Aquaporins are channel forming membrane proteins that have the ability to provide high flux and, at the same time, very selective for the transport of water and other small molecules across biological membranes. They belong to a conserved and ancient family of proteins called major intrinsic proteins (MIPS) with molecular weights around 26-34 kDa, and its members are represented in nearly all living organisms. Aquaporins show a tremendous diversity in plants and they are multifunctional proteins, allowing some small neutral solutes such as glycerol, CO$_2$, ammonia (NH$_3$), urea, boron, and hydrogen peroxide across cell membranes. Differential gene expression of aquaporins in different organs and membranes has implicated its importance in regulating water movement in normal development as well as under certain stress, such as drought or high salt. The objectives of this study were to search for the presence of peanut aquaporins or MIPS nucleotide sequences in a set of expressed sequence tags (ESTs), to identify possible new aquaporins, and to study gene expression profiles on these proteins. We have sequenced a total of 44,064 clones from 10 peanut cDNA libraries, derived from developing seeds at three reproduction stages (R5, R6 and R7) and from leaf tissues of a resistant and a susceptible cultivated peanuts, “Tifrunner” (a runner type, resistant to TSWV and leaf spots) and “GT-C20” (a Spanish type, susceptible to TSWV and leaf spots but resistant to Aspergillus/aflatoxin, bacteria wilt and rust). Resulting sequence data were searched against NCBI Translated Protein Database (BLASTx). A total of 181 transcripts matched to aquaporins which represent a 0.41% against total sequences. This corresponds to different members of aquaporins including 5 unknown Tonoplast Intrinsic Proteins (TIPs) and 11 unknown Plasma Membrane Intrinsic Proteins (PIPs) from peanuts. Future experiments will ascertain different aquaporin gene expression in peanut plants in response to drought. This information will be applied in peanut breeding program to develop or select peanut varieties that will have enhanced drought tolerance.