We were presented with the bacterium *Arhodomonas* sp. Seminole, the full DNA sequence of which is currently unknown. Our job was to track the DNA of a missing contig by utilizing database resources, such as BLASTX, and the technique of PCR amplification. Our group had a positive forward PCR product, which led us to the conclusion that two fragments of the original sequence and forward primer had aligned.

**RESULTS**

Before we started the experiment, we used BLASTX to compare our original contig sequence with a related protein sequence. Through that, we found that the fused contig is continuous on the head.

The image to the left is the gel image that contains our group’s PCR product. As our gel produced a visible band, we had a positive PCR product.

**DISCUSSION**

The goal of our experiment was to determine the DNA structure of a gap sequence found in *Arhodomonas* sp. Seminole. Fortunately our experiment provided us with a positive result in the forward primer, which allowed corresponding base pairs to be added to create the DNA strand for the missing contig.

Besides finding the DNA of the gap sequence, the original hypothesis desired to know if the new proteins would stabilize the environment and habitat of the bacteria. We were able to determine that by correlating the new protein back to what was predicted at the gap. We utilized the program, BLASTX, by blasting the new DNA sequence to the original fused contigs. This program allowed us to determine if there was a gap. Our results concluded that the two fragments had aligned, and therefore, supported the hypothesis.

We are happy with our result, but it is not completely ideal. In the future, we would recommend redesigning the forward and reverse primers in the hopes of receiving a positive result for the reverse primer sequence.

**REFERENCES**