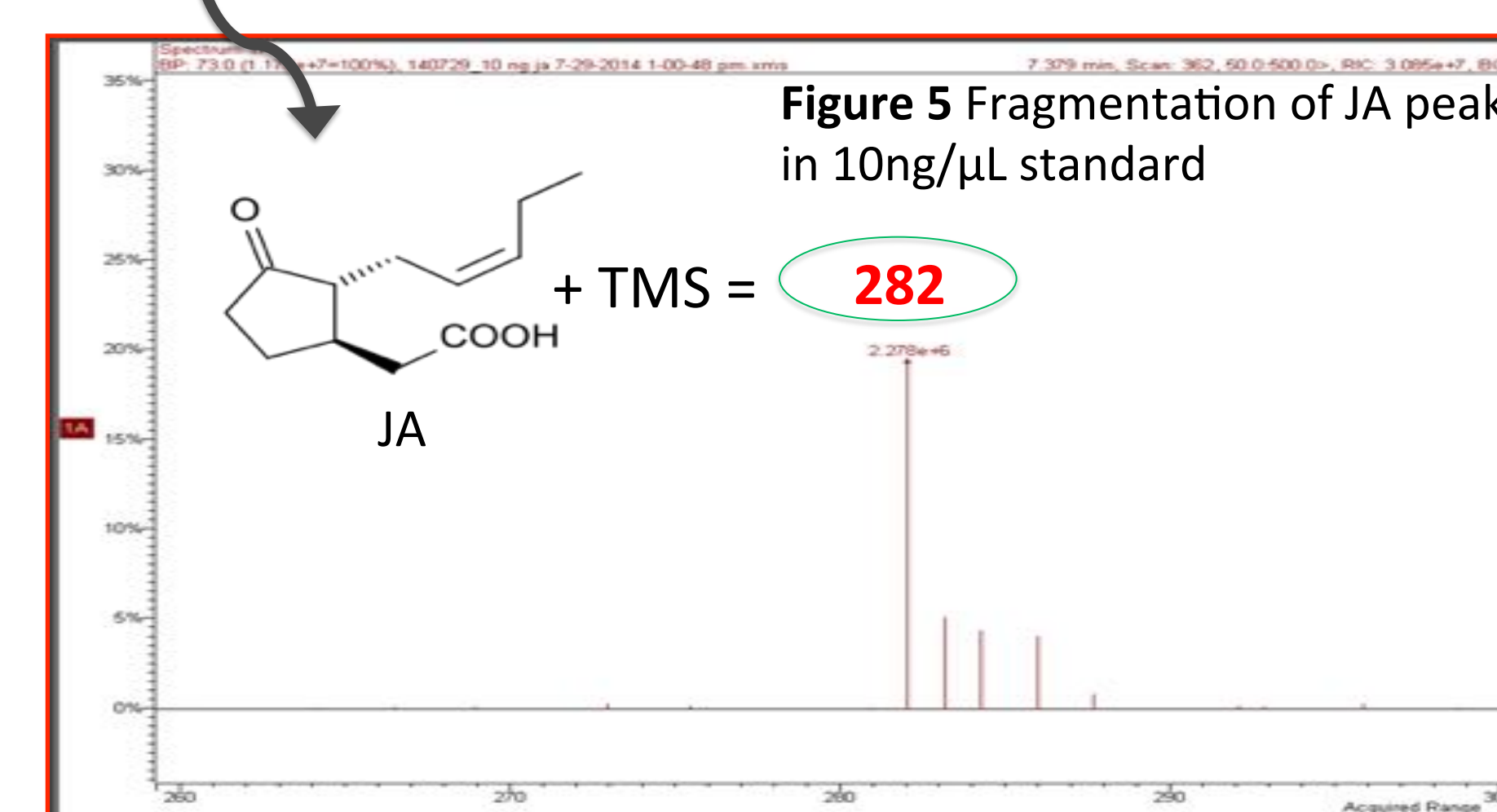


Figure 1 experimental setup



Gas chromatography-mass spectrometry (GC-MS) analysis of JA standards

Before experimentation began, we ran jasmonic acid standards with concentrations of 1, 10, and 100 ng/μL to test the machine's sensitivity to and retention time for the compound (Figures 2, 3, and 4, respectively). After trimethylsilyl (TMS) derivatization of the standards, the GC-MS was able to detect all three concentrations.



