



UNIVERSITI PUTRA MALAYSIA

**CREATION OF A POTENTIAL GENE CASSETTE FOR RECOMBINANT
PROTEIN EXPRESSION IN GREEN MICROALGAL SYSTEM**

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By

SAEID KADKHODAEI

**Thesis Submitted to the School of Graduate Studies, Universiti Putra Malaysia, in
Fulfillment of the Requirement for the Degree of Doctor of Philosophy**

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DEDICATION

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Abstract of thesis presented to the Senate of Universiti Putra Malaysia in fulfillment of the requirement for the degree of Doctor of Philosophy

CREATION OF A POTENTIAL GENE CASSETTE FOR RECOMBINANT PROTEIN EXPRESSION IN GREEN MICROALGAL SYSTEM

By

SAEID KADKHODAEI

July 2014

Chairman: Professor Arbakariya B. Ariff, PhD

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Development of efficient strategies and reliable systems for production of recombinant proteins in high quality and quantity to reach the market are gaining more attraction. On the economic side, improvement of the efficiency and cost effectiveness of production process is highly required to be commercially viable. Although many strategies have been theoretically established to increase the level of gene expression in different specific host systems, it is needed to be practically applied. Due to the lack of enough information for expression of recombinant proteins in microalgal systems, the present study aimed at creation of a gene cassette utilizing both upstream (bioinformatics and computational analysis, genetic engineering and molecular biology) and downstream factors (bioprocess engineering) which may have critical roles in gene expression with the emphasis on two microalgae species, *Dunaliella salina* and *Chlamydomonas reinhardtii*.

As the first step in evaluating the feasibility of molecular farming in microalgae, some of the important upstream factors including matrix attachment regions (MARs), translation initiation sites, signal peptides and gene optimization parameters were studied. An artificial universal MAR sequence was designed and developed considering the MAR specific rules and motifs. To explore the specific translation initiation site, all mRNA sequences in the microalgae *D. salina* were screened among which the non-redundant mRNAs were selected for bioinformatics analysis. A consensus sequence was finally created to be used in the specific expression vector. For the secretion systems in microalgae *D. salina*, a screening procedure was carried out to find the specific signal peptides using bioinformatics and *in silico* tools in DNA, RNA and protein databases. The predicted sequences were then selected for further characterizations and the highest

scored predicted signal was embedded in the secretion series of expression vectors. For optimization of the coding sequences, the most important parameters such as the host codon preference, RNA secondary structure, GC and CpG dinucleotides content were taken into consideration. The final expression cassette containing all of the required elements including MAR, signal peptide, translation initiation site, KDEL retention signal, His 6x purification tag, V5 epitope and protease cleavage site was integrated into 25 expression vectors (25 vectors containing different elements). To develop a proprietary series of microalgae specific expression vectors, nine fragments containing the Gateway recombination cassette, optimized genes of interest (2), promoters (2), 5'-UTR, interon, 3'-UTR (2), MARs (2) and pUC18 backbone were amplified using the most high fidelity enzyme available (KAPA). The fragments were successfully assembled in a single recombination reaction through the novel multiple overlap extension PCR (MOE-PCR) technique developed in this study.

To assess the efficient transformation techniques for microalgae, three different methods (electroporation, glass beads and PEG-mediated) were used to transform one *Dunaliella* and three *Chlamydomonas* strains using the developed expression vectors. Glass bead method with 10 s agitation time, 4% PEG and 300 ng/ μ L plasmid DNA, as an efficient and simple technique showed the best results despite a drop in viable cells. The use of specific expression vectors resulted in more number and more stable transformants comparing a commercially available vector (pCAMBIA-3301) without the abovementioned optimized elements. The expression cassette containing optimized genetic elements could be delivered into microalgae cells and confer the resistance to the transformants for at least 3 months. For the downstream processes, the culture condition of *D. salina* was optimized to be used for future studies of the transformants. An experiment was conducted based on response surface methodology (RSM) to realize the reaction of microalgae to different phototrophic conditions including heterotrophic, mixotrophic and phototrophic. It was observed that the higher the amount of supplemented glucose up to 15 g/L, the more glucose utilization, biomass concentration and consequently protein content obtain. The results demonstrated superiority of mixotrophic conditions in constant light in improving the growth of microalgae.

This study demonstrated that the upstream factors such as MARs, translation initiation sites and gene optimization along with the optimized transformation systems and downstream processes, could be a potential procedure to be efficiently used in overexpression of recombinant protein production using microalgae as the expression platform. Considering the close relatedness of the studied microalgae and other close species, the proprietary vector series could be generally used in genetic engineering of at least green microalgae.

