# Abstract

Digital analysis of whole chromatin DNA is a relatively new field of research made possible by recent advances in long-read genome sequencing technology. The study reported here attempted to determine characteristic parameters of SSR primer pairs in an *F. carica* genome reference assembly but instead found the genome contents do not match published analog descriptions of SSR primers in plants. Of the 11.8k instances of 15 standard marker primers in the genome, only 2.8k qualified as marker pairs, and less than 1% of those were found within 1k bp of each other. In addition, microsatellite sequences were found once every 60 bp on weighted average – a much shorter period than reported for other plants. Consequently SSR microsatellites are not a robust choice for genetic ID and genomic distance in *F. carica*.