Maize landraces represent a valuable source of genetic variation based on the following considerations: i) Only a small number of landraces served as sources for modern elite germplasm, therefore landraces can be expected to contain unexploited allelic variation. ii) Due to their adaptation to specific local environmental conditions they are likely to harbor unique favorable alleles for biotic and abiotic stress resistance. iii) Because of many generations of random mating, landraces are assumed to have low levels of linkage disequilibrium (LD) and no population substructure, making them ideal for genetic mapping. Up to date, these assumptions could not be appropriately tested as most previously reported diversity statistics and LD levels for maize landraces were based on measurements across landraces with only one individual per accession and/or low-density molecular marker data.

We investigated genetic diversity, population structure and LD in a broad panel of 35 European maize landraces by genotyping 22 to 48 individuals per landrace with 609,442 single nucleotide polymorphism markers. Percentage of polymorphic markers and average nucleotide diversity $\pi$ indicated high genetic variation within landraces and $F_{ST}$ values suggested substantial genetic variation between landraces. Population structure analyses revealed genetic clustering of landraces mainly according to geographical origin and kernel type (Dent/Flint), absence of population substructure within landraces and moderate levels of admixture between landraces. Unlike most previous studies, which reported very low LD levels based on measurements across many landraces with few individuals, we found that within most landraces, LD decay distances ($r^2 < 0.2$) were within 100 to 500 kb. Based on this unique and extensive dataset, we present results on the influence of sample size, sample composition and marker density on diversity and LD measurements within and across landraces.

Funding acknowledgement: This study was funded by the Federal Ministry of Education and Research (BMBF, Germany) within the AgroClastEr Synbreed - Synergistic plant and animal breeding (grant 0315528) and by KWS SAAT SE under a PhD fellowship for M. Mayer