The Cooperative Dry Bean Nursery has produced a multi-environment phenotype dataset with thousands of phenotypic datapoints measured over many decades. To study stable genetic effects in this dataset, we conducted genome-wide association using best linear unbiased predictions derived across years and locations for 21 phenotypes, using genotypic data (1.2M SNPs) for 327 genotypes. We find significant effects for all phenotypes, two genomic regions with significant effects on many phenotypes, and multiple genomic regions previously identified in other genome-wide association work in common bean. Our results demonstrate that multi-environment datasets not designed for genetic work can nonetheless support genetic discovery.