

BIOINFORMATIC ANALYSIS OF DEGRADOME DATA FROM AFRICAN OIL PALM
(*ELAEIS GUINEENSIS JACQ.*) INFLORESCENCE

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ABSTRACT

African Oil Palm (*Elaeis guineensis* Jacq.) is an economically important plant since it is the highest yielding oil-producing crop in the world. Long reproductive cycle and slow seed maturation result in lengthy breeding cycles and a slow rate of improvement through selection. Demand to increase oil palm yield can be supported by analysis of oil palm sequence data towards a functional genomic approach to support marker assisted selection.

In this study degradome data from inflorescence of the African Oil Palm was analysed to identify miRNA/siRNA cleavage products and SNPs in miRNA targets. Degradome analysis tools CleaveLand, SeqTar and PARESnip were used to analyse degradome data towards the objective of identifying miRNA/target pairs that may be important in oil palm flowering and hence yield of this major crop.

Total miRNA targets predicted by CleaveLand, SeqTar, PARESnip were 1304, 663318 and 12532 respectively. SeqTar is suitable to be used to predict a wide range of targets without missing any possibilities of the predicted targets in oil palm degradome data. SeqTar is also suitable to predict precursor novel miRNA targets in oil palm degradome data. CleaveLand can only be used to predict known miRNA targets and it is not suitable to predict novel miRNA targets in oil palm degradome data.

Of the three currently available tools for degradome analysis, PARESnip was found to be the fastest and most convenient tool. PARESnip is user friendly and user configurable tool. PARESnip also shows the highest number of prediction of highly significant miRNA targets compared to CleaveLand and SeqTar. Thus, PARESnip can be considered as a more reliable tool to analyse degradome data from African Oil Palm inflorescence.

Computational prediction methods have been successfully employed to find candidate miRNA targets in African Oil Palm inflorescence data.

ABSTRAK

Kelapa Sawit Afrika (*Elaeis guineensis* Jacq.) adalah tanaman yang penting dari segi ekonomi kerana ia merupakan pengeluar minyak yang tertinggi di dunia. Kitar reproduktif yang lama dan maturasi benih yang perlahan mengakibatkan kitar pembiakan yang panjang dan kadar perlahan peningkatan melalui pilihan. Permintaan untuk meningkatkan hasil kelapa sawit boleh disokong oleh analisis data turutan minyak kelapa sawit ke arah pendekatan genomik berfungsi untuk menyokong seleksi dibantu marker.

Dalam kajian ini, data degradome dari pembungaan kelapa sawit Afrika telah dianalisa untuk mengenal pasti produk hasil belahan miRNA/siRNA dan SNPs dalam target miRNA. Program-program penganalisis degradome seperti CleaveLand, SeqTar dan PARESnip telah digunakan untuk menganalisa data degradome ke arah objektif mengenal pasti pasangan miRNA target yang mungkin penting dalam pembungaan kelapa sawit dan seterusnya meningkatkan hasil tanaman utama ini.

Jumlah pasangan miRNA target yang diramalkan oleh CleaveLand, SeqTar dan PARESnip adalah 1304, 663 318 dan 12 532 masing-masing. SeqTar sesuai diguna untuk meramal miRNA target dalam pelbagai jenis tanpa sebarang kemungkinan ketinggalan pasangan target. CleaveLand hanya boleh digunakan untuk meramalkan miRNA target orthologus tetapi tidak sesuai untuk miRNA target novel dalam data kelapa sawit.

Antara ketiga-tiga program ini yang diguna untuk menganalisa degradome, PARESnip adalah paling pantas dan mudah untuk diguna. PARESnip merupakan mesra pengguna dan boleh dikonfigurasi. PARESnip juga menunjukkan bilangan tertinggi ramalan miRNA target yang amat ketara berbanding CleaveLand dan SeqTar. Oleh itu, PARESnip boleh dianggap sebagai program yang lebih sesuai untuk menganalisa data degradome dari pembungaan kelapa sawit Afrika.

