Supplemental Figure S1. The rate of change in the probability of data between successive $K$ values (delta $K$) calculated based on the Evanno method with $K$ varied from 1 to 10, each including five independent runs, applied to (A) the full set of 904 SNPs informative in the world landrace collection, (B) a random set of 195 SNPs informative in landraces and flanking every 3 cM interval based on a cowpea consensus map, (C) the full set of 322 SNPs informative in both wild cowpeas and landraces, and (D) 129 SNPs that are informative in both wild cowpeas and landraces, flanking every 3 cM interval. Scatter plots are correlations of cluster assignment likelihood (for genepool 1 at $K = 2$) between (E) full and reduced sets of SNPs informative in landraces, (F) full and reduced sets of SNPs informative in both wild cowpeas and landraces, (G) the full set of landrace SNPs and the full set of wild-landrace SNPs, and (H) the reduced set of landrace SNPs and the reduced set of wild-landrace SNPs.
Supplemental Figure S3. Population structure among 367 cowpea landraces in Africa and other continents (number of individuals in brackets). Colored bars are memberships of individuals assigned to $K$ sub-groups by the software STRUCTURE with $K$ varying from 2 to 10 applied to all 904 informative SNPs and their subset of 195 SNPs at every 3-cM interval based on the cowpea consensus map. The 195 SNP set seems to perform better than the full set at $K$ values from 3 to 7 by reducing fractional memberships. Likelihood scores for each $K$ applied to the 195 SNP set are provided in Supplemental Table S5.