Supplemental Figure S1. OS elicitation enhances the accumulation of uni-parental transcript patterns of WIPK and LOX3, but not NPR1 in N×o lines (2-5).

After elicitation with *M. sexta* oral secretions (OS), *N. ×obtusiata* (N×o) lines 2-5 induced an increase in the accumulation of *N. attenuata*-wound induced protein kinase (Na-WIPK), and *N. obtusifolia*- lipoxygenase 3 (No-LOX3), and attenuated levels of Na-LOX3, *Na* and *No* non-expressor of pathogenesis-related (NPR1) transcripts. Asterisks indicate levels of significant difference between the maximum values of the pairs plotted together on the same graph (*P<0.05; **P<0.01).
Supplemental Figure S2. Both cis and trans regulatory elements act on the expression of WIPK, LOX3 and NPR1 genes elicited by M. sexta OS.

Wound induced protein kinase (WIPK), lipoxygenase 3 (LOX3) and pathogenesis-related (NPR1) transcripts accumulation was compared among N. attenuata tetraploid (NaT), N. obtusifolia tetraploid (NoT) and N. ×obtusiata (N×o) using the approach described by Zhang and Borevitz (2009). Briefly, the authors consider that a given gene is under the control
of only cis genetic elements if the specific parental expression difference is equal to the allele expression difference in the hybrid; otherwise, both cis and trans elements are involved. Our analysis revealed that the parental WIPK, LOX3 and NPR1 transcript accumulation difference between NaT and NoT is not equal to the difference of Na and No transcripts in N×o, suggesting that the regulation of the expression of these genes involves not only cis, but also trans elements. In this analysis, we considered only the maximal relative values of transcript accumulation elicited by M. sexta oral secretions (OS).
Supplemental Figure S3. Patterns of OS-elicited SA and JA accumulation in N×o 2-5 after OS elicitation.

After elicitation with *M. sexta* oral secretions (OS), *N. xobtusiata* (*N×o*) lines 2-5 accumulated high levels of *salicylic acid* (SA) and low levels of *jasmonic acid* (JA). Only the accumulation of JA was associated with a delay in the synthetic polyploids compared to their parental lines.
Supplemental Figure S4. *N*×*o* lines (2-5) enhance the accumulation of only one parental transcript of JAR4 and TPI, and accumulated different levels of JA-Ile and TPI activity after *M. sexta* OS elicitation.

After elicitation with *M. sexta* oral secretions (OS), *N. obtusiata* (*N*×*o*) lines 2-5 accumulated only *N. obtusifolia*-jasmonate-resistant4 (*No*-JAR4) transcripts and *N. attenuata*-trypsin protease inhibitor (*Na*-TPI) transcripts, but not that of *Na*-JAR4 and *No*-TPIs. The maximum levels of accumulated jasmonic acid–isoleucine (JA-Ile) and active TPIs were different among *N*×*o* lines. All polyploid lines showed a delay in the accumulation of JAR4, JA-Ile as well as transcript and active TPI levels compared to their parental lines. Asterisks
indicate levels of significant difference between the maximum values of the pairs plotted together on the same graph (\*\*P<0.01).
Supplemental Figure S5. Methyl jasmonate treatment of \textit{N\times o1}-5 elicits transcripts of both parental LOX3, JAR4 and TPIs, demonstrating that the uniparental pattern of transcript accumulation observed after OS elicitation is not due to gene inactivation.

After methyl jasmonate (MeJA) application, \textit{N.\ xobtusiata} line 2-5 (\textit{N\times o} 2-5) accumulated both parental lipoxygenase 3 (LOX3), jasmonate-resistant 4 (JAR4) and trypsin protease inhibitor (TPI). Application of MeJA restored the delay in the accumulation of JAR4 and TPI transcripts observed after OS elicitation. Asterisks indicate levels of significant difference between the maximum values of the pairs plotted together on the same graph (*P<0.05; **P<0.01)
Supplemental Figure S6. PCR products amplified in \textit{N. attenuata} (Na) and \textit{N. obtusifolia} (No) cDNA using RT primer pairs specific for Na and No- wound induced protein kinase (WIPK), lipoxygenase 3 (LOX3), jasmonate-resistant 4 (JAR4), trypsin protease inhibitor (TPI) and non-expressor of pathogenesis-related (NPR1)

PCR products (10 µL/well) were run in a 1.5% agarose gel and visualized with ethidium bromide staining.