*Porphyromonas gingivalis* is a bacterium of the oral microbiome that is normally present in small amounts in healthy individuals. However, if it grows too much it is known to promote dysbiosis and is considered the 'keystone pathogen' of gum disease. In severe cases, it is also able to enter the bloodstream where it can promote cardiovascular diseases and even Alzheimer's disease by penetrating the blood brain barrier. Previous research has used traditional and quantitative PCR methods to detect *P. gingivalis* but the targeting of virulence genes specifically, and the use of digital PCR for increased sensitivity, is limited. Digital PCR (dPCR) is a newer method that works by partitioning a reaction mixture so that either zero or one template molecule is present in each discrete PCR reaction. The number of partitions that amplify the template (determined by fluorescent probes) indicate the absolute number of template molecules in the original sample. My research focused on developing a dPCR based method for quantification of the bacterium *Porphyromonas gingivalis* and characterization of its virulence gene expression in human oral samples. Two genes unique to *P. gingivalis,* which are also involved in its virulence, were selected as gene targets. These genes, a lysine specific cysteine protease (Kgp) and a haemophore-like heme binding protein (hmuY), along with a species-specific region of the 16S rRNA gene were targeted in a single PCR assay. Primers and TaqMan fluorescent probes were designed for each target to build the multiplex assay for use on genomic DNA (gDNA) and reverse-transcribed RNA (cDNA) samples. The multiplex assay showed good reproducibility with qPCR standard curves and high sensitivity on the dPCR. Both gDNA and cDNA extracted from oral samples from ten participants were also run on qPCR and dPCR, with dPCR showing higher sensitivity.