Abstrak tesis yang dikemukakan kepada Senat Universiti Putra Malaysia sebagai memenuhi keperluan untuk ijazah Doktor Falsafah

**PENCIPTAAN KASET GEN BERPOTENSI UNTUK EKSPRESI REKOMBINAN
PROTEIN DALAM SISTEM MICROALGAL HIJAU**

Oleh

SAEID KADKHODAEI

Julai 2014

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Pembangunan sesuatu strategi yang cekap dan sistem yang boleh dipercayai, khususnya untuk pengeluaran protein rekombinan yang berkualiti tinggi dan dalam kuantiti yang mencukupi untuk pasaran semakin mendapat perhatian. Dari sudut ekonomi, penambahbaikan ke atas kecekapan dan keberkesanan kos adalah sangat diperlukan untuk satu-satu proses pengeluaran itu mampu berdaya saing. Terdapat pelbagai strategi yang secara teorinya dikenalpasti dapat meningkatkan tahap ekspresi gen di dalam sistem perumah yang berbeza, yang mana secara praktikalnya ianya perlu dibangunkan khusus untuk organisma tertentu. Bagi mencapai matlamat tersebut, pelaksanaan kajian ini telah menjurus kepada penerokaan kedua-dua faktor hulu dan hiliran yang mungkin mempunyai peranan kritikal dalam ekspresi gen, dengan penekanan diberikan kepada dua spesies mikroalga, *Dunaliella salina* dan *Chlamydomonas reinhardtii*. Oleh yang demikian, kajian ini telah digariskan kepada tiga bidang yang berbeza tetapi saling berkait, a) bioinformatik dan analisa perkomputeran, b) kejuruteraan genetik dan biologi molekular, dan c) kejuruteraan bioproses.

Sebagai langkah pertama dalam menilai daya saing kaedah pertanian molekul ke atas mikroalga, beberapa faktor hulu yang penting seperti kawasan pelekatan matriks (MARs), tapak permulaan translasi, peptida isyarat dan parameter-parameter pengoptimuman gen telah dikenalpasti untuk kajian lanjutan. Satu turutan MAR buatan yang universal telah direka dan dibangunkan dengan mengambilkira syarat-syarat spesifik dan motif MAR. Kualiti turutan yang direka kemudiannya disahkan menggunakan platform Genomatix SMARTest. Berkenaan tapak-tapak permulaan translasi di dalam mikroalga, oleh kerana terdapat beberapa variasi yang signifikan di

kalangan pelbagai eukariot, dan di sebaliknya pula terdapat kekurangan maklumat yang sedia ada untuk mikroalga, maka turutan ini telah cuba diterokai di dalam pangkalan-pangkalan data. Semua turutan mRNA bagi mikroalga *D. salina* di dalam NCBI disaring, yang mana mRNAs tidak-berlebihan dipilih untuk tujuan analisa bioinformatik. CLC – Bio Main Workbench telah diguna untuk menganalisa turutan-turutan berkenaan melalui penetapan kawasan penjajaran hulu dan hiliran pada codon permulaan. Akhirnya, turutan yang konsensus telah digunakan dalam pembangunan vektor. Disebabkan kurangnya maklumat eksperimen mengenai sistem rembesan di dalam mikroalga *D. salina*, satu kaji selidik telah dijalankan untuk mencari peptida isyarat yang spesifik dengan menggunakan bioinformatik dan peralatan *in silico* dalam pangkalan-pangkalan data DNA, RNA dan protein. SignalP 4.1 sebagai platform dalam talian yang paling dikenali dengan ambang yang mempunyai nilai p yang tinggi (> 0.9) telah digunapakai dalam penyaringan dataset urutan. Urutan ramalan kemudiannya telah dipilih untuk pencirian selanjutnya. Isyarat ramalan terunggul dengan skor rembesan tertinggi kemudiannya digunakan untuk berada pada bahagian hulu turutan pengkodan di dalam siri-siri rembesan vektor-vektor ekspresi untuk kajian sistem rembesan di dalam mikroalga hijau pada masa depan. Bagi tujuan mengoptimumkan turutan pengkodan, parameter yang paling penting seperti keutamaan codon perumah, struktur RNA sekunder, kandungan dinukleotida GC dan CPG, dan lain-lain telah diambil kira. Kaset ekspresi mutakhir yang mengandungi semua unsur-unsur yang diperlukan seperti MAR, peptida isyarat, tapak permulaan translasi, isyarat pengekal KDEL, tag penulenan His 6x, epitop V5 dan tapak belahan protease diintegrasikan ke dalam vektor ekspresi (25 vektor yang mengandungi elemen-elemen yang berbeza). Untuk membangunkan satu siri proprietari vektor ekspresi yang spesifik kepada mikroalga, sembilan serpihan yang mengandungi kaset rekombinan Gateway, gen sasaran yang telah dioptimum (2), promoter (2), 5'- UTR, interon, 3' - UTR (2), MAR (2) dan tulang belakang pUC18 telah diampifikasi dengan menggunakan enzim yang berkesesuaian paling tinggi yang boleh diperolehi (KAPA). Serpihan-serpihan berkenaan telah dipasang melalui teknik terbaru iaitu pertindihan berganda dalam pemanjangan PCR (MOE-PCR) yang dibangunkan khusus dalam kajian ini. MOE-PCR telah berjaya menghimpunkan pelbagai fragmen secara serentak dalam satu tindakbalas rekombinan tunggal.

