



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

Berline Fopa Fomeju, Aurélie Berard, Isabelle Le Clainche, Aurélie Canaguier, Elodie Belmonte, Veronique Gautier, Charles Poncet, Marie-Christine Le Paslier, Guillaume Frémondière, Damien Hinsinger, et al.

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EPGV
Etude du Polymorphisme
des Génomes Végétaux

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GENTYANE
PLATE-FORME de
GENOTYPAGE et SÉQUENÇAGE en AUVERGNE

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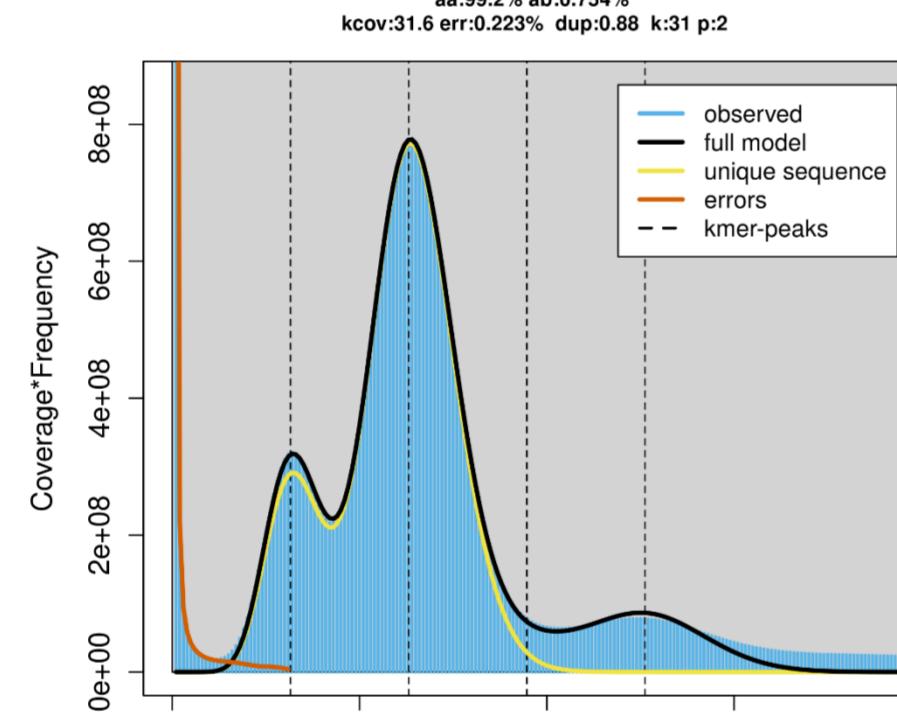
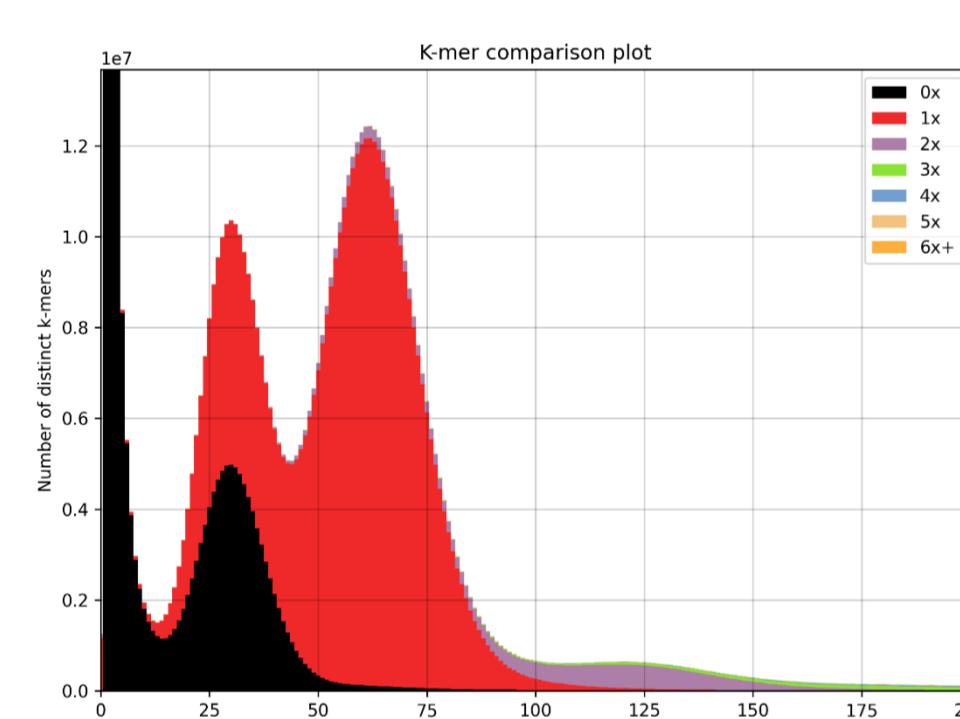
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Metrics of Lavender assemblies

