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Sweet corn transcriptome pinpoints vitamin genes

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First author Jenna Hershberger harvests an ear of sweet corn for RNA extraction. Photo courtes

First author Jenna Hershberger harvests an ear of sweet corn for RNA extraction. Photo courtesy of Jenna Hershberger.

Elevating vitamin levels in sweet corn has the potential to benefit human health. A better understanding of the genetic control of vitamin traits in sweet corn would help this process, known as biofortification. However, previous genome-wide association studies have been limited by low statistical power and mapping resolution. Using transcriptome-based analyses, which provide both gene-level resolution and insight into regulatory variation, researchers recently clarified the relationship between the sweet corn genome and vitamin traits.

Using 3′mRNA transcript abundances from fresh sweet corn kernels, researchers conducted transcriptome-wide association studies and transcriptome- and genome-wide marker predictions for carotenoids (provitamin A, lutein, zeaxanthin, and antioxidants) and tocochromanols (vitamin E and antioxidants). This work, reported in *The Plant Genome*, revealed significant associations for four causal genes on a transcriptome-wide level, with additional associations identified on a biosynthetic pathway level. Transcriptomic data boosted predictive ability over genome-wide marker data alone for some traits, but joint transcriptome- and genome-wide marker models achieved the highest predictive abilities.

These findings will be leveraged to speed up development of biofortified sweet corn cultivars through genomics-enabled breeding approaches.

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Hershberger, J., Tanaka, R., Wood, J. C., Kaczmar, N., Wu, D., Hamilton, J. P., ... & Gore, M. A. (2022). Transcriptome-wide association and prediction for carotenoids and tocochromanols in fresh sweet corn kernels. *The Plant Genome*, *e20197*. **https://doi.org/10.1002/tpg2.20197**

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