

Genetic Dissection of Sclerotinia Stem Rot Resistance in Quinoa Reveals Resistance-Associated Loci and Candidate Defense Genes

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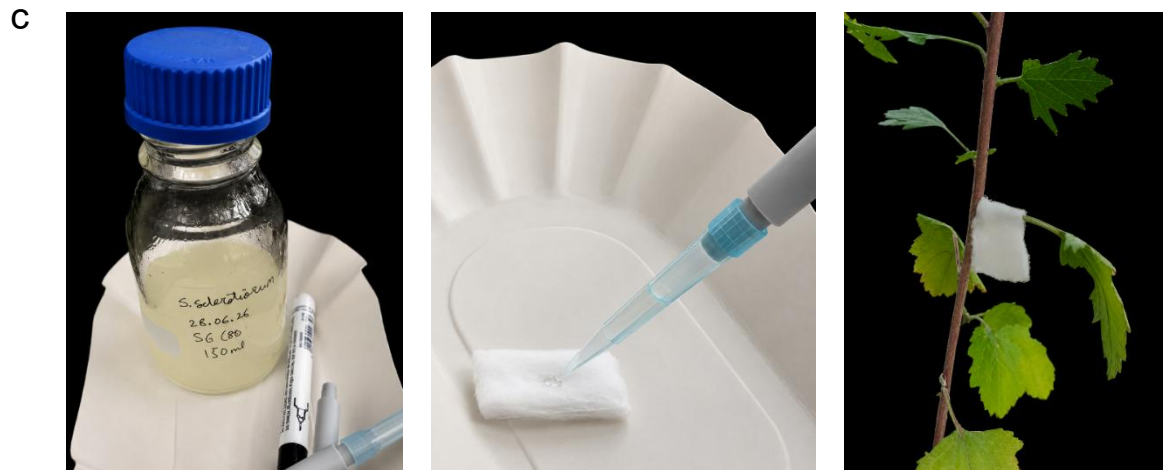


Fig. S1 **a** stem inoculation using mycelial plug. **b** soil inoculation using mycelial plug. **c** Cotton pad inoculation using mycelial suspension.

