
The chromosome-scale genome assembly of Visayan warty pig provides insight into porcine evolutionary history

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We generated the *Sus cebifrons* (the Visayan warty pig) assembly using linked-read sequencing and Hi-C-based chromatin interaction maps. The assembly is on chromosome level, it consists of 17 chromosomes and 1,568 unplaced scaffolds. The N50 length for the scaffold is 141,782,568 while the contigs N50 is 159,621. BUSCO analysis suggests the assembly is highly complete, with 95.7% of BUSCOs complete. The alignment of the *Sus cebifrons* assembly and Duroc assembly (Sscrofa11.1) reveals a high degree of collinearity. In the meantime, we also observed chromosome fission and fusion, which reveal the chromosome rearrangement in Suidae evolutionary history. In total, 38,300 protein-coding genes and 788.86 Mb of repetitive sequences were identified. These highly contiguous assembly provide a comparative framework to common pigs, extending our understanding of the genome evolution in a short period of evolutionary history (~3 Million years).