
Figures and figure supplements

Evidence for suppression of immunity as a driver for genomic introgressions and host range expansion in races of *Albugo candida*, a generalist parasite

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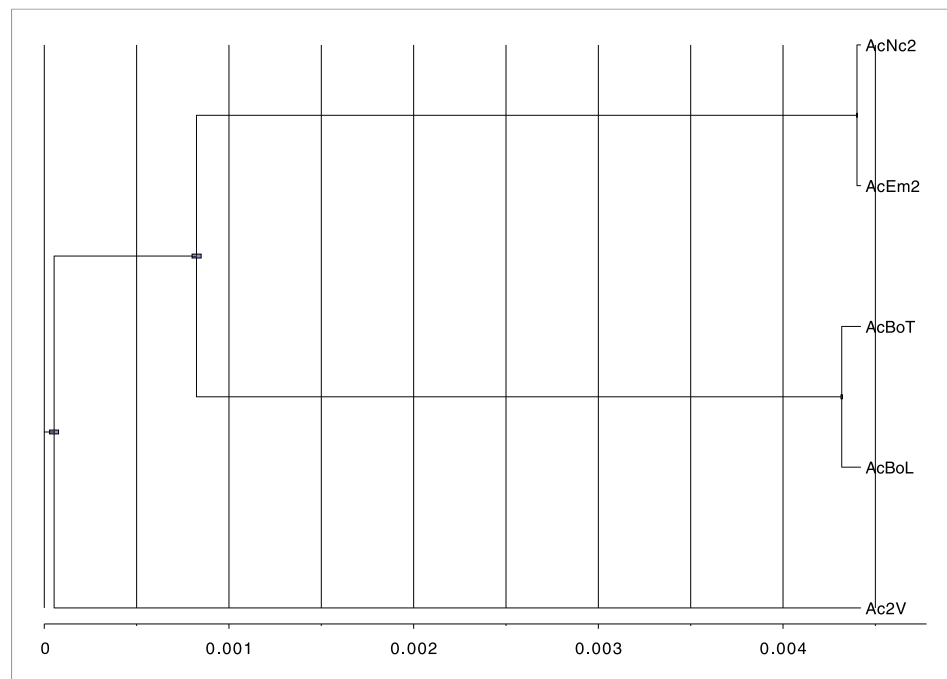


Figure 1. Phylogeny shows that the five sequenced *Albugo candida* isolates fall into three divergent races. BEAST tree constructed based on using contig 1 (398,508 bp) shows the divergence among the three *A. candida* races (AcEm2 and AcNc2; AcBoT and AcBoL; Ac2V). Blue bars represent the 95% Higher Posterior Density (HPD). Here, we used a strict molecular clock fixed at 1.0 in order to show the relationship in the scale of substitutions per site.
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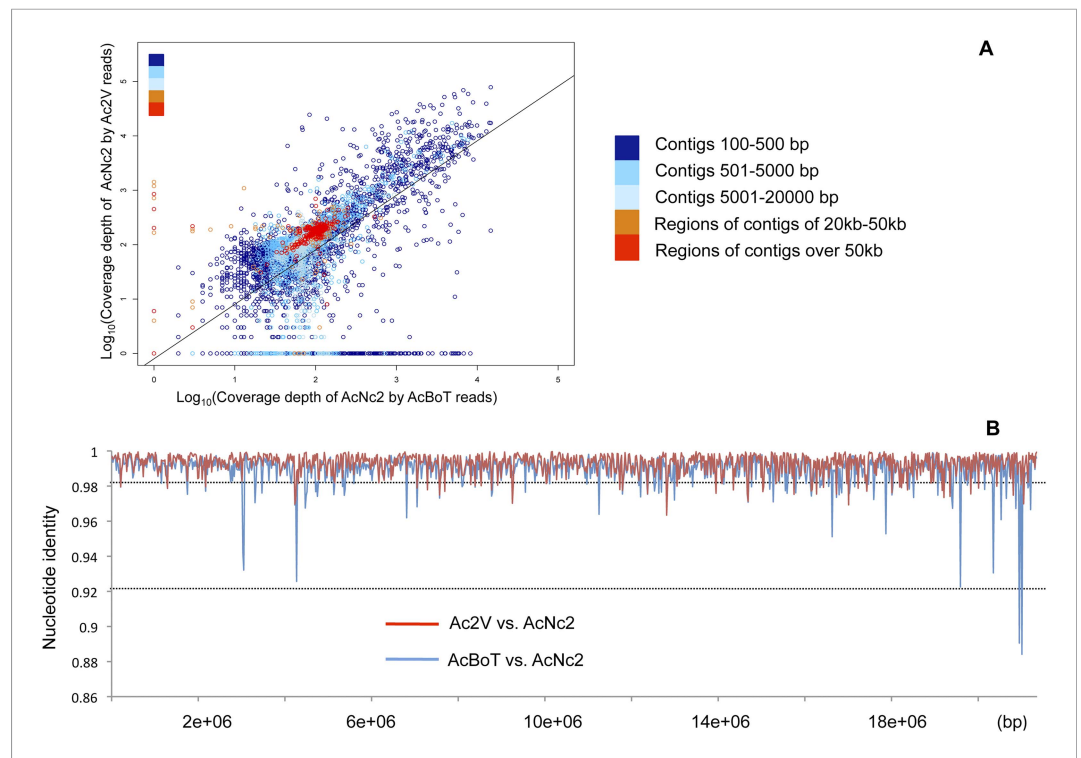