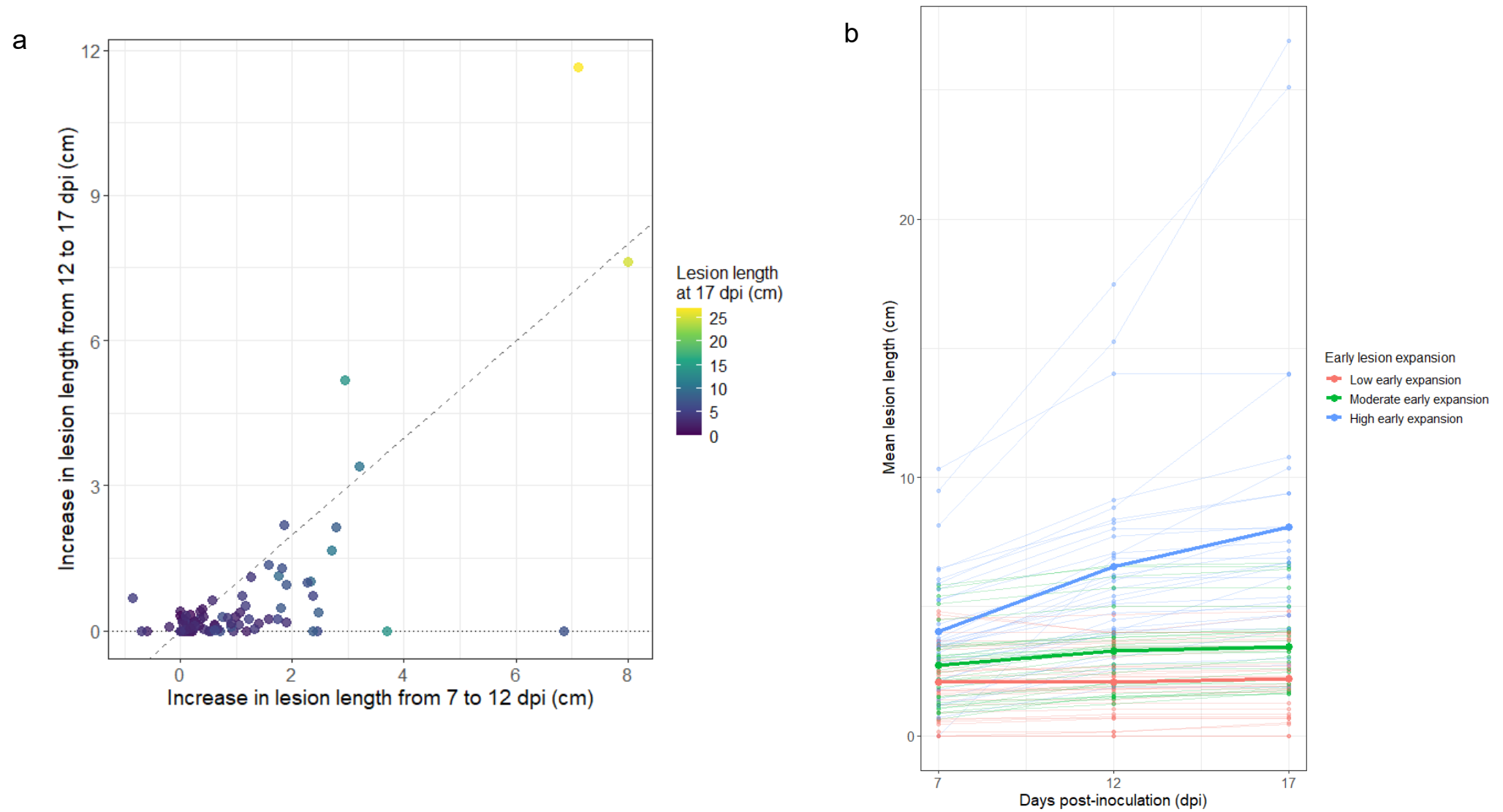


Fig. S2 Changes in lesion length during early and late disease development across 91 quinoa accessions. **a** Each point represents the mean response of one accession. The x-axis shows the increase in lesion length from 7 to 12 days post-inoculation (dpi), and the y-axis shows the increase from 12 to 17 dpi. Point colour indicates mean lesion length at 17 dpi. The dashed diagonal indicates equal lesion expansion during the two intervals, while the dotted horizontal line indicates no change between 12 and 17 dpi. Points below the diagonal represent accessions with slower lesion expansion during the later interval. **b** Lesion-length progression among quinoa accessions grouped by early expansion from 7 to 12 dpi. Thin lines represent individual accession means, while thick lines represent group means.

