Long Reads for Long-Term Goals: A Genome Resource for Lavander Genetic Improvement


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Long Reads for Long-Term Goals: A Genome Resource for Lavender Genetic Improvement

Lavender (Lavandula angustifolia L.) is both a patrimonial and economically important species, used for its essential oils in cosmetics and perfumery products. Naturally adapted to poor soil and dry environment, lavender represents a promising culture in the context of climate change. However, increasing pathogenic pressure related to climate change challenges present varieties yields and quality of essential oils. The cultivar ‘Maillette’, that is most-valued for the quality of its essential oil, is widely used in genetic improvement programs in France. Useful genomic resources available for these programs remain nevertheless scarce, despite a short-reads assembled genome available. To support the emerging programs for genetic improvement in lavender, we generated genomic resources based on long-reads sequences, in complement with Illumina short-reads sequences.

Materials & methods
Young leaves from an individual of the cultivar ‘Maillette’ were collected and immediately flash frozen. The protocol of ‘Plant Leaves’ (dx.doi.org/10.17504/protocols.io.bpp2014y7gev1) was slightly modified and the obtained DNA medusa was used for long reads sequencing. A Pacbio HiFi library was built following the manufacturer’s instructions, then sequenced on a Sequel II at Gentyane (INRAE, Clermont-Ferrand) and HiFi reads generated. Assembly was performed with HiFiAsm using default parameters. Assembly quality was assessed using BUSCO, Merqury and KAT. Repeated Sequences were identified with RepeatModeler/RepeatMasker.

Synteny with JingXu2 (JX)
- 54 Maillette contigs anchored on 27 chr. JX
- 839 markers from 3,766 loci (NEBnext direct Genotyping Solution V2)
- + 36 Maillette contigs anchored in 80 JX scaffolds (not shown)
- Contigs with telomere repeats (one end)
  - 12 anchored on JX chr (green contigs in view)
  - 24 anchored on scaffolds
- 6 without anchorage

Conclusions
- Assembly more contiguous
- Better completion
- 839 markers used to check collinearity
- Synteny with JingXu2 (supported by several markers)
- Hypothesis: JingXu2 chr4 and chr25 = one chromosome in Maillette (partially contig 28)

Perspectives
- Expand contigs with available Nanopore long reads (data not shown)
- Scaffolding to pseudomolecules with genetic map (currently under construction)
- Gene and repeat annotations
- Compare with scaffolding from Hi-C linked reads

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