ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

| TxID | 3116505 | |
|---------|-------------------|--|
| ToLID | icCedAzor3.2 | |
| Species | Cedrorum azoricus | |
| Class | Insecta | |
| Order | Coleoptera | |

| Genome Traits | Expected | Observed |
|-------------------|-----------------------|-------------|
| Haploid size (bp) | 729,929,118 | 567,877,672 |
| Haploid Number | 19 (source: ancestor) | 16 |
| Ploidy | 2 (source: ancestor) | 2 |
| Sample Sex | Unknown | Unknown |

EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 7.7.Q65

The following metrics were automatically flagged as below EBP recommended standards or different from expected:

- . Observed Haploid size (bp) has >20% difference with Expected
- . Observed Haploid Number is different from Expected
- . Kmer completeness value is less than 90 for collapsed
- . Not 90% of assembly in chromosomes for collapsed

Curator notes

- . Interventions/Gb: 292
- . Contamination notes: ""
- Other observations: "The assembly of CEDRORUM AZORICUS (icCedAzor3) is based on 43X PacBio data and 189X Arima Hi-C data generated as part of the European Reference Genome Atlas (ERGA, https://www.erga-biodiversity.eu/) via the Biodiversity Genomics Europe project (BGE, https://biodiversitygenomics.eu/). The assembly process included the following steps: initial PacBio assembly generation with Hifiasm, removal of contaminant sequences using Context, removal of haplotypic duplications using purge_dups, and Hi-C-based scaffolding with YaHS (and no contig correction). In total, 9 contigs were identified as contaminants (bacterial, archaeal, or viral), totaling 11 Mb (with the largest being 2 Mb). Additionally, 730 regions totaling 427 Mb were identified as haplotypic duplications and removed. The mitochondrial genome was assembled using OATK. Finally, the primary assembly was analyzed and manually improved using Pretext. Manual curation was performed using the normal resolution map, and the genome was reviewed on the BGE GitHub with a normal resolution q0 map (find in this EAR.pdf). Every effort was made to improve this genome, but full

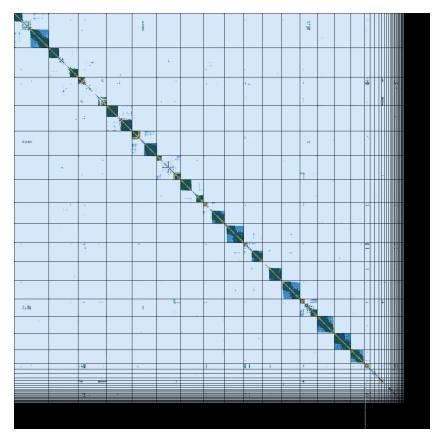
confidence has not been reached. During manual curation, 4 haplotypic regions were removed, totaling 416,211 pb (with the largest being 156,079 pb). Chromosome-scale scaffolds confirmed by $\rm Hi-C$ data were named in order of size. "

Quality metrics table

| Metrics | Pre-curation collapsed | Curated collapsed |
|--------------|------------------------|-------------------|
| Total bp | 568,266,305 | 567,877,672 |
| GC % | 28.76 | 28.75 |
| Gaps/Gbp | 17.6 | 105.66 |
| Total gap bp | 1,000 | 11,100 |
| Scaffolds | 348 | 302 |
| Scaffold N50 | 16,796,384 | 28,853,378 |
| Scaffold L50 | 14 | 8 |
| Scaffold L90 | 56 | 23 |
| Contigs | 358 | 362 |
| Contig N50 | 10,971,072 | 10,971,072 |
| Contig L50 | 16 | 16 |
| Contig L90 | 66 | 69 |
| QV | 65.7836 | 65.6817 |
| Kmer compl. | 84.2012 | 84.1826 |
| BUSCO sing. | 98.4% | 95.5% |
| BUSCO dupl. | 0.5% | 0.3% |
| BUSCO frag. | 0.4% | 2.9% |
| BUSCO miss. | 0.7% | 1.3% |

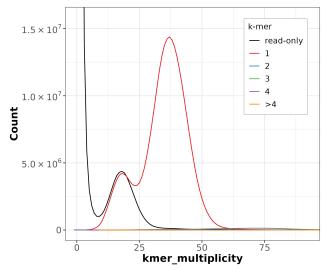
Warning! BUSCO versions or lineage datasets are not the same across results:
BUSCO: 5.4.3 (euk_genome_met, metaeuk) / Lineage: endopterygota_odb10 (genomes:56, BUSCOs:2124)
BUSCO: 5.8.2 (euk_genome_met, metaeuk) / Lineage: endopterygota_odb12 (genomes:76, BUSCOs:3754)

HiC contact map of curated assembly

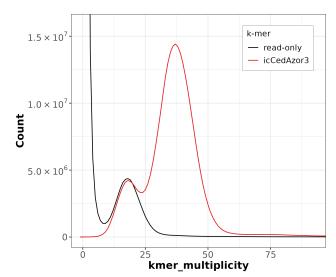


collapsed [LINK]

K-mer spectra of curated assembly

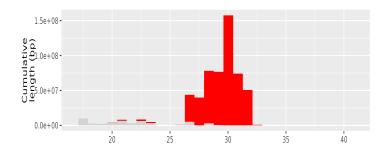


Distribution of k-mer counts per copy numbers found in asm

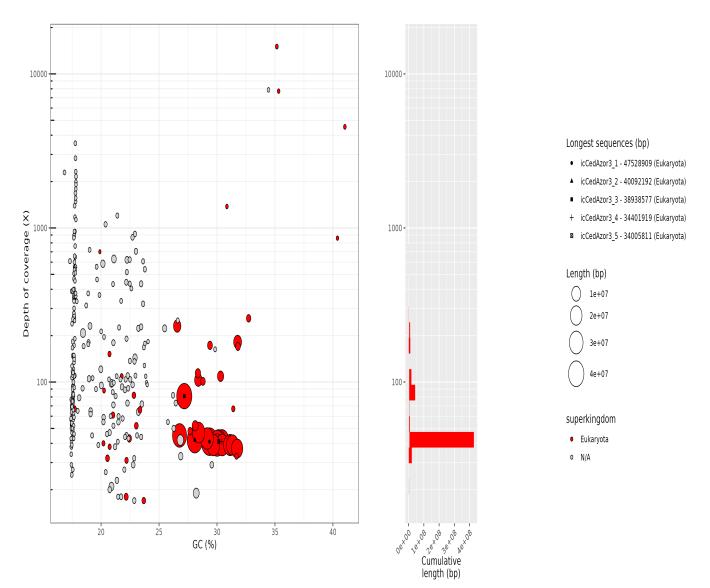


Distribution of k-mer counts coloured by their presence in reads/assemblies

Post-curation contamination screening



TAPAs summary Graph



collapsed. Bubble plot circles are scaled by sequence length, positioned by coverage and GC proportion, and coloured by taxonomy. Histograms show total assembly length distribution on each axis.

Data profile

| Data | PACBIO Hifi | Arima |
|----------|-------------|-------|
| Coverage | 43 | 189 |

Assembly pipeline

Curation pipeline

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Date and time: 2025-05-19 13:06:07 CEST