

Article

Supplementary material : Management practices and breeding history of varieties strongly determine the fine genetic structure of crop populations: A case study based on European wheat populations

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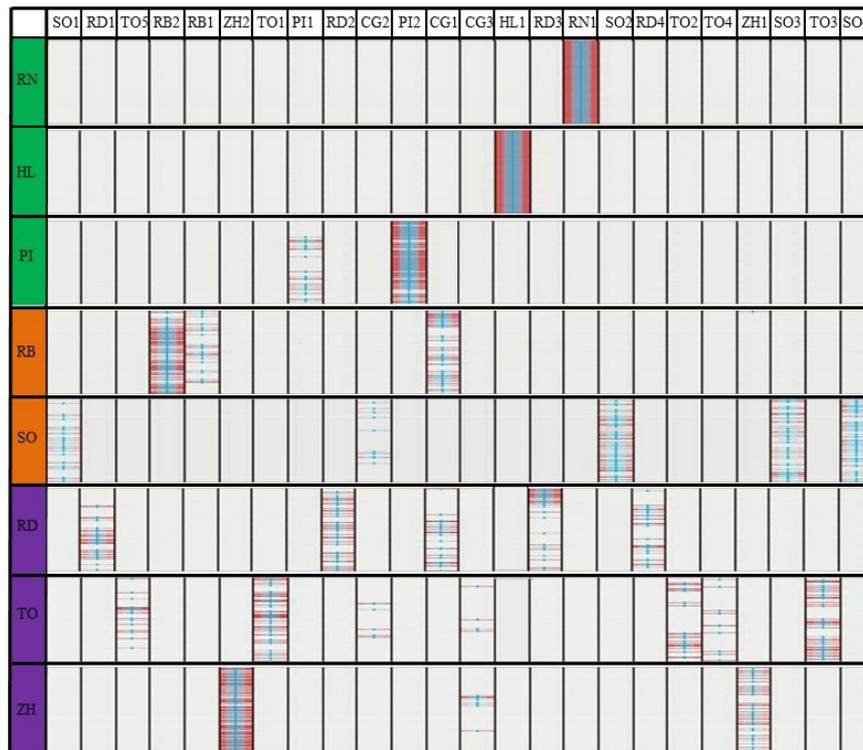
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Supplemental Material, Figure S2. Distribution of the 1325 genotypes among their samples in line and among their genetic groups in column. Assignment of genotypes to genetic groups was done using the DAPC method with an optimal number of cluster equal to 24.

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Table S1. Pairwise F_{ST} computed between the 8 sample populations. 95% confidence interval (CI) was estimated based on 1000 bootstraps.

Pairwise	F_{ST}	95%CI
HL-RN	0.99	(0.98-1)
PI-RN	0.92	(0.88-0.95)
HL-PI	0.91	(0.87-0.94)
HL-ZH	0.85	(0.79-0.9)
RN-ZH	0.83	(0.75-0.88)
RN-SO	0.80	(0.71-0.87)
HL-SO	0.74	(0.63-0.82)
RD-RN	0.74	(0.65-0.81)
PI-SO	0.73	(0.64-0.8)
SO-ZH	0.72	(0.63-0.8)
PI-ZH	0.70	(0.6-0.79)
RN-TO	0.70	(0.62-0.75)
RB-RN	0.68	(0.61-0.76)
HL-RD	0.64	(0.54-0.71)
PI-TO	0.61	(0.51-0.68)
HL-RB	0.60	(0.52-0.68)
RD-ZH	0.59	(0.49-0.68)
RB-ZH	0.56	(0.48-0.66)
PI-RB	0.55	(0.46-0.63)
PI-RD	0.54	(0.45-0.63)
TO-ZH	0.54	(0.43-0.63)
HL-TO	0.46	(0.35-0.56)
SO-TO	0.44	(0.32-0.54)
RD-SO	0.43	(0.3-0.53)
RB-SO	0.37	(0.24-0.48)
RD-TO	0.31	(0.2-0.4)
RB-TO	0.28	(0.2-0.36)
RB-RD	0.25	(0.17-0.33)