

RGC Reference <b>CUHK3/CRF/11G</b>
<i>please insert ref. above</i>

**The Research Grants Council of Hong Kong  
Collaborative Research Fund Group Research Projects  
Completion Report**

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*(for completed projects only)*

**Part A: The Project and Investigator(s)**

**1. Project Title**

Genomic and molecular studies of a salinity tolerance locus in the wild soybean genome  
野生大豆內一個耐鹽位點的基因組及分子生物學研究

**2. Investigator(s) and Academic Department/Units Involved** *(please highlight approved changes in the composition of the project team and quote the date when RGC granted approval of such changes)*

Research Team	Name/Post	Unit/Department/Institution	Average number of hours per week spent on this project in the current reporting period
Project Coordinator	LAM Hon-Ming/ Professor	School of Life Sciences/CUHK	5
Co-Principal investigator(s)	CHAN Ting-Fung Philos/Asst. Professor	School of Life Sciences/CUHK	3
	GUO Dianjing Diane/ Asso. Professor	School of Life Sciences/CUHK	0
	NGAI Sai-Ming/ Asso. Professor	School of Life Sciences/CUHK	3
	ZHANG Jianhua/ Chair Professor	School of Life Sciences/CUHK	2
	LIM Boon-Leong Wallace/ Asso. Professor	School of Biol. Sci/HKU	2
	XU Xun/ Vice President of R&D	BGI-Shenzhen	0
Collaborators/ Others			

**3. Project Duration**

	Original	Revised	Date of RGC Approval <i>(must be quoted)</i>
Project Start Date	01/04/2012		
Project Completion Date	31/03/2015	30/09/2015	16/03/2015
Duration ( <i>in month</i> )	36	42	16/03/2015
Deadline for Submission of Completion Report	31/12/2015	30/09/2016	16/03/2015

**Part B: The Final Report**

**5. Project Objectives**

5.1 Objectives as per original application

1. To perform detailed bioinformatics and genomic analysis of the putative salinity tolerance locus in the wild soybean genome.
2. To select, clone and examine the salt-tolerance functions of selected candidate genes within the putative salinity tolerance locus in the wild soybean genome.
3. To characterize the stress response transcription factors located within the putative salinity tolerance locus in the wild soybean genome.

5.2 Revised objectives

Date of approval from the RGC: \_\_\_\_\_

Reasons for the change: \_\_\_\_\_

## **6. Research Outcome**

### 6.1 Major findings and research outcome

(maximum 1 page; please make reference to Part C where necessary)

**Genomic analysis of the major salinity tolerance locus in the wild soybean genome:** We employed whole genome sequencing to refine the *de novo* sequencing data of a salt tolerant wild soybean (W05). Using a tailor-made recombinant inbred (RI) population that was a result of a cross between the salt tolerant W05 and a salt sensitive cultivated soybean (C08), we performed genotyping using low-coverage whole genome sequencing. Together with multi-year phenotypic data, we successfully constructed a map for quantitative trait loci. These novel strategies have successfully identified a major salt tolerant locus. Further molecular studies and functional tests have led to the identification of a casual gene conferring salt tolerance in W05. The gene encodes a putative cation/proton antiporter (Publication #11).

To make better use of the genomic and RNA-Seq data, we have developed several research platforms. We investigated the impacts of nucleotide fixation during soybean domestication (Publication #16) and summarized how whole genome sequencing could consolidate molecular markers for plant breeding (Publication #18). Using our RNA-Seq data, we evaluated a set of reference genes suitable for gene expression studies in soybean (Publication #19). We developed methods for organism-specific rRNA capturing (Publication #3) and a tunable resistive pulse sensing system with pore-based techniques (Publication #2). We also performed small RNA analyses (Publications #20 and Submitted Manuscript #28).

We have identified a transcriptional factor close to the salt tolerance locus of interest and found that it is associated with ABA signals. Transcriptional activity studies show that it is likely a transcriptional repressor. A manuscript is under-preparation to report these newest findings.

**Mechanisms of stress/salt tolerance in soybean:** Comprehensive surveys were performed to understand how omic researches could help to delineate possible mechanisms related to stress tolerance in soybean (Publications #4, 6, 20 and 24). While the cation/proton antiporter GmCHX1 is a key player of salt tolerance via regulating the level and distribution of sodium ions (Publication #11; see above), to balance the charge, regulation of anions such as chloride ions is also important. We have cloned the gene encoding a putative chloride/proton antiporter GmCLC1 from soybean. The function of GmCLC1 was demonstrated by electrophysiology and *in planta* gain-of-function tests (Publications #5 and 26).

Besides ion transportation, sequestering of reactive oxygen species (ROS) is also an important mechanism for salt tolerance. We showed that ROS scavengers could alleviate stress responses (Publications #9 and 10). Secondary compounds such as phenolic compounds may also play a role in stress tolerance of wild soybeans (Publication #8) and we found that wild soybean may accumulated more phenolic compounds in seeds which is regulated by a unique genomic region (Publication #25). In addition, salt/stress tolerance of soybean is also associated with proteomic and phospho-proteomic changes especially in roots (Publications #22 and 24). We also performed physiological studies in relation to stress responses (Publications 12, 13, 14, 15, 17, 21 and 23). We showed the importance of phytohormone signals (Publications 1, 13 and 21) and the importance of roots (Publications #15, 17 and 23). We characterized additional regulators such as 14-3-3 protein (Publication #1), protein phosphatases (Publications #14), and copper ions (Publication #13).

