Hydrothermal vents are considered to be one of the most ancient continuously inhabited ecosystems on the planet, and may have been a site for the origin of life on Earth and the earliest microbial communities. Yet despite an intense research focus on hydrothermal vent microbiology, little is known about the viral ecology of these ecosystems. Through the process of transduction, viruses may play a crucial role in the evolution of microbial communities by acting as mediators of horizontal gene transfer, a process that may be particularly important in the dynamic environment of vents. To explore these concepts, we are investigating genetic characteristics of subseafloor diffuse flow viral communities at Hulk vent in the Main Endeavour Field of the Juan de Fuca Ridge. Viruses were concentrated and purified from 170 liters of diffuse flow fluid that was collected at the base of Hulk vent. DNA was extracted from this sample, and the viral metagenome will be obtained through 454 pyrosequencing. The target of our analysis will be metabolic genes that appear to have been laterally transferred in the virome: it has been hypothesized that since microbes inhabiting dynamic ecosystems such as hydrothermal vents are subject to rapidly changing temperature, pH, and nutrient conditions, selection is likely to favor the lateral transfer of metabolic genes that may improve fitness in these dynamic environments. This may include genes related to functions such as sulfur and iron reduction, nitrogen fixation, and biofilm formation. In this scenario, the viral gene pool would effectively act as a “genetic toolbox” from which microbes can gain genes that allow them to adapt to varying conditions. Finally, viruses are increasingly thought to have been present at the earliest stages in the evolution of life; thus, studying viruses in an ancient environment such as vents may elucidate their role in the evolution of life in its earliest stages.