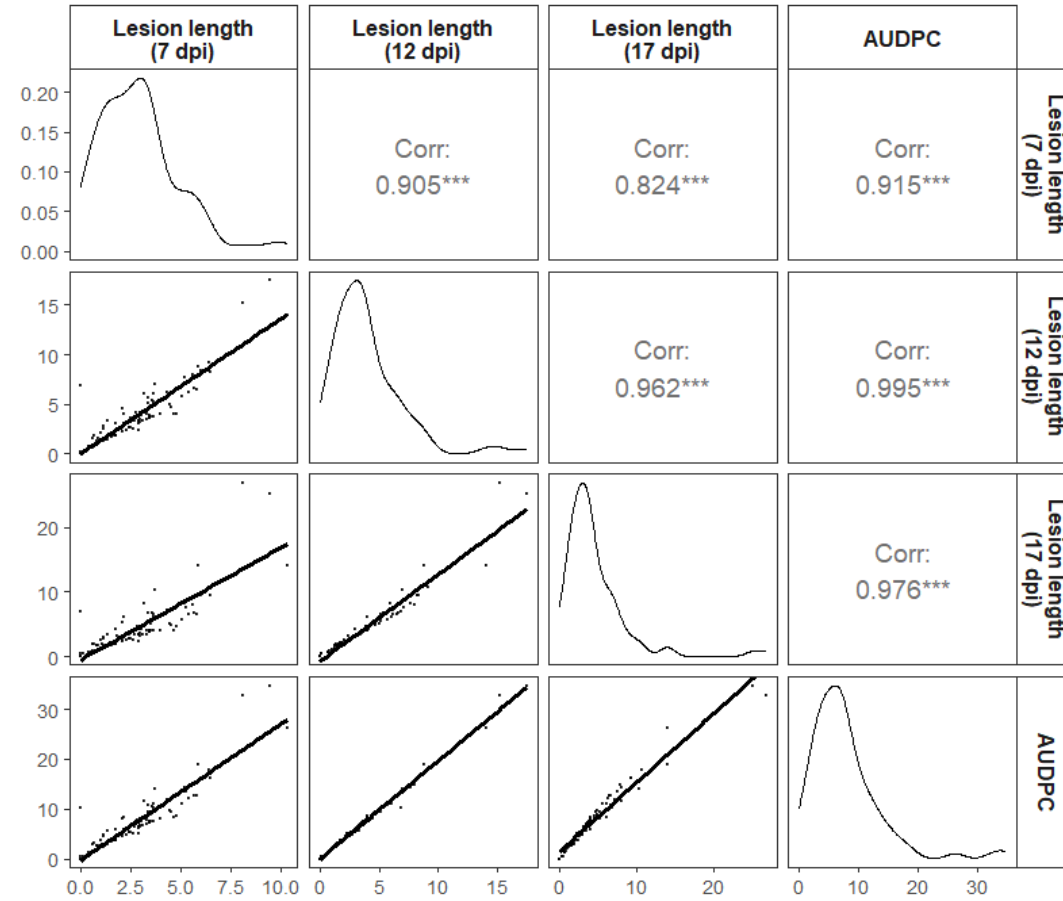


Fig. S3 Pairwise correlations among lesion length at 7, 12, and 17 days post inoculation (dpi) and AUDPC across 91 quinoa accessions. Density distributions are shown on the diagonal, scatterplots in the lower triangle, and Pearson correlation coefficients in the upper triangle (***) $P < 0.001$).

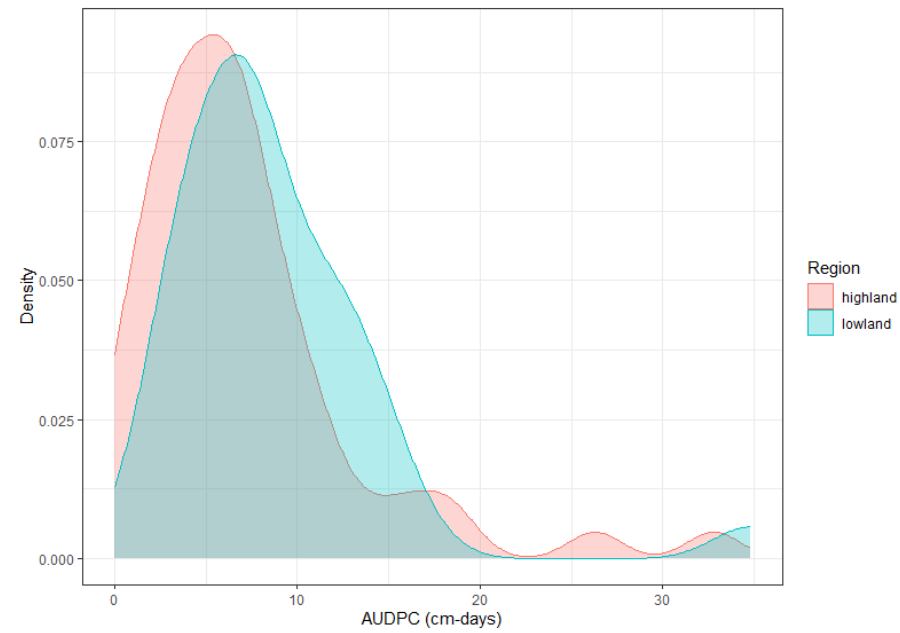


Fig. S4 Density distribution of Area Under the Disease Progress Curve (AUDPC) values among 91 quinoa accessions. Kernel density estimates are shown separately for highland and lowland ecotypes.

