Vanessa v2 genome alignment with Melitaea cinxia genome v2

**Methods**

In order to obtain further insights into the accuracy of the v2 assembly, we aligned this genome against the closest related Nymphalid with a high quality chromosomal assembly, which was *Melitaea cinxia*. These species last shared a common ancestor approximately 42 million years ago (Chazot et al. 2019) and the chromosomal structure of *M. cinxia* has been shown to be similar in large scale synteny (chromosomal gene order) with the other butterflies (Ahola et al. 2014). We used the latest version of the *M. cinxia* genome, v2, which was produced using Pacific Biosciences sequencing, combined with a linkage map from population crosses (Blande et al. 2020). Using nucmer, of the Mummer alignment package (v.4.0.0beta2; Marçais et al. 2018), we generated one to one alignments of best hits between these two genomes with a alignment identity of between 80 – 90%, for regions of at least 200 bp in length, for scaffolds of >= 1 Mbp in length. A circle plot of the alignment was made using custom R scripts (R v.4.0.1), with packages (tidyverse v 1.3.0 (Wickham et al., (2019); circlize v 0.4.10 (Gu et al. 2014); RColorBrewer v. 1.1-2). Please see bioinformatic scripts for additional details.

References

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