Abstract:

Cannabis is most frequently used drug of abuse not only in Pakistan but also in the whole world. Its use is mounting drastically every year. GCMS allows analysis of *cannabis sativae* and there is a divergence between the constituents of this plant. From where this plant belongs to we can straightforwardly locate plant's geographical region by knowing the plant constituents. In this way we can obstruct production if we know the region in which it is produced. GCMS is a useful technique for the comparison of constituents of this drug of abuse which will assist the investigator concerning the origin of plant. Comparison also aids about the understanding and acquaintance of similarities of different samples of cannabinoids. It is supposed that cannabinoids are highly bounded to plasma proteins which have been proved here by HPLC analysis of pure extract and analysis of plasma protein bound drug that revealed us that cannabinoids have high affinity towards plasma. Another approach about the estimation of plasma protein binding we used here is estimation of total phenol contents in pure plant drug extract and drug extract incubated with blood sample. Decreased amount of phenolic content in sample incubated with blood as compared to pure plant sample clearly showed the high affinity towards protein .