Polydnaviruses are rarely studied for their natural variation in immune suppressive abilities. The polydnavirus harboring braconid Cotesia sesamiae, a widespread endoparasitoid of Busseola fusca and Sesamia calamistis in sub-Saharan Africa exists as two biotypes. In Kenya, the western biotype completes development in B. fusca larvae. However, eggs of the coastal C. sesamiae are encapsulated in this host and ultimately, no parasitoids emerge from parasitized B. fusca larvae. Both biotypes develop successfully in S. calamistis larvae. Encapsulation activity by B. fusca larvae towards eggs of the avirulent C. sesamiae was detectable six hours post-parasitization. The differences in encapsulation of virulent and avirulent strains were associated with differences in nucleotide sequences and expression of a CrV1 polydnavirus (PDV) gene, which is associated with haemocyte inactivation in the Cotesia rubecula/Pieris rapae system. CrV1 expression was faint or absent in fat body and haemolymph samples from B. fusca parasitized by the avirulent C. sesamiae, which exhibited encapsulation of eggs. Expression was high in fat body and haemolymph samples from both B. fusca and S. calamistis larvae parasitized by the virulent C. sesamiae, encapsulation in the former peaking at the same time points as CrV1 expression in the latter. Non synonymous difference in CrV1 gene sequences between virulent and avirulent wasp suggests that variations in B. fusca parasitism by C. sesamiae may be due to qualitative differences in CrV1-haemocyte interactions.