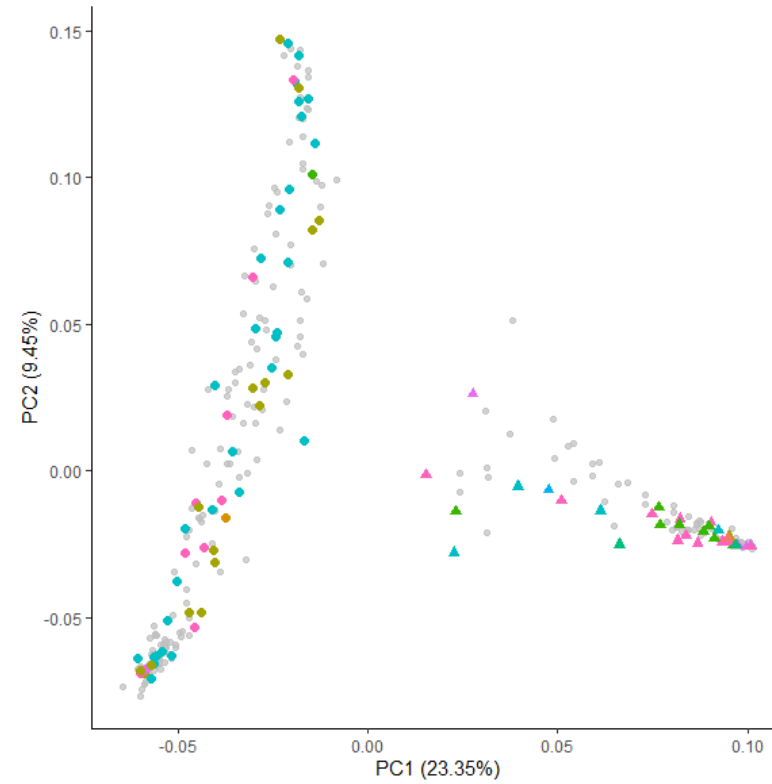


Fig. S5 Distribution of the 91-accession GWAS panel within the source diversity panel. Principal component analysis of the previously characterized quinoa diversity panel comprising 303 accessions (Patiranage et al., 2022). The 91 accessions selected for the present study are highlighted, whereas the remaining accessions are shown in grey. PC1 and PC2 explained 23.35% and 9.46% of the genetic variance, respectively.

