PBB$_1$) and plume moth (*PPM*$_1$) in interspecific mapping populations (F_2, F_3 and BC_1) derived from a cross involving *Cajanus cajan* (*cv*. ICP-26) × *Cajanus scarabaeoides* (*acc*. ICPW-94) appeared to be under monogenic control either by a single major gene or a cluster of tightly linked genes. Bulked segregant analysis using 237 [85 simple sequence repeats (SSR), 143 random amplified polymorphic DNA (RAPD) and nine inter simple sequence repeats (ISSR)] parental polymorphic primers led to the identification of 43 markers that distinguished the resistant and susceptible bulks alike to parents, and which were also segregating among F_2 progenies. Linkage analysis of these markers along with interaction phenotype score for both traits generated a linkage group consisting of 11 markers (two SSR, seven RAPD and two ISSR) and two trait loci (*PBB*$_1$ and *PPM*$_1$). This linkage group distributed over 133.9 cM with an average marker interval of 10.3 cM. The *PBB*$_1$ and *PPM*$_1$ loci were linked to each other by 11.2 cM (rf 0.110), and were flanked by ISSR marker UBC872$_{2000}$ (15.9 cM), and RAPD marker OPA09$_{910}$ (15.3 cM), respectively. On the basis of sequence homology of linked marker OPA09$_{910}$ these two loci were assigned to chromosome 2 (CcLG02). Composite interval mapping led to the detection of two major quantitative trait loci (*qPBB2.1* and *qPPM2.1*) controlling blue butterfly and plume moth resistance, respectively and the quantitative trait locus peaks coinciding with *PBB*$_1$ and *PPM*$_1$ loci on the map.