Comparative analyses identify the contributions of exotic donors to disease resistance in a barley experimental population

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Figure S1  SNP positions and allele frequency comparison of the Closed and Reopened panels on each linkage group. The frequency of the minor allele in the Closed panel is shown. The increase in frequency of some SNPs in the Reopened panel results in SNP states exceeding 50% in frequency. The red lines correspond to the SNPs in the high $F_{ST}$ blocks.
Figure S1 cont.
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Figure S2  Population history, $N_0$, $N_1$ and $N_2$ stand for the Ancestral population, the Closed population and the Reopened population. $T_1$ is the start of the bottleneck population, ~8000 generations before present. $T_2$ is the end of the bottleneck and $T_3$ is the start of the Reopened population, ~15 generations before present. Migration is from the Ancestral population to the Reopened population.
Figure S3  (A) Observed SFS in the Ancestral panel. (B) Simulated SFS in the Ancestral panel using a discovery panel with eight chromosomes and a minor allele count of three.
Figure S4  $F_{ST}$ value versus minor allele frequency. The horizontal dashed line corresponds to genome-wide 97.5\textsuperscript{th} percentile of $F_{ST}$ values. All SNPs below the threshold are shown as solid black points. SNPs above the threshold are shown in three symbols corresponding to each of the three linkage groups. Minor allele frequency is based on the whole dataset, including both the Closed and Reopened panels.
Figure S5  Prior and posterior density of relative size of the Closed panel from simulations.
Figure S6  The heatmap of bottleneck. The x-axis is the timing of the end of the bottleneck. The y-axis is the relative size of the bottleneck.
Figure S7  Prior and posterior density of migration rate from the Ancestral panel to the Reopened panel.
Figure S8  IBS and LD plot on linkage group 6H. The upper panel shows the number of IBS segments between the donor lines and their progeny in the Reopened panel. The vertical dashed lines delimit the high $F_{ST}$ block. The middle and lower panels are the LD heatmaps of the Reopened and Closed panels respectively.
Figure S9  IBS between each of the donor lines and their respective progeny in the Reopened panel on 4H and 6H. The vertical dashed lines delimit the high $F_{St}$ block.
Figure S10  Percent of adjacent SNPs at varying levels of LD in the Closed and Reopened panel.
The Minnesota (MN) barley breeding population (the basis of the Closed panel) has greatly reduced diversity relative to donor lines (Table 1). To generate simulations consistent with this difference in diversity among populations, we simulate the establishment of bottleneck associated with the establishment of the MN population. In ms simulations, we use values $U(0.000025, 0.008)$ and $U(0, 0.02)$ for the end of the bottleneck and relative size of the Closed panel. The population represented by the Reopened panel started ~15 generations ago. For scaling in ms, with time scaled in $4N_0$, we use $N_0 = 150,000$ based on $\theta = 4N_0\mu = 0.003$ and $\mu = 5 \times 10^{-9}$, where $\mu$ is mutation rate per site per generation. We assume one generation per year. The bottleneck started at 8000/$4N_0 = 0.013$. The Reopened panel started 15 generations before present, 15/$4N_0 = 0.000025$. The end of the bottleneck can be anytime between the start of the Reopened panel (0.000025) and the start of the bottleneck (0.013). Therefore, the relative size of the Closed panel is sampled from a uniform distribution $U(0, 0.02)$. The end of bottleneck is also sampled from a uniform distribution $U(0.000025, 0.013)$. Based on initial simulations, we refined the interval to be $U(0.000025, 0.008)$ in the final simulation.

The command line for simulating the ancestral population and the Closed panel is:
```
ms 240 1000000 -t 150 -r 1000 1000 -l 2 120 120 -n 2 0.025 -en tbs 2 tbs -ej 0.013 2 1
```

The command line for simulating all populations is
```
ms 360 1000000 -t 150 -r 1000 1000 -l 3 120 120 120 -n 2 0.025 -en 0.0015 2 0.01 -n 3 0.09 -ej 0.0133 2 1 -m 3 1 tbs -ej 0.000025 3 2 0
```
Table S1  The donor line/lines of each line in the Reopened panel.

