The stem borer *Chilo tumidicostalis* Hampson is one of the most important pests of sugarcane and is difficult to control because of their living inside of the stem. However, the larval parasitoid *Cotesia flavipes* Cameron is an efficient biological agent for the control of the sugarcane stem borer. The objectives of this study were to investigate the biology, behavior of larval parasitoid *C. flavipes*, its efficiency to control the stem borer, as well as the genetic relationships among the populations of *C. flavipes*. The crop losses by the stem borer *C. tumidicostalis* were monitored in the sugarcane planted areas in the Northeast during November 2001 – March 2002. The results showed that the percentage of destroyed stems was between 1.2 – 18.2%, and the percentage of parasitization was between 0 – 16.9% in the field. The average percentage of stem borer eggs emerging in the laboratory was 96.34 ± 5.65%. The total life cycle in the laboratory of *C. tumidicostalis* was between 42 – 63 days and the average survival rate was between 63.88 – 95.98%. According to the laboratory test, the female parasitoids *C. flavipes* prefer to parasitize on the 3rd – 6th stage of stem borer larval. The time used for laying egg of parasitoid female into the 3rd – 4th instars of stem borer is less than the bigger larval size of stem borer at 5th – 6th stage. The number of larval parasitoid progeny produced from the 3rd, 4th, 5th and 6th instars was 19.23 ± 6.61, 29.69 ± 10.41, 36.95 ± 9.58 and 37.28 ± 6.88 respectively. The total development time for parasitoid *C. flavipes* on the 5th – 6th instar (16 – 18 days) was shorter than the 3rd – 4th instar (23 – 25 days). PCR assays using primer sets (NAD1F, NAD1R and CS16SF,CS16SR ) from mitochondrial DNA amplified 350 fragments at parts of the genes 16S rRNA and NADH dehydrogenase subunit I (mitochondrial genes). Direct sequencing of amplified fragments showed no nucleotide difference between all *C. flavipes* populations. In addition the random amplified polymorphic DNA (RAPD-PCR) was used to
investigate the genetic variation of *C. flavipes* populations. Eight out of 60 random primers were selected and showed polymorphic bands among *C. flavipes* populations (OPA – 2, OPH – 5, OPH – 7, OPH – 15, OPH – 18, OPH – 20, OPG – 16 and OPAE – 1). A dendrogram based on similarity of *C. flavipes* was constructed and showed six main groups of the parasitoid populations based on a similarity coefficient. The Manja-Kiri population from Khon Kaen, Muang population from Khon Kaen and the Sa-teak population from Buriram were genetically distant from the other populations (similarity coefficient 80%, 86.5% and 88.5% respectively). No significant of the number of parasitized on stem borer from using different genetic distance population of larval parasitoids.