The chromatogram was filtered for molecular ion 282, TMS-derivatized JA. The samples were found to have a retention time of about 7.5 minutes, as shown by the consistency of the peaks in Figures 2, 3, and 4. In the fragmentation of the filtered chromatogram (Figure 5), the peak was shown to come from molecular ion 282, confirming the presence of JA.

Results

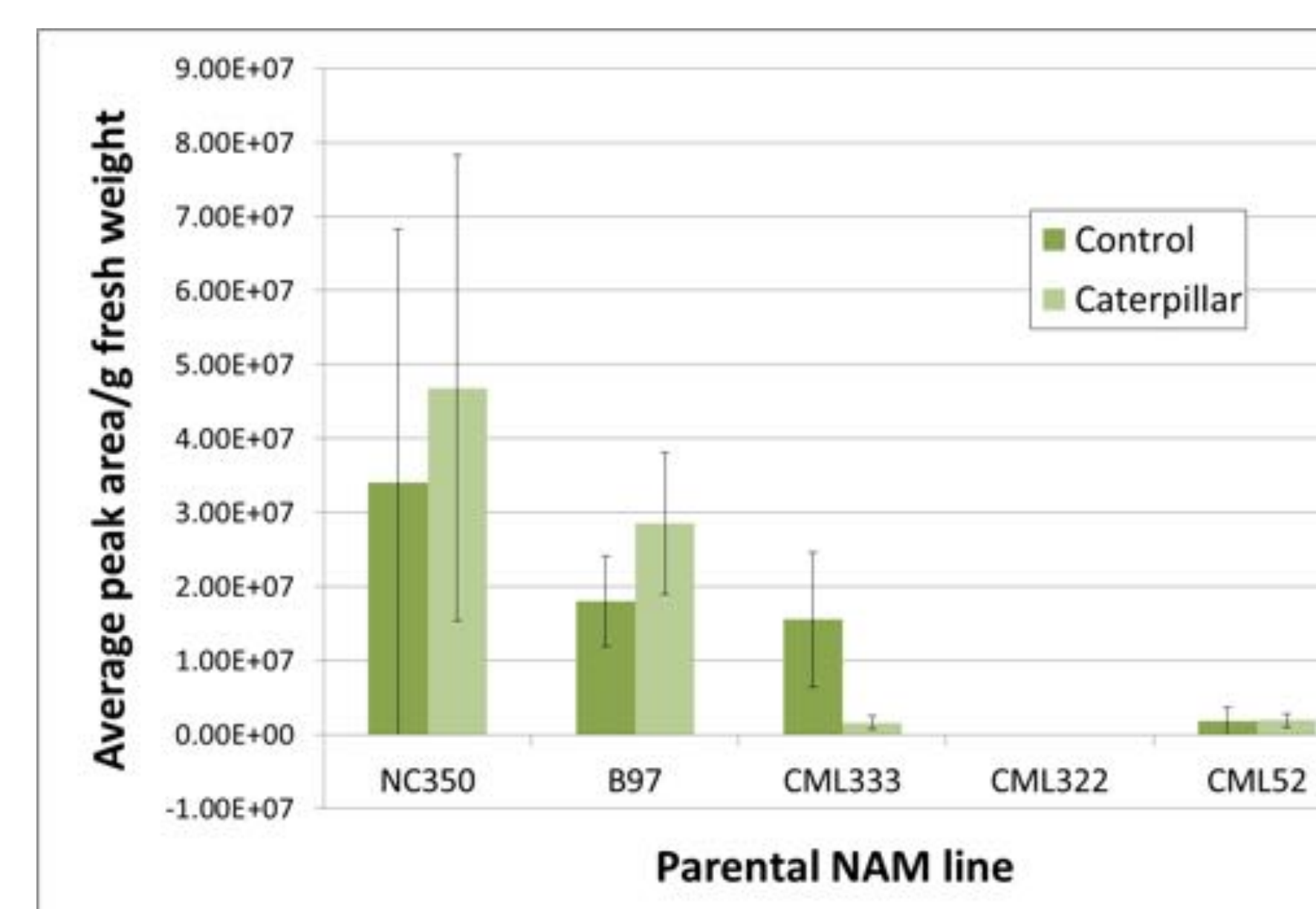


Figure 8 JA levels among 5 selected parental NAM lines