Figure 2. Comparison of *A. candida* races using alignments of Illumina reads against the AcNc2 assembly. **(A)** Positive correlation between the depths of coverage of the reference assembly (AcNc2) by the Ac2V and AcBoT reads. For the reference contigs less than 20 kb, the mean coverage was calculated across the whole contig length and log-transformed. For the contigs over 20 kb, the mean coverage was calculated for the sliding window of 20 kb and log-transformed. Y-axis shows the log-transformed depth of the reference coverage by the Ac2V reads; X-axis shows the log-transformed depth of the reference coverage by the AcBoT reads. **(B)** Nucleotide identity amongst the homologous genomic regions of Ac2V, AcBoT and AcNc2. The mean identity was calculated for the sliding window of 20 kb.

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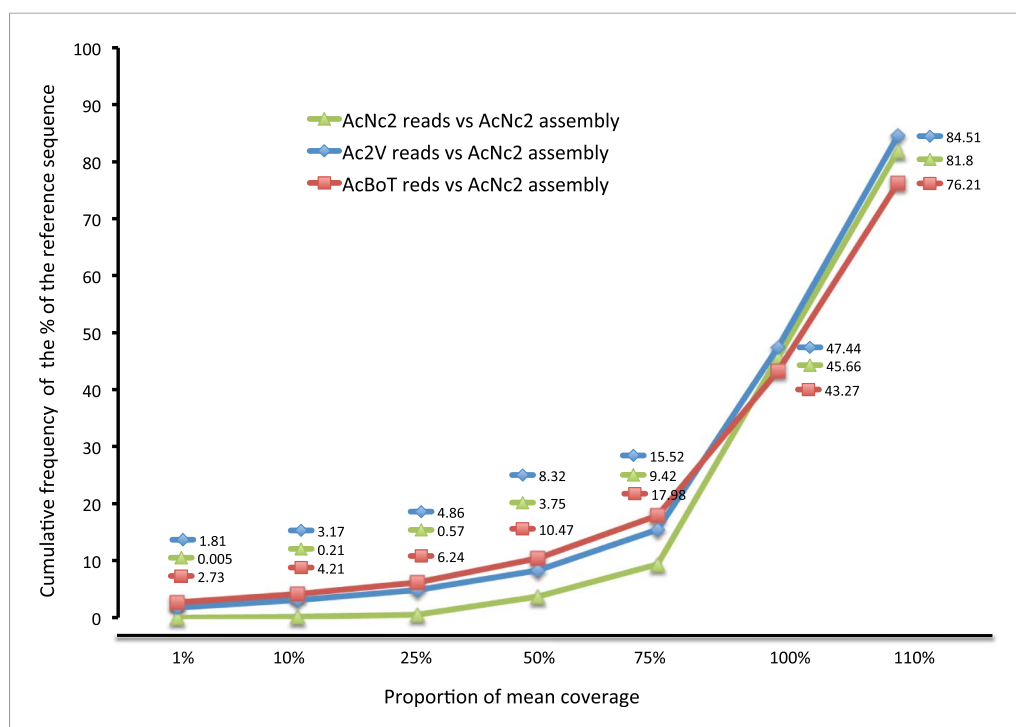


Figure 2—figure supplement 1. Coverage of the reference assembly (AcNc2) by Ac2V and AcBoT. Proportion of mean coverage is a measure relative to the depth of coverage of the reference reads mapped back to the reference assembly. The proportion of AcNc2 assembly not covered by AcBoT and/or Ac2V reads ($\leq 10\%$ of the mean coverage) was 3.17% (971,030 bp) in Ac2V and 4.21% (1,285,877 bp) in AcBoT.

