

Predicting and mapping of major QTL for hull color using inheritance model and a high-density genetic map in foxtail millet (*Setaria italica* (L.) P. Beauv.)

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Abstract: 【Background】 Hull color is an important morphological marker for color selection in seed production of foxtail millet. However, the molecular mechanism for hull color is unknown. **【Results】** An F₇ recombinant inbred line (RIL) population containing 215 lines derived from Hongjiugu × Yugu18 was employed to analyze inheritance and detect QTL for four hull color traits using major gene plus polygene mixed inheritance model analysis and the composite interval mapping (CIM) in four environments. Genetic analysis revealed that hull color L* value (HCL*) was controlled by two major genes plus additive polygenes, hull color a* value (HCa*) was controlled by three major genes, hull color b* value (HCb*) was controlled by two major genes plus polygenes, and hull color C* value (HCC*) was controlled by four major genes. A high-density genetic linkage map covering 1227.383 cM of the foxtail millet genome, with an average interval of 0.879 cM between adjacent bin markers, was constructed using 1420 bin markers. Based on the genetic linkage map and the phenotypic data, a total of 39 QTL were detected for these four hull color traits across four environments, and each explaining 1.50%–49.20% of the phenotypic variation. Of them, six environmentally stable major QTL colocalizations for multiple hull color traits played a major role in hull color, containing 556 annotated genes. Via the function of homologous genes in *Arabidopsis* and KEGG and GO gene annotation, five genes were preferentially predicted as candidate genes for further study.

【Conclusions】 This is the first study to use inheritance model and QTL mapping in the genetic mechanisms of hull color trait in foxtail millet. Six environmentally stable major QTL were identified. Five potential candidate genes were predicted to be associated with hull color. The results advance the current understanding of the genetic mechanisms of hull color trait in foxtail millet and provide additional resources for application in genomics assisted breeding and potential isolation and functional characterization of the candidate genes.

Acknowledgements: Shaanxi Province Key Research and Development Program (2023-ZDLNY-06), National Program on Key Basic Research Program of China (2021YFD1600600, 2021YFD1600605, 2020YFD1000800, 2020YFD1000803), Ministry of Finance and Ministry of Agriculture and Rural Affairs: Technology Systems of National Modern Agricultural Industry (CARS-06-A26), Technical System of Minor Grain Crops Industry in Shaanxi Province (NYKJ-2018-YL19).

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