# Tracking Viral Evolution: Disease Diversity of Cloned Deformed Wing Virus in Honeybee Populations

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Responsible for 80% of global agricultural crop pollination, bees are essential to food production efforts. Deformed wing virus (DWV) is the leading cause of death, disability, and colony collapse disorder in honeybees (Apis mellifera). DWV does not only jeopardize the health of bees but global food security as well, inhibiting goods production. This study investigates the viral diversity of DWV and how viral mutations influence strain virulence across multiple honeybee generations, allowing researchers to accurately predict future DWV polymorphisms/prevalence aimed toward cross-reference in vaccine development. Honeybee pupae were sampled (n=64) from three source colonies (#57, #75, and #78). Then inoculated with a tagged nano-luminescent DWV strain (10^6 viral particles) via injection. After 72 hours of growth at 35°C, viral mRNA was extracted using the QIAGEN Viral RNA Extraction Kit and isolated by creating cDNA, which was used to perform qPCR to quantify viral loads and then deep sequenced. Procedures were replicated thrice with two parent-to-child colony injections and a final three-way cross. The susceptibility of recipient colonies influences the virulence strength of DWV strains rather than the donor strain, as colony #75 experienced elevated DWV levels in reaction to all donor pools. Experimentation found seemingly no interaction link between source colony and viral levels indicative of virulence patterns consistent with the laws of natural selection, suggesting an increase in the prevalence of inheritable traits promotes DWV growth in isolated to exposed populations over time.

**Awards Won:**
Fourth Award of $500