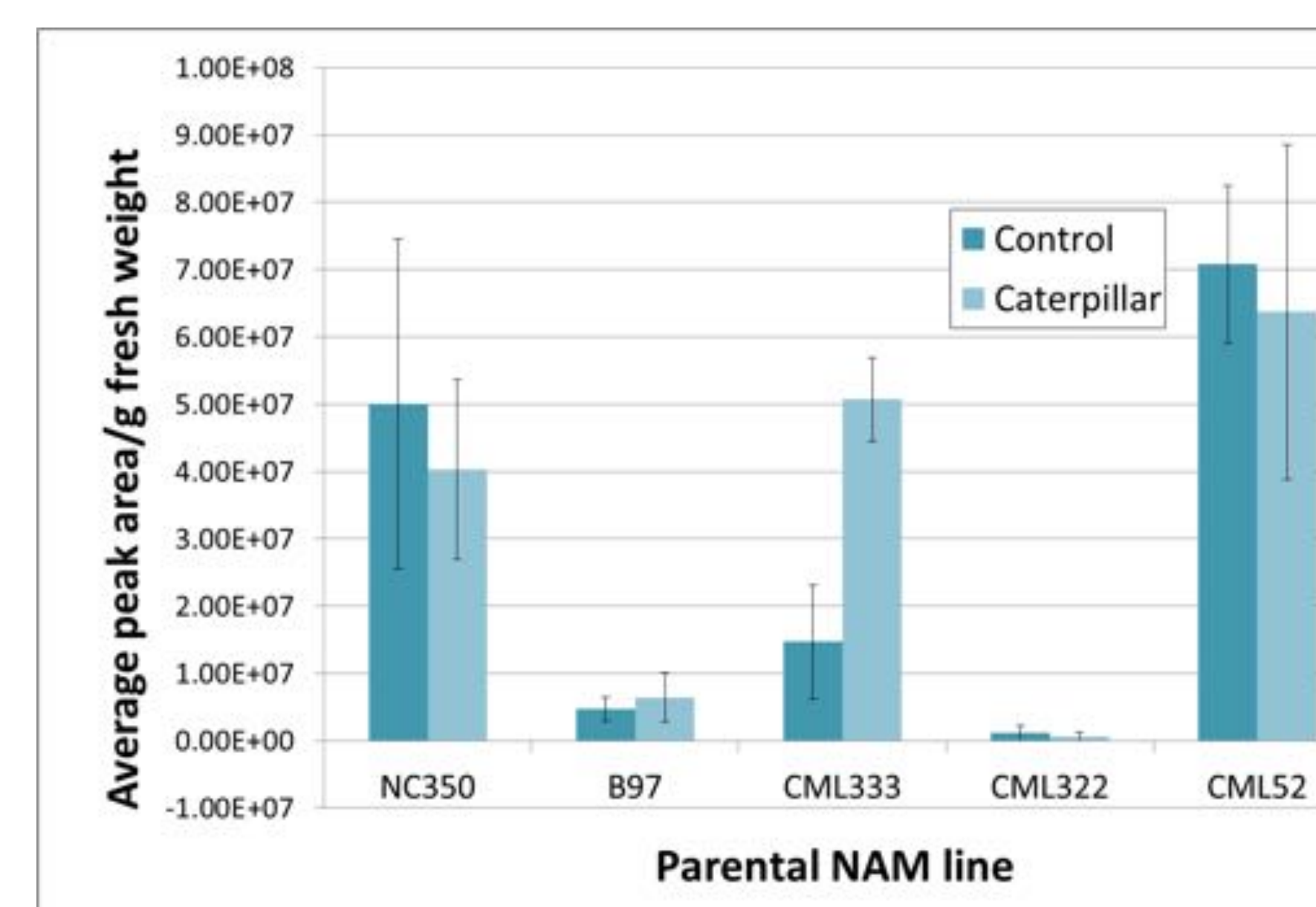
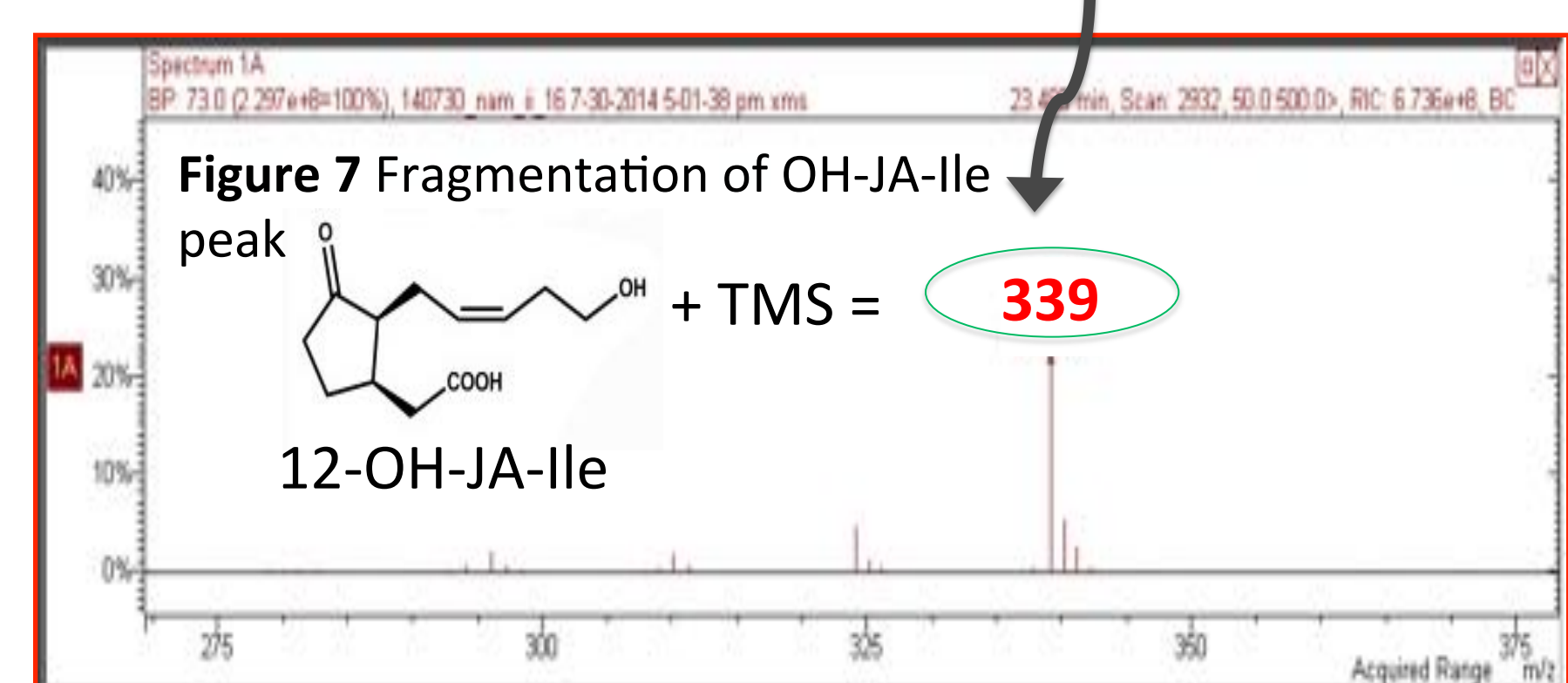
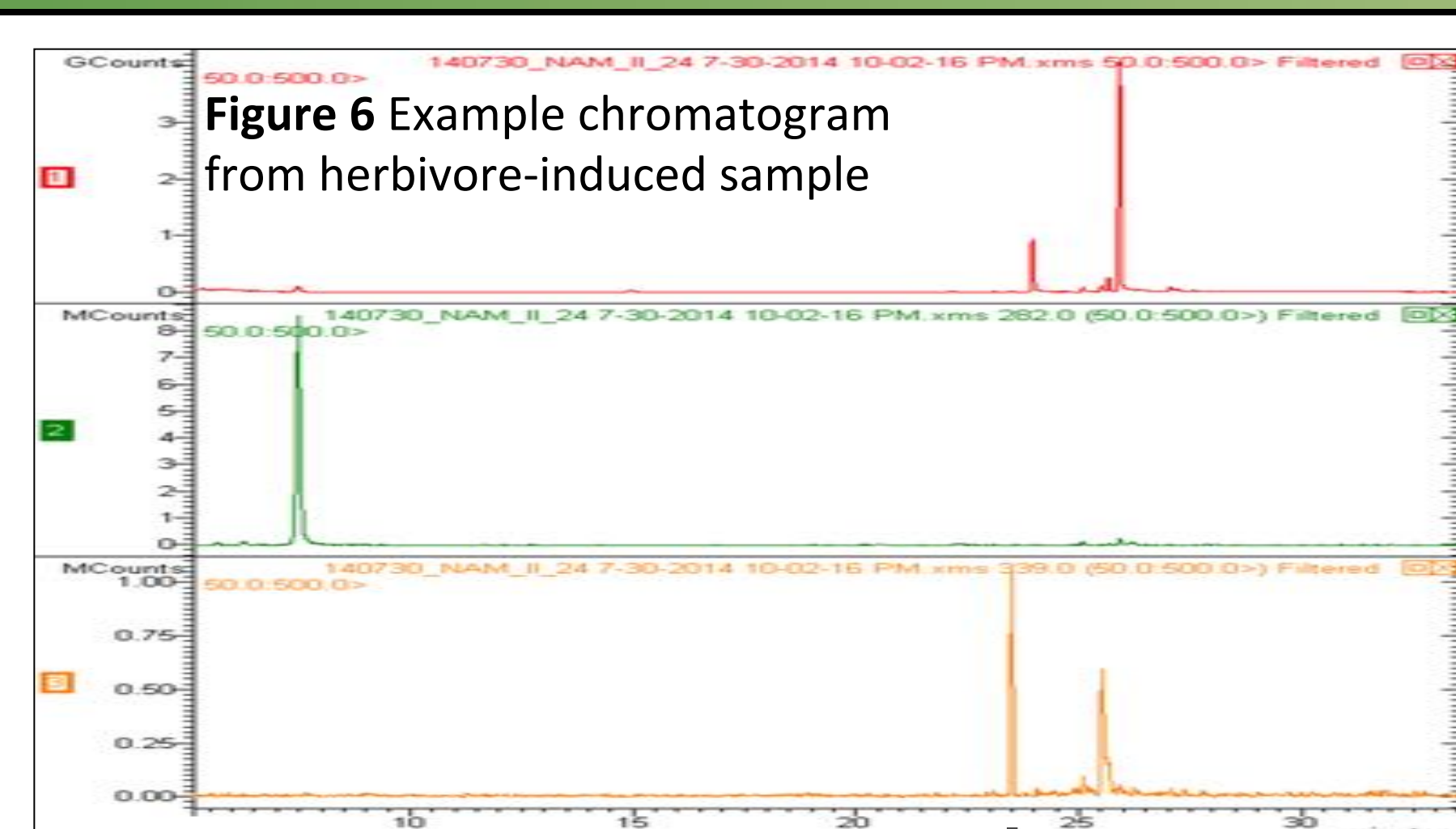


Figure 9 OH-JA-Ile levels among 5 selected parental NAM lines

GC-MS analysis of experimental and control samples after phytohormone extraction

Peaks having the proper molecular ion and retention time for JA were found in many samples (see Figure 6). In addition to JA peaks, we looked for OH-JA-Ile peaks by filtering the chromatograms for molecular ion 339, as some lines may have rapidly metabolized the JA spike into OH-JA-Ile prior to the collection of tissue 3 hours after initial herbivore induction. As seen in Figure 6, the OH-JA-Ile had a consistent retention time of 23.5 minutes, and was ultimately visible in more samples than JA.



■ overall chromatogram
■ filtered for molecular ion 282
■ filtered for molecular ion 339

Conclusions and perspectives

- We observed variability among the 5 selected parental NAM lines analyzed with respect to both JA levels and rate of metabolism to 12-OH-JA-Ile.
- The variability quantified here can be used as a starting point for pinpointing genes responsible for magnitude of JA signaling.
- The high presence of JA and OH-JA-Ile in some control lines, sometimes even surpassing that of the experimental, remains to be explored.

Literature

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