| Reopened lines | Donor lines        |
|----------------|--------------------|
| C113.004       | Chevron            |
| C119.002       | Chevron            |
| FEG59.09       | Ac Oxbow           |
| FEG60.27       | BT463              |
| FEG61.37       | Clho6613           |
| FEG63.16       | Chevron            |
| FEG63.56       | Chevron            |
| FEG65.02       | Zhedar1            |
| FEG66.05       | Zhedar1            |
| FEG66.08       | Zhedar1            |
| FEG66.21       | Zhedar1            |
| FEG66.31       | Zhedar1            |
| FEG67.12       | Frederickson       |
| FEG69.24       | PFC88209           |
| FEG69.38       | PFC88209           |
| FEG73.13       | Hor211             |
| FEG73.49       | Hor211             |
| FEG74.18       | Hor211             |
| FEG74.19       | Hor211             |
| FEG75.39       | Hor211             |
| FEG80.06       | Zhedar1            |
| FEG80.53       | Zhedar1            |
| FEG81.58       | Harrington         |
| FEG81.60       | Harrington         |
| FEG82.16       | Chevron            |
| FEG86.03       | Hor211             |
| FEG86.53       | Hor211             |
| FEG88.73       | Atahualpa, Zhedar1 |
| FEG88.87       | Atahualpa, Zhedar1 |
| FEG89.73       | Hor211             |
| FEG90.31       | Zhedar1, Atahualpa |
| FEG90.35       | Zhedar1, Atahualpa |
| FEG91.28       | PFC88209, Frederickson |
| FEG93.12       | Frederickson       |
| FEG93.36       | Frederickson       |
| FEG94.20       | Zhedar1            |
FEG94.41  Zhedar1
FEG96.06  Ac Oxbow
FEG96.55  Ac Oxbow
FEG97.14  Ac Oxbow
FEG97.44  Ac Oxbow
FEG98.53  PFC88209
FEG99.10  Ac Oxbow
FEG99.51  Ac Oxbow
FEG100.17 Zhedar1
FEG100.33 Zhedar1
FEG100.41 Zhedar1
FEG100.47 Zhedar1
FEG103.44 Ac Oxbow, Harrington
FEG103.45 Ac Oxbow, Harrington
FEG104.63  Zhedar1
FEG104.89  Zhedar1
FEG105.33  PFC88209
FEG105.59  PFC88209
FEG109.13  Ac Oxbow
FEG109.44  Ac Oxbow
FEG109.54  Ac Oxbow
FEG111.10  Ac Oxbow, Zhedar1
FEG111.13  Ac Oxbow, Zhedar1
FEG111.24  Ac Oxbow, Zhedar1
FEG112.14  Ac Oxbow, Atahualpa
FEG113.85  Ac Oxbow, Zhedar1
FEG114.33  Clho6613
FEG116.05  Zhedar1
FEG117.24  Zhedar1
FEG118.05  PFC88209
FEG118.41  PFC88209
FEG118.69  PFC88209
FEG121.03 Zhedar1, Ac Oxbow
FEG121.16 Zhedar1, Ac Oxbow
FEG121.29 Zhedar1, Ac Oxbow
FEG121.43 Zhedar1, Ac Oxbow
FEG122.36 Hor211, PFC88209
FEG122.50 Hor211, PFC88209
FEG122.92 Hor211, PFC88209
| Sample ID | Description |
|-----------|-------------|
| FEG124.35 | PFC88209    |
| FEG125.46 | Zhedar1     |
| FEG125.69 | Zhedar1     |
| FEG126.08 | Zhedar1     |
| FEG126.14 | Zhedar1     |
| FEG129.41 | Frederickson|
| FEG129.60 | Frederickson|
| FEG132.05 | Zhedar1, Frederickson |
| FEG132.63 | Zhedar1, Frederickson |
| FEG138.08 | Zhedar1, Hor211 |
| FEG138.27 | Zhedar1, Hor211 |
| FEG141.18 | Ac Oxbow    |
| FEG141.20 | Ac Oxbow    |
| FEG142.13 | Zhedar1, Hor211 |
| FEG142.28 | Zhedar1, Hor211 |
| FEG142.55 | Zhedar1, Hor211 |
| FEG144.21 | Ac Oxbow, Hor211 |
| FEG144.27 | Ac Oxbow, Hor211 |
| FEG144.68 | Ac Oxbow, Hor211 |
| FEG146.09 | Frederickson|
| FEG146.46 | Frederickson|
| FEG146.68 | Frederickson|
| FEG147.03 | Zhedar1, Atahualpa |
| FEG147.14 | Zhedar1, Atahualpa |
| FEG147.63 | Zhedar1, Atahualpa |
| FEG148.22 | Ac Oxbow    |
| FEG148.56 | Ac Oxbow    |
| FEG149.18 | ND20407     |
| FEG149.65 | ND20407     |
| FEG150.42 | ND20493     |
| FEG150.49 | ND20493     |
| FEG153.22 | Zhedar1     |
| FEG155.07 | Ac Oxbow    |
| FEG156.09 | Zhedar1     |
| FEG161.03 | Ac Oxbow    |
| FEG162.22 | Ac Oxbow    |
| FEG163.21 | Zhedar1     |
| FEG164.33 | Hor211, PFC88209 |
| FEG166.38 | Zhedar1     |
| Code     | Description |
|----------|-------------|
| FEG168.09 | Comp351     |
| FEG169.47 | Hor211      |
| FEG170.07 | Hor211      |
| FEG172.40 | Hor211      |
| FEG175.57 | Zhedar1, Hor211 |
Table S2  The observed pairwise diversity (scaled by the number of segregating sites) for each linkage group and the median of simulated pairwise diversity in the Ancestral panel, Closed, and Reopened panel.