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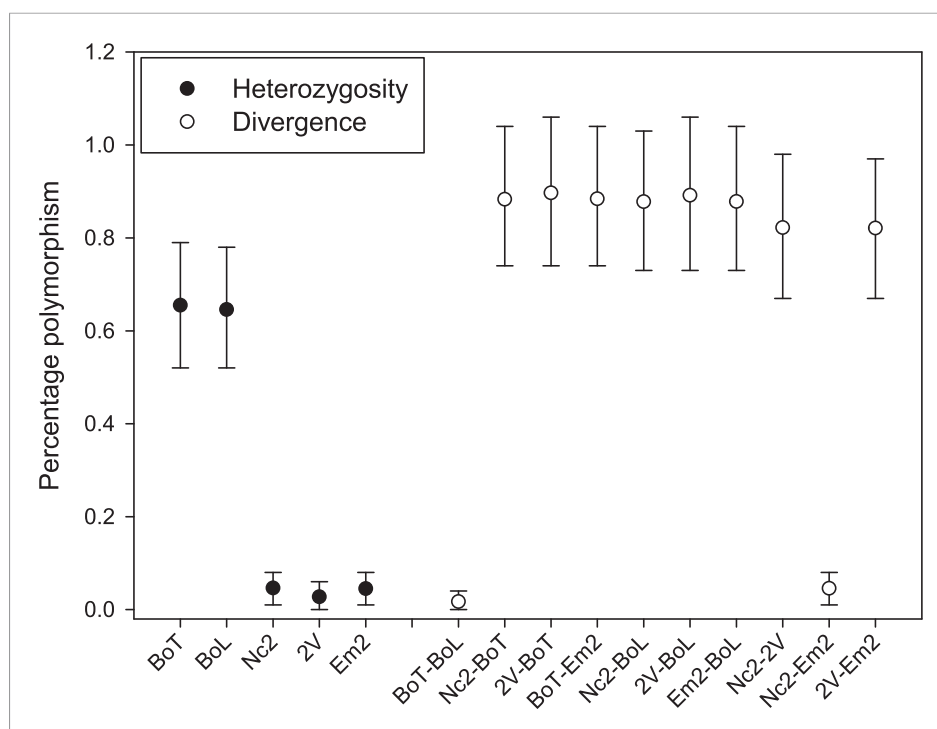


Figure 3. Nucleotide polymorphism within and between *A. candida* isolates. Mean ($\pm 5-95\%$ CI) polymorphism expressed as the percentage observed heterozygote sites (solid symbols) and percentage nucleotide divergence (open symbols) at contig 1. Confidence intervals were calculated using a bootstrap of contig 1 after removal of indels. Isolates infecting the same host plant (i.e., AcBoT-AcBoL and AcEm2- AcNc2) show little nucleotide divergence, which indicates that they are genotypically almost identical (i.e., diverged by less than 0.05%). Nevertheless, the *Brassica oleracea* infecting race (AcBoT and AcBoL) possess a relatively high heterozygosity compared to the isolates of the *Arabidopsis thaliana* infecting race. Moreover, most of this heterozygous polymorphism is shared (low nucleotide divergence) and presence of the majority of heterozygous sites is consistent with clonal reproduction.

