The study was aimed to develop molecular markers that were linked to resistance to anthracnose in chili at green fruit stage which was previously identified as \textit{col} (Pakdeevaraporn \textit{et al.}, 2005). Two approaches, mapping and bulked segregant analysis (BSA) were applied to the study. A backcross population (BC$_r$F$_2$P$_2$) containing 140 plants derived from an interspecific cross between \textit{C. annuum} 'Bangchang' (susceptible variety) and \textit{C. chinense} 'PBC932' (highly resistant line) was used as mapping population with 35 STMS (sequenced tagged microsatellite site) 10 EST (expressed sequence tags) and 8 morphological markers. Eleven linkage groups were formed covering 770.8 cM. The \textit{col} was located in linkage group 1 with STMS PMC3 36.9 cM apart. QTL analysis found that the PMC3 was a major QTL of anthracnose resistance with the LOD score value of 4.09 ($P = 0.0001$) which was highly significant (>99%).

Two DNA bulks were generated from resistant plants of BC$_r$F$_1$P$_1$ population and from susceptible plants of susceptible lines of BC$_r$F$_2$P$_1$. Total 51 AFLP primers were screened on parents bulk R and bulk S. Two AFLP markers 932-1 and 932-2, appeared to be associated with resistance trait 84 and 68\% respectively.