| LG | Ancestral panel | Closed panel | Reopened panel |
|----|-----------------|--------------|----------------|
| 1H | 0.049           | 0.002        | 0.004          |
| 2H | 0.060           | 0.004        | 0.004          |
| 3H | 0.072           | 0.001        | 0.005          |
| 4H | 0.057           | 0.001        | 0.005          |
| 5H | 0.068           | 0.004        | 0.007          |
| 6H | 0.059           | 0.007        | 0.011          |
| 7H | 0.044           | 0.002        | 0.002          |
| Simulated | 0.054 | 0.007 | 0.014 |
Table S3  Markers from previous studies that are within or flanking (~5 cM) the high $F_{ST}$ blocks and their estimated positions.

| Linkage group | Marker | Position (cM) |
|---------------|--------|---------------|
| 2H            | ABC252 |               |
|               | CDO373 |               |
|               | F3hA   |               |
|               | MWG5208|               |
|               | pKABA1 |               |
|               | Ebmc0415| 142.42 – 143.72|
|               | Cnx1   |               |
|               | BCD135 |               |
|               | Gln2   | 146.05 – 147.93|
|               | KG004.1|               |
|               | KG004.2|               |
|               | ABC157 | 148.58 – 150.55|
|               | Zeo1   | 150.55 – 152.64|
| 4H            | HVM40  | 19.27 – 20.26 |
|               | CDO669A| 20.68 – 21.33 |
|               | Ole1   | 24.49 – 25.23 |
|               | BCD402B| 26.47         |
|               | CDO542 | 29.08 – 29.49 |
|               | DsT-29 |               |
|               | CDO122 | 30.10         |
|               | BCD351D| 30.10 – 31.41 |
|               | INT-C  | 30.37         |
|               | MWG635A| 31.41 – 32.62 |
|               | BCD265B| 34.92 – 37.54 |
|               | BCD808B|               |
| 5H            | Sccsr05939| 94.25 – 94.66 |
|               | ksuD17 | 65.89 – 69.87 |
|               | G57    |               |
|               | ABC163 | 71.52 – 72.17 |
|               | ABG379 |               |
|               | Bmac0218C| 73.18 – 73.98 |
|               | ABG388 | 74.60 – 75.34 |
|               | CDO507 |               |
|               | ABC175 | 77.82 – 78.46 |
|               | RZ323  |               |
| Sample   | Description | Range          |
|----------|-------------|----------------|
| 6H       | ksuA3D      | 79.34 – 80.13  |
|          | ABC1708     |                |
|          | Scsn21226   | 81.05 – 82.53  |
|          | MWG820      | 83.71 – 85.17  |
|          | cMWG684D    | 88.08 – 88.78  |
|          | MWG514      | 136.17 – 137.84|
|          | MWG798A     |                |
|          | ABG725      |                |
|          | DAK213C     | 138.49 – 140.92|
|          | DsT-71      |                |
Table S4  BOPA, POPA and SCRI SNPs within genes of known function in the high \(F_{ST}\) blocks and their respective gene products.

| LG  | SNP          | GenBankID       | cM     | Silent | Gene            | Product                                |
|-----|--------------|-----------------|--------|--------|-----------------|----------------------------------------|
| 2H  | SCRI_RS_173  | NM_001073041    | 139.9  | No     | Os12g0256900    | hypothetic protein                     |
|     | 017          |                 |        |        |                 |                                        |
|     | 11_10446     | XM_003560174    | 140.69 | No     | LOC100837523    | serine carboxypeptidase-like           |
|     | 11_20480     | AY162186        | 140.69 | Yes    | exin1           | Extracellular invertase                |
|     | SCRI_RS_151  | DQ163025        | 141.5  | Yes    | VTE5            | phytol kinase                          |
|     | 19           |                 |        |        |                 |                                        |
|     | 11_21459     | AM039897        | 143.18 | No     | ahh1            | S-adenosyl-L-homocysteine hydrolase    |
|     | 11_10656     | XM_003580700    | 145.69 | Yes    | LOC100826196    | U3 small nucleolar ribonucleoprotein   |
|     | 11_10383     | AY136627        | 147.37 | Yes    | Ha1             | U3 small nucleolar ribonucleoprotein   |
|     | 12_30942     | GQ169685        | 147.37 | Yes    | GS2             | U3 small nucleolar ribonucleoprotein   |
| 4H  | 11_20422     | XM_003560743    | 28     | Yes    | LOC100820964    | microsomal glutathione S-transferase   |
|     | SCRI_RS_157  | XM_003560569    | 30     | Yes    | LOC100840876    | vam6/Vps39-like protein-like           |
|     | 832          |                 |        |        |                 |                                        |
| 6H  | SCRI_RS_143  | XM_003570599    | 72.9   | No     | LOC100831957    | RINT1-like protein-like                |
|     | 317          |                 |        |        |                 |                                        |
|     | SCRI_RS_206  | XM_003570630    | 74.6   | No     | LOC100841641    | microtubule-associated protein         |
|     | 976          |                 |        |        |                 | TORTIFOLIA1-like                       |