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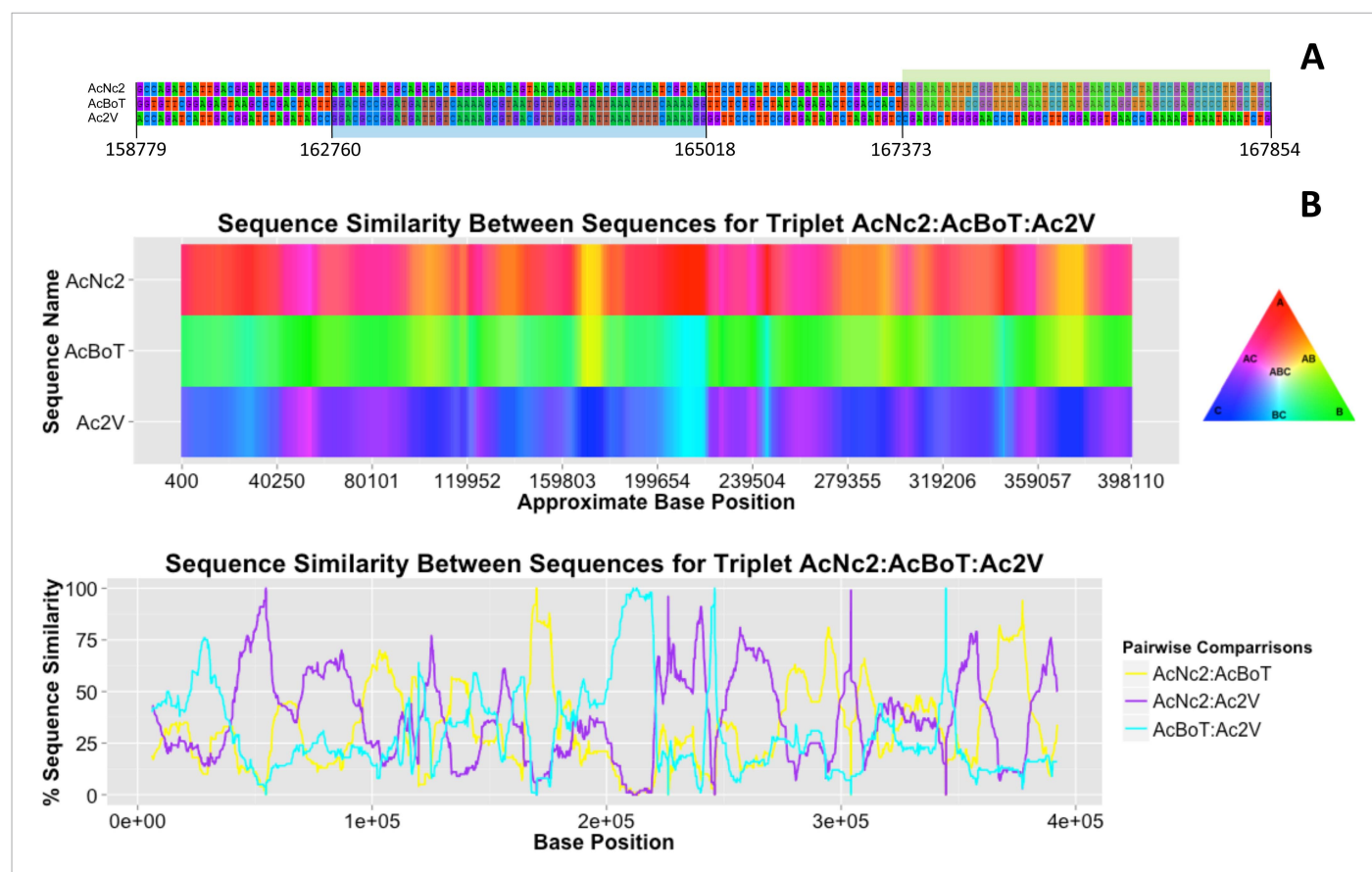


Figure 4. Variation in sequence similarity between races. **(A)** Alignment of nucleotides in between positions 158,779 and 167,382 within 'contig 1' of three *A. candida* races (AcNc2, AcBoT and Ac2V) illustrating two recombination blocks coloured blue and green. Both blocks show high sequence similarity between races. Also shown is the sequence divergence in between blocks. Alignment gaps and monomorphic sites have been removed. **(B)** The sequence similarity at 'contig 1' amongst three *A. candida* races was visualised using the colours of a RGB colour triangular in the software HybRIDS (<http://www.norwichresearchpark.com/HybRIDS>). Areas where two contigs have the same colour (yellow, purple or turquoise) are indicative of two races sharing the same polymorphisms. The linear plot of the proportion of SNPs shared between the three pairwise comparisons between the races. Shown on the X-axis is the actual base position. The graphs were made in the R package HybRIDS (<http://www.norwichresearchpark.com/HybRIDS>).

