

MPOB INFORMATION SERIES • ISSN 1511-7871 • JUNE 2015

MPOB TS No. 148

he Malaysian Oil Palm Genome Programme (MyOPGP) was initiated by MPOB in 2004 to selectively the hypomethylated sequence regions of the genome (Low et al., 2014), and was subsequently expanded to the whole genome, facilitated by advancements in sequencing technologies and bioinformatics. These efforts led to the publication of the oil palm (Elaeis guineensis) genome (Singh et al., 2013). The genome information has since been shared via the Genomsawit website (Rosli et al., 2014). To expand the capabilities of Genomsawit, MYPalmViewer was developed (Figure 1). MYPalmViewer is a web-based genome browser, developed to display and explore the chromosomes of the oil palm. It also has search capabilities for information, such

ISSN 1511-7871

as the position and annotations in the oil palm genome. The genome browser is able to visualise the Elaeis guineensis (EG) genome build, which is the genome assembly representing genetic scaffolds (16 chromosomes) derived from a comparison of the Oil Palm Genome Assembly to markers in two genetic maps (T128 and P2). The assembly also contains scaffolds that were not incorporated into the 16 chromosomes. The E. oleifera genome was also mapped to the EG genome build. Other information, such as the predicted genes, transcripts and markers from oil palm publications has also been mapped to the EG genome build. The browser can be accessed via a link in the Genomsawit website (http:// genomsawit.mpob.gov.my) or directly via http:// gbrowse.mpob.gov.my.

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Figure 1. MYPalmViewer oil palm genome browser.





MATERIALS AND METHODS

MYPalmViewer was built using Gbrowse version 2.0 (Stein, 2013) with the EG genome build dataset as the reference sequence. The browser is hosted on Ubuntu version 12.04 (x86_64) and the browser dataset is archived using MySQL 14.14 (http://www.mysql.com) database. The browser's web interface, which resembles the Genomsawit web interface was developed using HTML coding and Bootstrap packages 3.3.4 as the CSS styling codes. Google Analytics website monitoring system tracks usage and traffic in the browser.

INFORMATION AVAILABLE

MYPalmViewer comes with the EG genome build dataset of the oil palm genome. As of May 2015, nine categories of annotation tracks, namely Comparative Genomics, Gene Predictions. GenBank Sequences, Experimental Results, Reference Genomes, Public Database Sequences, Gaps, Markers and General have been made available in MYPalmViewer. For example, the Pisifera build-5 (P5) GlimmerHMM Gene Models (Gene Prediction Category) that contain 30 752 gene models with similarity to RefSeq sequences are available as a track in the EG5 genome build. The gene prediction was trained using putative full-length oil palm transcriptome sequences. The oil palm sequences from GenBank's protein database (REFSEQ v53), Arabidopsis thaliana (version 9) genes from The Arabidopsis Information Resource (TAIR; https://www. arabidopsis.org/) and Oryza sativa (version 7) genes from the Rice Genome Annotation project (http://rice.plantbiology.msu.edu/) are also available in MYPalmViewer. In addition to genome browsing, MYPalmViewer offers several other capabilities, such as search engines, detailed view pages for each gene, interactive genome navigation and download functions.

BENEFITS OF MYPalmViewer

- Enhanced visualisation of the oil palm genome with powerful navigation tools.
- Comprehensive functional and structural annotation of the oil palm genome.
- Interactive user interface for data sharing.

ACCESSIBILITY

MYPalmViewer has been made available to the public since 20 March 2015. It can be accessed via a web browser (Preferred Browsers: Internet Explorer 11 and Firefox 23.0.1, and above version). Hence, there is no need for any installation of

desktop software to browse and use the genome annotations. The browser is accessible via a link provided in the Genomsawit website (http:// genomsawit.mpob.gov.my) or at MyPalmViewer's URL (http://gbrowse.mpob.gov.my).

REFERENCES

LOW, E T L; ROSLI, R; JAYANTHI, N; MOHD-AMIN, A B; AZIZI, N; CHAN, K L; MAQBOOL, N J; MACLEAN, P; BRAUNING, R; MCCULLOCH, A; MORAGA, R; ONG-ABDULLAH, M and SINGH, R (2014). Analyses of hypomethylated oil palm gene space. *PLoS ONE*, *9*(1): e86728.

ROSLI, R; AB HALIM, M-A; CHAN, K L; AZIZI, N; JAYANTHI, N; NIK MOHD SANUSI, N S; AMIRUDDIN, N; ABDUL RAZAK, A S; KADRI, F and LOW, E T L (2014). Genomsawit website. *MPOB Information Series No. 134*.

SINGH, R; ONG-ABDULLAH, M; LOW, E T L; ABDUL MANAF, M A; ROSLI, R; RAJANAIDU, N; OOI, L C-L; OOI, S E; CHAN, K L; HALIM, M A; AZIZI, N; JAYANTHI, N; BACHER, B; LAKEY, N; SMITH, S W; HE, D; HOGAN, M; BUDIMAN, M A; LEE, E K; DESALLE, R; KUDRNA, D; GOICOECHEA, J L; WING, R A; WILSON, R K; FULTON, R S; ORDWAY, J M; MARTIENSSEN, R A and SAMBANTHAMURTHI, R (2013). Oil palm genome sequences reveals divergence of interfertile species in old and new worlds. *Nature*, 500(7462): 335-339.

STEIN, L D (2013). Using GBrowse 2.0 to visualize and share next-generation sequence data. *Briefings in Bioinformatics*, 14(2): 162-171.

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