	Maillette (this study)	Maillette (Mallie et al. 2019)	JingXu2 (Li et al. 2021)
Chromosome number	25	25	27
Sequencing technologies	Pacbio HiFi	Illumina + transcriptome	PacBio CLC + 10X + Hi-C
Estimate of genome size (Mb)	721.73	~850	1016.25
Total length of contigs (Mb)	891.5	688.04	911.14
Total number of contigs	579		1383
N50 of contigs (Mb)	20.35		1.22
Largest contig (bp)	35,738,470		9,968,313
Total length of scaffolds (Mb)		869.79	914.49
Total number of scaffolds		84,291	306
N50 of scaffolds (Mb)		0.097	36.20
Largest scaffold (Mb)		0.94	46.64
GC content (%)	39.18	38.1	38.58
Complete BUSCOs (%)	97.1	89.7	91.4
Repeat density (%)	68.23	42.8	58.28
Number of protein-coding genes	ongoing	62,141	65,905

Assembly

BUSCO (eudicot_odb10, n:2326)	C:97.1%[S:24.7%,D:72.4%],F:0.6%,M:2.3%
Mercury completeness	83.0479
Mercury QV (error rate)	41.7636 (6.66247e-05)

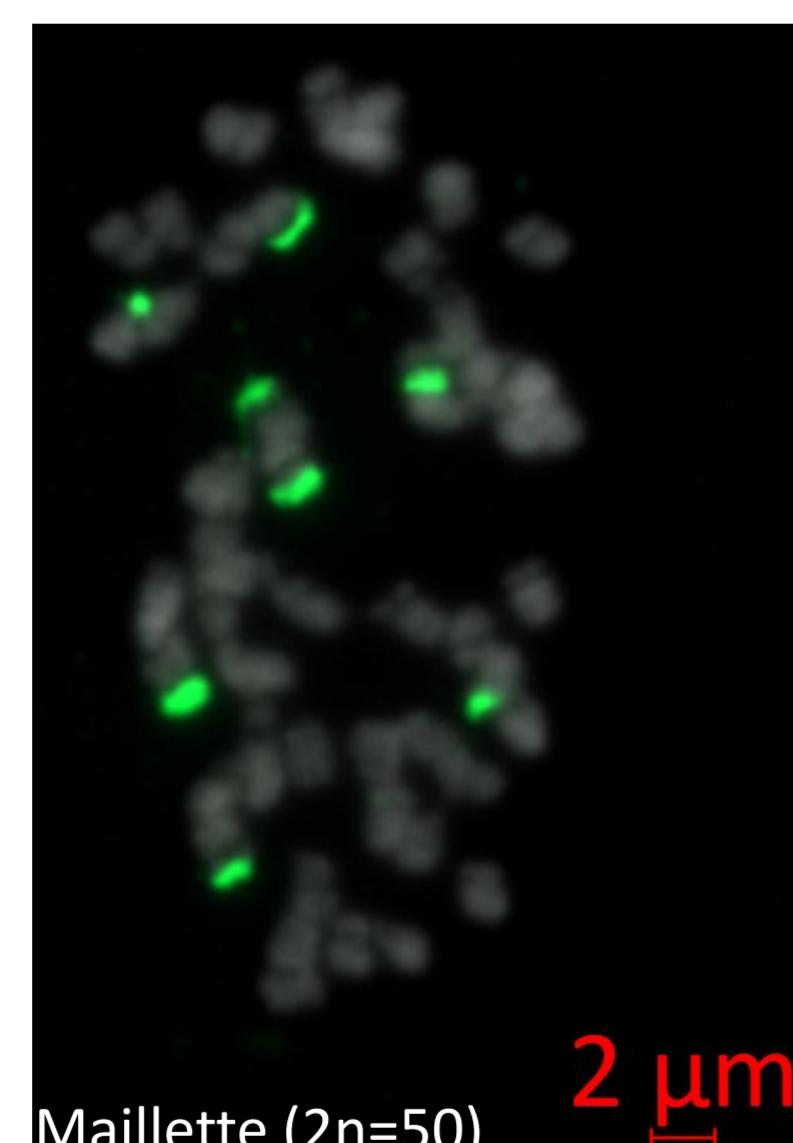


The lavender genome is composed of 68.23% of repeated sequences (mainly Copia – 36.13%).

Other Results

Cytology

Using chromosome counting and rDNA staining (realised at the Molecular Cytogenetics platform – INRAE Le Rheu), we found 25 chromosomes, as well as 8 45S rDNA clusters, in 'Maillette' root tip cells.



Conclusions

- Assembly more contiguous (N50 of contigs)
- 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

Acknowledgements

Molecular Cytogenetics platform – INRAE Le Rheu

Genolavande



Associated publication :

Genospace lavande : Fopa Fomeju B, Brunel D, Bérard A, Rivoal J-B, Gallois P, Le Paslier M-C, et al 2020

Quick and efficient approach to develop genomic resources in orphan species: Application in *Lavandula angustifolia*.

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