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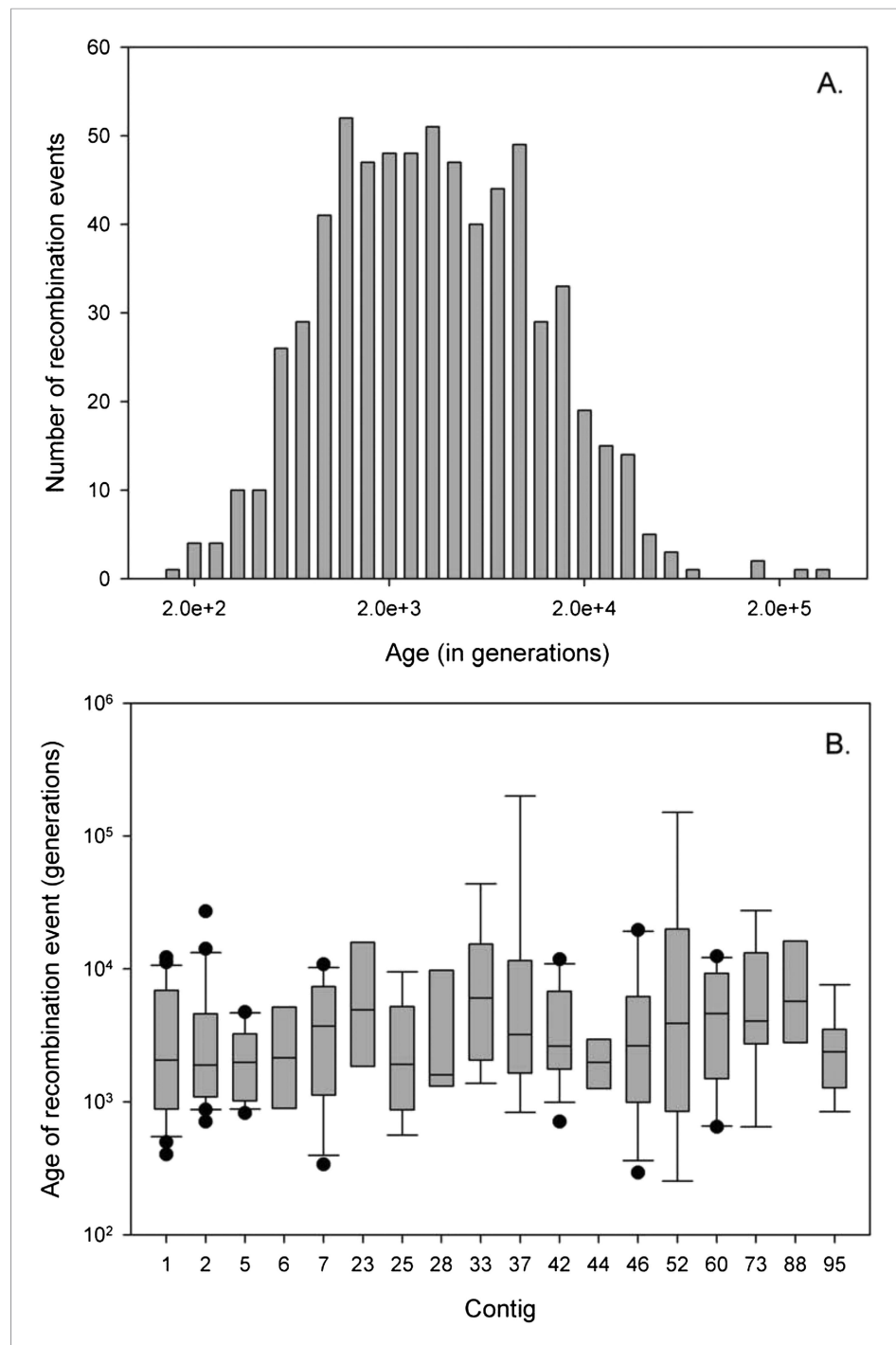


Figure 5. Age of recombination blocks. (A) Age of the 675 recombination blocks (mutation rate of $\mu = 10^{-6}$) estimated using binomial mass function; (B) Boxplot of the median (plus first nation blocks and third quartile) log-age of recombination events in contigs. Only contigs with eight or more events are shown. There is no significant difference in age of events between contigs (GLM: $F_{22, 233} = 1.06$, $p = 0.387$).