Dalam usaha untuk memilih dan melakukan kajian lanjutan terhadap transformants yang berjaya, satu ujian sensitiviti telah dijalankan untuk menentukan rintangan mikroalga (*D. salina* dan *C. reinhardtii*) kepada antibiotik dan racun rumpai yang berbeza, dan juga mencari amalan rintangan racun-racun yang efektif. Mikroalga-mikroalga telah menunjukkan sensitiviti yang tinggi terhadap BASTA pada kepekatan sekurang-kurangnya 6 mg / L.

Untuk menilai teknik transformasi yang berkesan untuk mikroalga, tiga kaedah yang berbeza (elektroporasi, manik kaca dan pengantaraan PEG) telah digunakan untuk mengtransformasi satu strain *Dunaliella* dan tiga strain *Chlamydomonas* dengan menggunakan vektor ekspresi yang telah dibangunkan. Kaedah manik kaca sebagai teknik yang cekap dan mudah telah menunjukkan keputusan yang terbaik walaupun

terdapat penurunan dalam jumlah bilangan sel-sel yang hidup. Penggunaan vektor ekspresi yang spesifik telah menyebabkan bilangan yang tinggi dan transformants yang lebih stabil berbanding vektor diperolehi secara komersial (pCAMBIA - 3301) di mana ia tidak mengandungi unsur-unsur dioptimumkan seperti yang dinyatakan di atas. Sebagai salah satu proses hiliran, keadaan kultur *D. salina* telah dioptimumkan untuk digunapakai dalam kajian ke atas transformants yang selanjutnya. Satu eksperimen telah dijalankan berdasarkan kaedah sambutan permukaan (RSM) untuk memahami tindakbalas alga terhadap keadaan phototrophic yang berlainan, ini termasuklah heterotrofik, mixotrofik dan fototrofik. Keputusan diperolehi menunjukkan keadaan mixotrophic dengan pencahayaan tetap adalah paling sesuai dalam meningkatkan pertumbuhan mikroalga.

Kajian ini telah menunjukkan bahawa faktor-faktor hulu seperti MAR, tapak permulaan translasi, pengoptimuman gen, dan lain-lain bersama dengan sistem transformasi yang dioptimumkan, dan juga proses hiliran boleh menjadi prosedur yang berpotensi untuk digunapakai secara cekap di dalam pengeluaran protein rekombinan yang menggunakan mikroalga sebagai platform ekspresi. Memandangkan perkaitan rapat mikroalga yang dikaji dengan spesies terhampir yang lain, siri-siri vektor proprietari ini boleh diguna secara umum untuk kejuruteraan genetik yang sekurang-kurangnya melibatkan microalga hijau.

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I certify that a Thesis Examination Committee has met on 18 July 2014 to conduct the final examination of Saeid Kadkhodaei on his thesis entitled "Creation of Potential Gene Cassette for Recombinant Protein Expression in Green Microalgal System" in accordance with the Universities and University Colleges Act 1971 and the Constitution of the Universiti Putra Malaysia [P.U.(A) 106] 15 March 1998. The Committee recommends that the student be awarded the Doctor of Philosophy.

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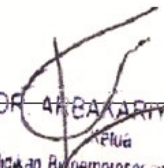
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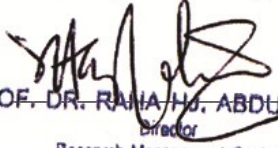
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