

MICRO-INTERNSHIP

Comparative analysis of the chloroplast genomes of *Quercus x morehus* and the presumptive parents *Q. wislizeni* and *Q. kelloggii* (Fagaceae) from California



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Quercus morehus Kellogg, Abram's oak, was originally proposed from a single specimen from near Clear Lake, California, USA. It was described as a small tree (9.14 meters) with black bark, oblong-lanceolate leaves, and oblong nuts. Greene was the first to study *Q. morehus* and concluded it was a hybrid between the interior live oak *Q. wislizeni* A. DC. and the black oak *Q. kelloggii* Newb. Subsequent authors agreed with this hypothesis, including Jepson who itemized six observations supporting the hybrid conclusion (3-7).

Many oak chloroplast genomes have been sequenced to date, however the genomes of

Quercus x morehus, *Q. wislizeni*, and *Q. kelloggii* have not been analyzed. To contribute to the bioinformatics of *Quercus x morehus*

and these closely related *Quercus* species, we assembled and characterized the complete chloroplast genomes of the presumptive hybrid and parents. The genomes are 161,119–161,130 bp and encode 132 genes. *Quercus x morehus* and *Q. wislizeni* are identical in sequence, but differ from *Q. kelloggii* by three indels and eight single nucleotide polymorphisms. Analysis of the chloroplast genomes support the hybrid designation for *Quercus x morehus* as well as contributes to the systematics and chloroplast evolution of Fagaceae.



Quercus x morehus