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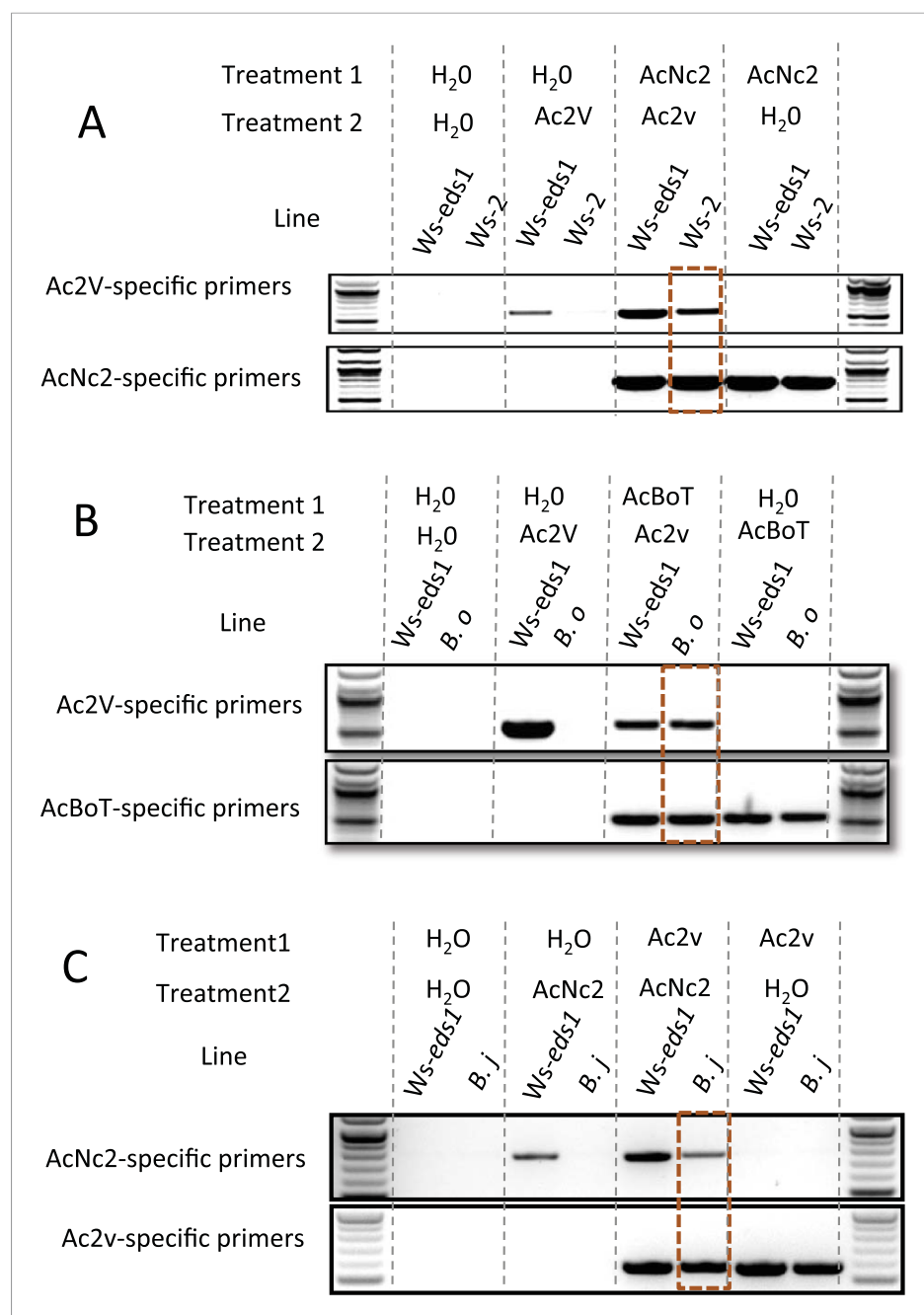


Figure 6. PCR with race-specific markers on DNA prepared from plant tissue generated from co-infection assays. **(A)** Co-infection assay of AcNc2 followed by Ac2V onto *Ws-eds1* and *Ws-2*. **(B)** Co-infection of AcBoT followed by Ac2V onto *Ws-eds1* and *B. oleracea* (*B.o*). **(C)** Co-infection of Ac2V followed by AcNc2 onto *Ws-eds1* and *B. juncea* (*B.j*). Bands highlighted in orange indicate amplification of secondary inoculum on usually non-host plants upon primary inoculation with virulent *A. candida*. These experiments were repeated multiple times with similar results (see **Supplementary file 6**).

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