Genetic diversity, population structure, and association mapping of agronomic traits in waxy and normal maize inbred lines

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ABSTRACT. Understanding genetic diversity, population structure, and linkage disequilibrium is a prerequisite for the association mapping of complex traits in a target population. In this study, the genetic diversity and population structure of 40 waxy and 40 normal inbred maize lines were investigated using 10 morphological traits and 200 simple sequence repeat (SSR) markers. Based on a population structure analysis, the 80 maize inbred lines were divided into three groups: I, II, and admixed. Significant marker-trait associations were identified between the markers and the 10 morphological traits, which were studied according to the model used to confirm the association. Using a general linear model, the lowest R^2 value (9.03) was detected in umc1139, which was associated with ear number, and the highest (43.97) was in umc1858, which was associated with plant height. Using a mixed linear model, the lowest R^2 value (18.74) was in umc1279, which was

associated with ear weight; the highest (27.66) was in umc1858, which was associated with 100-kernel weight. The SSR markers identified in the present study may serve as useful molecular markers for selecting important yield and agronomic traits. These results will be useful for marker-assisted selection in maize breeding programs, to help breeders choose parental lines and markers for crosses.