Kaedah ramalan komputer telah berjaya digunakan untuk mencari calon-calon miRNA target dalam data pembungaan kelapa sawit Afrika.

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TABLE OF CONTENTS

CHAPTER 1: INTRODUCTION	1
CHAPTER 2: LITERATURE REVIEW	
2.1 Importance of African Oil Palm (<i>Elaeis guineensis</i> Jacq.)	3
2.2 Small RNA (sRNA) in Plants	4
2.3 Degradome Data and Parallel Analysis of RNA Ends (PARE)	5
2.4 MicroRNAs and Expressed Sequence Tags (EST)	6
2.5 Bioinformatic Tools for Degradome Analysis	7
2.5.1 CleaveLand	7
2.5.2 SeqTar (SEQUencing-based sRNA TARget prediction)	7
2.5.3 PARESnp	8
CHAPTER 3: METHODOLOGY	
3.1 Degradome and sequence data sets used	10
3.2 The CleaveLand Pipeline	10
3.3 The SeqTar pipeline	13
3.4 PARESnp	15
CHAPTER 4: RESULTS	
4.1 Predicted miRNA targets by CleaveLand, SeqTar and PARESnp	17
4.2 Run Time of Tools	19
4.3 Prediction comparisons	20
4.4 P-Values	21

CHAPTER 5: DISCUSSION	
5.1 Run Time of Tools	27
5.2 Predicted Target Comparisons	27
5.3 User Friendly Tool	28
5.4 Validation of results	29
CHAPTER 6: CONCLUSIONS	30
BIBLIOGRAPHY	31
APPENDIX	34

LIST OF FIGURES

Figure 3.2 Workflow of CleaveLand	12
Figure 3.3 Workflow of SeqTar	14
Figure 3.4 Workflow of PARESnip	15
Figure 3.5 Parameters used in PARESnip	16
Figure 4.1.1 Number of Predicted targets by CleaveLand, SeqTar and PARESnip	18
Figure 4.2.1 Run time for CleaveLand, SeqTar and PAREsnip	19
Figure 4.3.1 Venn diagram showing the comparison of miRNA target predictions by CleaveLand, SeqTar and PARESnip	20
Figure 4.4.1 Cumulative Plot showing number of predicted targets versus p-value reported by CleaveLand	21
Figure 4.4.2 Cumulative Plot showing number of predicted targets versus mismatch p-value reported by SeqTar	22
Figure 4.4.3 Cumulative Plot showing number of predicted targets versus valid p-value reported by SeqTar	23
Figure 4.4.4 Category I miRNA target pairs classified by their Pv and Pm-values.	24
Figure 4.4.5 Cumulative Plot showing number of predicted targets versus p-value reported by PARESnip	25
Figure 4.4.6 Number of highly significant miRNA targets according to small p-value predicted by CleaveLand, SeqTar and PARESnip	26

LIST OF TABLES

Table 2.5.1 Mismatch-based scoring scheme	7
Table 2.5.2 Rules used in modified Smith–Waterman algorithm	8
Table 2.5.3 5-category system in PAREsnip	8
Table 2.5.4 sRNA target binding rules applied in traversing the partitioned 4-way tree	9
Table 4.1.1 Example of a predicted miRNA target by CleaveLand, SeqTar and PARESnip	17

APPENDIX

APPENDIX A

Compiled scripts	34
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APPENDIX B

Linux Commands	38
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APPENDIX C

List of Similar prediction of miRNA targets by CleaveLand, SeqTar and PARESnip	40
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APPENDIX D

List of Category I miRNA target pairs predicted by SeqTar	44
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APPENDIX E

Supplementary Tables S1, S2 and S3	46
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APPENDIX F

Summary of mapped degradome	47
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APPENDIX G

Number of sequences in miRNAs and number of predicted targets according to CleaveLand, SeqTar and PARESnip	48
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