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**Locus-dependent selection in crop-wild hybrids of lettuce under field conditions and its implication for GM crop development**

Hooftman, D.A.P.; Flavell, A.J.; Jansen, H.; den Nijs, H.C.M.; Syed, N.H.; Sørensen, A.P.; Orozco-ter Wengel, P.; van de Wiel, C.C.M.

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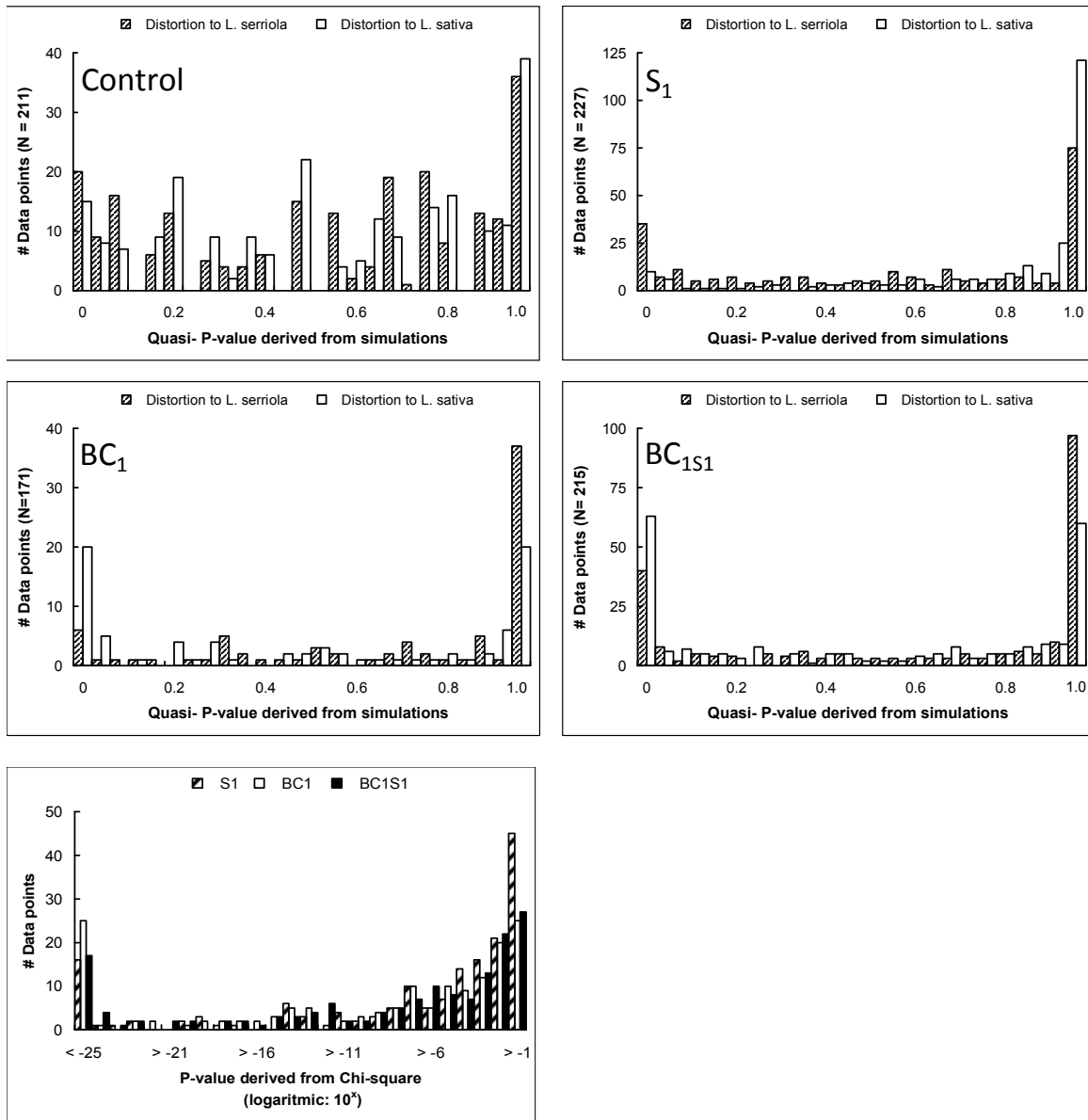
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**Figure S1. Histograms of P-value distributions for distortion** in the direction of containing more *L. serriola* or *L. sativa* alleles based on a Monte Carlo algorithm, 50,000x drawing N virtual plants from the expected distribution per locus. The observed distribution was compared to these confidence intervals. Each locus was independently drawn per virtual plant. Left-above: control population grown in the greenhouse, Right-above: S<sub>1</sub> generation under field exposure; Left-middle: BC<sub>1</sub> generation under field exposure. Right-middle: BC<sub>1S1</sub> generation under field exposure. Left-below: P-value distribution for all 3 populations for significant alterations in LD compared to the control generation; note the 10<sup>x</sup> scaling of x-axis. Chi-square testing was used for testing of statistical significance, using LD and (1-LD) for both expected (control) and observed (one of the populations) as variables (df = 1).