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, J.C.M.; Syed, N.H.; Sørensen, A.P.; Orozco-ter Wengel, P.; van de Wiel, C.C.M.

Published in: Evolutionary Applications

DOI: 10.1111/j.1752-4571.2011.00188.x

Citation for published version (APA):

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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:** S₁ generation under field exposure; **Left-middle:** BC₁ generation under field exposure. **Right-middle:** BC₁S₁ 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 $10^8$ 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).