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MABDE is an INCO MED funded project working to improve understanding of adaptation of barley to hostile environments, including drought, salinity, high and low temperatures, which are a major cause of cereal crop yield and quality loss in rainfed environments around the Mediterranean. Identifying genomic regions influencing the response of yield and its components to water deficits will aid in our understanding of the genetics of drought tolerance and the development of more drought-tolerant cultivars. We assembled 192 genotypes that represented landraces, old and contemporary cultivars; the majority from the Mediterranean basin and the remainder from the rest of Europe. The genotypes were grown in irrigated and rainfed trials in each of seven Mediterranean countries for harvest 2004 and 2005. The 192 genotypes were genotyped with a stratified set of 50 genomic and EST derived molecular markers, 49 of which were Simple Sequence Repeats (SSRs). We also used Diverse Arrays Technology (DArT®) to generate 1130 biallelic markers. Yield data gathered from 28 field trials in 2004 and 2005, together with the marker data were used to search for associations using single marker regression. Landraces and old varieties showed strong local adaptation, particularly in the harshest environments. The most significant contrast among testing sites was the region of origin of the genotypes. QTLs were identified for grain yield, days to heading, thousand kernel weight and plant height under varying levels of water stress. Stable QTLs were consistently located on the same chromosomes in trials with similar environmental characteristics. Several yield QTLs were detected that exhibited strong QTL x Environment interactions across trials grown under markedly contrasting conditions.