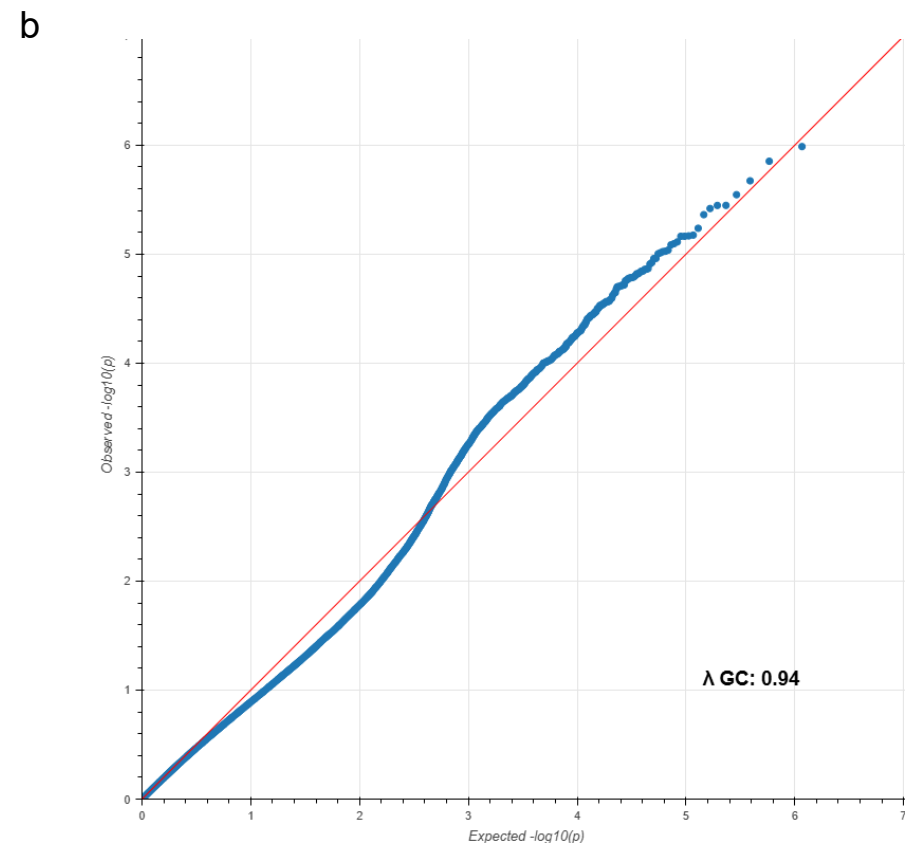
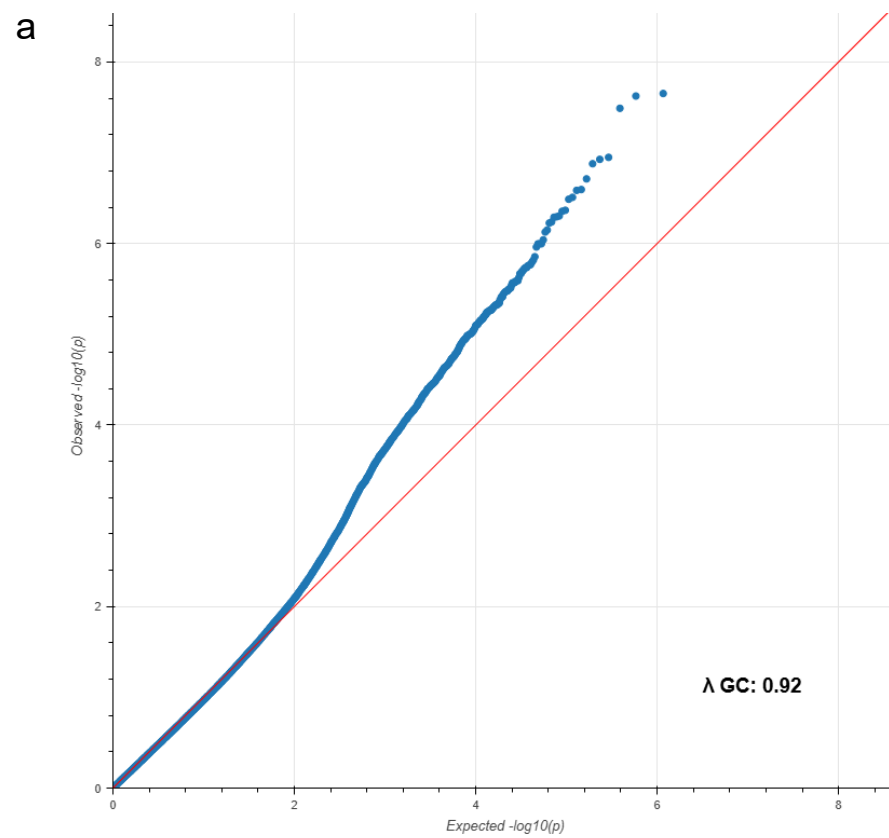


Fig. S6 a Quantile-Quantile plot for General linear model, **b** Quantile-Quantile plot for Mixed linear model.