Deep pedigree verification using mtDNA and Y-chromosome data: advancing MaGelLAn 2.1

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Low-coverage whole genome sequencing (lcWGS) has become powerful and cost-effective approach in population genomics and genome-wide association studies (GWAS). Here we present the utilization of lcWGS data to test a new version of the MaGelLAn 2.1 software. The main aim and capability of the previous version was to analyse maternal lineage using mitogenome polymorphism from the whole mitogenome sequence and the GGP100K SNP array, while it has now been extended to analyse paternal lineage using Y-chromosome markers. In addition, the software has been updated with a new graphical user interface, keeping the existing modules into the command line interface. Computational cost of the sampling procedure, which has been greatly reduced through the implementation of two efficient algortihms, has been tested on large Holstein cattle pedigre using retrived mtDNA and Y chromosome markers from lcWGS. With the new visualisation module, we were able to check the insight into important parts of pedigrees. The software is fully functional under Windows and Linux operating systems. This research was supported by grant HRZZ-IP-2022-10-6914. Key words: software, pedigree, lcWGS, mtDNA markers, Y-chromosome markers