**Viggo Blomquist, New York**  
**Project:** A Novel Suppression Technique of Premature Termination Codons and its Application to Congenital Long QT Syndrome 2  
**Mentor:** Dr. Christopher Ahern, University of Iowa

**Summary:** The human ether-à-go-go related gene (hERG) codes for the pore-forming subunit of the voltage dependent potassium ion channel in cardiac cells. Potassium channels are voltage gated protein channels within the plasma membrane that allow potassium to move down the electrochemical gradient. The channel’s central role is to initiate the repolarization of cardiac action potential. Premature termination codons in hERG result in a hereditary and potentially deadly disease called Long QT Syndrome 2 (LQTS2). The purpose of this investigation was to test if novel codon edited V10 tryptophan tRNA would be able to recognize the premature stop codon within the mRNA strand and add tryptophan to the growing polypeptide chain, preventing premature termination and rescue of Kv11.1. In order to prove successful suppression, Western blotting, patch clamp technique, and immunofluorescence microscopy were conducted on HEK293 cells transfected with DNA plasmids containing a gene for codon edited V10 Tryptophan tRNA and the mutated hERG gene. I determined that codon edited V10 Tryptophan tRNAs were capable of suppressing the W1001TGA premature stop. Successful suppression of premature stops by using such tRNAs could lead to major medical advances in gene therapy for not only LQTS2, but also for other diseases caused by premature termination codons.

**Eric Hwang, South Korea**  
**Project:** Development of tools to test novel narrow-spectrum insecticides in *Drosophila melanogaster*  
**Mentor:** Dr. April Burch, Berkshire School

**Summary:** The effects of global warming are wide and varied starting with shifts in temperature and precipitation that induce shifts in flora and fauna. A major end result of such shifts is the more silent, but equally impactful, spread of tropical vector-borne diseases. Efforts to control this mosquito migration have proven ineffective, even while drastically harming the environment as a result of broad-spectrum pesticides that also kills beneficial insects, including pollinators such as bees. Therefore, the need to find an environmentally friendly narrow spectrum pesticides derived from sources natural to tropical regions such as South America is a rising need. Tracing this requirement, chemical compounds of various plants for insecticidal functions and found Graviola (*Annona muricata*), a plant native to the
Amazon to be a promising source. Six different compounds – namely Kampferol (K), Cathechine (C), Quercetin (Q), Chlorogenic Acid (CA), Rutin (R), and Solamin (Benzethonium Chloride, BC) – extracted from Graviola leaves were obtained. Compounds that were proven to possess insecticidal potential were then combined into a cocktail to prevent the evolution of a specific chemical immune population of mosquitoes.

**Claire Lemker, Minnesota**  
**Project:** Isolation and Characterization of Phage CL1, a novel pathogen of *Anabaena variabilis* and potential natural mediator for freshwater algal blooms  
**Mentor:** Dr. April Burch, Berkshire School  

**Summary:** Anabaena is a freshwater filamentous cyanobacterium. Cyanobacterial blooms are known to produce BMAA, which is a non-proteinogenic amino acid. BMAA has been linked to neurological diseases, such as ALS, Parkinson’s, and Dementia, and has been found in the autopsied brains and spinal cords of these patients. A potential non-chemical way of controlling algal blooms could be by using bacteriophages. To the best of our knowledge no known phage for freshwater cyanobacteria exists. Since algal blooms are common in freshwater lakes in New England, water was screened from the region for the presence of a bacteriophage. Phage CL1 was isolated from one water sample which was also determined to contain Anabaena. This paper explains the isolation and characterization of phage CL1, a novel predator of Anabaena and possible implement for controlling algal blooms.

**Ryan Zang, China**  
**Project:** Genetic studies on the phiX174 pilot protein  
**Mentor:** Drs. April Burch (Berkshire School) and Dr. Bentley Fane (University of Arizona)  

**Summary:** The ways that viruses use to transport their DNA during infection have fascinated scientists for decades, and they are essential topics in scientific fields nowadays because many infectious diseases, such as HIV, SARS, and Zika, are responsible for millions of deaths around the globe. The present study focuses on the H protein of the virus phiX174, which is a pilot protein that forms a tube to inject the viral DNA into the bacteria during the infection. To gain a better insight of this process, several mutations were designed on the gene coding for the H protein. These mutations were made in the area that encodes the “waist” part of the tube formed by the H protein because it was predicted that the “waist” plays a crucial role in the shape and structure of the tube. One mutation, which includes the change from amino acid 193 (Tyr) into Glycine, was successfully isolated and tested. Two methods were designed to test the effect of this mutant. The first method incorporates mutagenic DNA fragment into the wild type viral genome, while the second one incorporates mutagenic DNA fragment into the H plasmid and uses the method of complementation. Results show that the mutated virus is still able to grow and reproduce under the method of complementation, albeit less than wild-type phiX174.