Vampirovibrio chlorellavorus (Gromov and Mamkaeva 1972) [Cyanobacteria] is a predatory bacterial pathogen of several Chlorella spp. (Chlorophyta) selected as biofuel and bioproduct strains for outdoor cultivation systems. Algal cells and the associated V. chlorellavorus were collected from a Ukrainian freshwater lake, leading to the first description of this predatory bacterium. Lyophilized, archived cells were used to produce a full genome sequence that provided the basis for its classification and detailed life cycle description. It has since been linked to costly culture decline and death at various locations, including cultures grown at commercial and testbed biomass production facilities in southern Arizona. Full genome assemblies were produced for two strains of V. chlorellavorus collected from algal ponds at the UA-Tucson testbed site. Analysis revealed surprising variation relative to the Ukrainian strain, and between one another. To determine the extent of genotypic variation among southwestern AZ naturally-occurring field isolates, samples were collected from a variety of freshwater sites, and incubated under conditions developed for enrichment of V. chlorellavorus. To identify candidates for full-length genome sequencing viable cultures were screened by PCR amplification using primers specific for V. chlorellavorus 16S rRNA, and confirmed by DNA sequencing. In addition, one previously sequenced Arizona strain was used to inoculate replicated laboratory cultures of the C. sorokiniana algal host, maintained in the UA laboratory. The latter cultures were sampled at five timepoints for RNA isolation, prepared for dual host-pathogen RNA-seq analyses. Tracking relative expression of pathogenicity genes and others unique to the infection cycle will aid in establishing the fundamental underpinnings of pathogen-host interactions and thereby the development of targeted V. chlorellavorus mitigation strategies for algal biofuel production systems.