INTRODUCTION

Fritillaria gentneri is an endangered plant native to Oregon. It grows in community with a sister species, Fritillaria recurva, which dominates the shared habitat. The two plants are virtually indistinguishable when not flowering, inhibiting the recovery efforts of Fritillaria gentneri. The purpose of this experiment is to create a genomic test that enables the identification of the endangered Fritillaria gentneri from its sister plant Fritillaria recurva.

METHODS

▪ Whole chloroplast genome sequencing from leaf tissue samples were evaluated for differences in genetic code
▪ Primers were custom designed for the 16 viable sites found
▪ 4 polymerase chain reaction (PCR) primers were tested using PCR and gel electrophoresis to determine efficacy
▪ PCR reactions were conducted with colored green buffer, colorless, and ExoSAP cleaned PCR
▪ Restriction enzyme digestions were tested using gel electrophoresis and analyzed based on sample fluorescence and PCR product size to determine success

CONCLUSION

▪ More research is required to determine whether the BamHI restriction enzyme and associated custom primers can be used to effectively differentiate the two species, Fritillaria gentneri and Fritillaria recurva. PCR product size and gel electrophoresis can be used to determine success
▪ Past work indicated Fritillaria recurva digests product in a similar fashion to Fritillaria gentneri, suggesting that changing the ratios of the components in the PCR product; such as adding more DNA, could lead to a successful test.
▪ Failure to design an effective test would require the use of additional primers to differentiate the two species, Fritillaria gentneri and Fritillaria recurva.

REFERENCES
