Microgastrine endoparasitoids co-inject symbiotic viruses known as polyDNAviruses (PDV) together with other wasp factors such as the venom and calyx fluid proteins during oviposition in hosts. These factors disrupt the host immune system allowing the parasitoids to develop successfully. In Kenya, the endoparasitoid Cotesia sesamiae (Cameron) (Hymenoptera: Braconidae) exists as two biotypes that differ in their ability to parasitize the stem borer Busseola fusca (Lepidoptera: Noctuidae). Cotesia sesamiae from western Kenya completes development in B. fusca larvae hence it is virulent. The coastal C. sesamiae biotype does not complete development and eggs oviposited get encapsulated in B. fusca larvae, and therefore it is avirulent. It is not yet known if intermediate C. sesamiae populations exist between western and coastal Kenya. On the other hand, several B. fusca biotypes have been described recently and it is not clearly understood whether this host also contributes to variation in C. sesamiae parasitism. In this study, B. fusca acceptance and suitability of different strains of C. sesamiae were examined. The avirulent strains were reluctant to oviposit in B. fusca larvae while the virulent strain readily oviposited in this host. Egg loads of the virulent C. sesamiae from Kitale were significantly lower compared to those of the avirulent Mombasa and Taita C. sesamiae females. Development of C. sesamiae in B. fusca larvae was tested in an interaction matrix. Results showed that both C. sesamiae and B. fusca contributed to the variation in the parasitoids' success. 39% of the variation was attributed to the geographic locality of C. sesamiae, 35% by the host locality and 27% by their interaction. Geographic variation in successful parasitism of hosts by their parasitoids was attributed to the co-evolutionary dynamics and selection pressures in C. sesamiae local community. Results from this study showed that the avirulent C. sesamiae strains have been under selection pressure to evolve a system that suppresses *B.* fusca 's immune reaction. The CrV 1 gene homolog was tested on various C. sesamiae strains using Polymerase Chain reaction (PCR). The CrV 1 gene was present in all the C. sesamiae strains. However, restriction enzyme tests showed that the gene is differently organized in the virulent and the avirulent C. sesamiae strains. The CrV 1 gene expression was found in fat bodies and haemolymph tissues of *B.* fusca larvae using the Reverse Transcriptase-PCR (RTPCR). Results showed that this gene was expressed in the fat bodies and haemolymph tissues of *B.* fusca and S. calamistis parasitized by the virulent C. sesamiae strains. For the avirulent C. sesamiae strains, CrV 1 gene expression was only evident on the permissive host S. calamistis but not *B.* fusca tissues. Differences in calyx fluid contents of the virulent and avirulent C. sesamiae populations were evaluated using the 2D-gel electrophoresis and results showed that more protein spots were present in calyx fluid of the virulent C. sesamiae than that of the avirulent strain. Changes in protein profiles in *B.* fusca larvae parasitized by the two C. sesamiae strains was evaluated by SDS-PAGE gel on fat body and haemolymph tissues. Results showed parasitism-specific protein bands in both tissues parasitized by the two C. sesamiae strains.