**Food and nutritional security:** We have composed two important analytical reviews to prestigious scientific journals (*Lancet* and *Nature Plants*). We analyzed the factors affecting food security in China and the importance of legumes (including soybean) in global food and nutritional security.

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### 6.2 Potential for further development of the research and the proposed course of action

*(maximum half a page)*

Through this research, we have built important research platforms (bioinformatics, genetics, molecular biology, biochemistry and physiology), consolidated strong collaborations (local, China, and global), generated useful genomic information and genetic materials. These are valuable resources to research in crop sciences.

To build on this solid background, the extended local team has submitted a proposal to the Area of Excellence Scheme titled “Center for Genomic Studies on Plant-Environment Interaction for Sustainable Agriculture and Food Security”. As a team, we will continue to seek funding opportunities to maintain our research momentum.

Another effort is to build an international consortium of legume research. The current task is to assess the impacts of legume research and cultivation in developing countries. We have already received positive responses from scientists from USA, UK, Australia, Netherlands, South Africa, Argentina, Japan, and China. We are plan to apply for international funding to support our endeavor.

### 6.3 Research collaboration achieved *(please give details on the achievement and its relevant impact)*

- a. Collaboration with BGI Shenzhen, Chinese Academy of Agricultural Sciences, Kazusa DNA Research Institute (Japan) and University of Hong Kong (HKU)

Through collaborations with colleagues in BGI-Shenzhen, the Chinese Academy of Agricultural Sciences, and Kazusa DNA Research Institute, we developed a bioinformatics platform to study soybean germplasm and identified important genes therein. One prominent example was to clone the casual gene of a major salt tolerance QTL in wild soybean (*Nature Communications* 5:4340).

- b. Collaboration with agricultural institutes in Mainland China

Since we have constructed new genetic materials and obtained important information during our basic scientific research, we have established collaboration with various agricultural institutes in Mainland China. One successful example of these collaborations is the generation of two new stress tolerant soybeans cultivars, Longhuang 1 and Longhuang 2. These lines have obtained approval from Gansu Province in 2015 to release to farmers for cultivation use (see Certificates).

- c. Collaboration with World Universities Network (WUN) Soybean Research Team

Our research achievement has attracted attention of international colleagues. We are included in a team of scientists from the World University Network to promote legume research and application worldwide. Together, we have submitted a white paper to the UN ([http://www.wun.ac.uk/files//researchgroups/wun\\_legumes\\_policy\\_document.pdf](http://www.wun.ac.uk/files//researchgroups/wun_legumes_policy_document.pdf)) and published an important perspective (*Nature Plants* 2:16112).

## **7. The Layman's Summary**

*(describe in layman's language the nature, significance and value of the research project, in no more than 200 words)*

In this completed project, we have successfully employed state-of-the-art genomic technologies to uncover important genes and stress tolerance mechanisms in soybean. We demonstrated the importance of utilization of wild germplasms in crop improvement. These findings have been published in important scientific journals.

We have also composed analytical reviews published in prestigious scientific journals (*Lancet* and *Nature Plants*) to discuss on the factors that affect food supplies and food safety in China and how neglecting legumes has compromised global food and nutritional security. We carefully argued that adequate supplies and high quality food is the key for good health, while cultivation of legumes such as soybean contributes to the sustainable agriculture in China and worldwide.

In addition to academic research, we collaborated with breeders in China to develop stress tolerant soybean cultivars. Two newly-bred stress tolerant soybean lines were approved by the Gansu Province to release to farmers.

We have established a strong research team in Hong Kong comprised of scientists of complementary expertise. We also formed an extensive and strong research networks with scientists in China and worldwide. We have made Hong Kong an important player of international crop genomic researches, for both academic advancements and potential applications.

**Part C: Research Output**

**8. Peer-reviewed journal publication(s) arising directly from this research project**  
*(Please attach a copy of the publication and/or the letter of acceptance if not yet submitted in the previous progress report(s). All listed publications must acknowledge RGC's funding support by quoting the specific grant reference.)*

The Latest Status of Publications				Author(s) (denote the corresponding author with an asterisk*)	Title and Journal/Book (with the volume, pages and other necessary publishing details specified)	Submitted to RGC (indicate the year ending of the relevant progress report)	Attached to this report (Yes or No)	Acknowledged the support of RGC (Yes or No)	Accessible from the institutional repository (Yes or No)
Year of publication	Year of Acceptance (For paper accepted but not yet published)	Under Review	Under Preparation (optional)						
2013				(#1) W. Xu, L. Jia, W. Shi, F. Baluška, H. J. Kronzucker, J. Liang and <b>J. Zhang*</b>	The Tomato 14-3-3 Protein TFT4 Modulates H <sup>+</sup> Efflux, Basipetal Auxin Transport, and the PKS5-J3 Pathway in the Root Growth Response to Alkaline Stress. <i>Plant Physiol.</i> <b>163</b> : 1817-1828.	2013	Yes	Yes	No
2013				(#2) A.C.-S. Yu, J.F.-C. Loo, S. Yu, S.-K. Kong* and <b>T.-F. Chan*</b>	Monitoring bacterial growth using tunable resistive pulse sensing with a pore-based technique. <i>Appl. Microbiol. Biotechnol.</i> <b>98</b> : 855-862.	2013	Yes	Yes	No
2013				(#3) S.-K. Li, J.-W. Zhou, A. K.-Y. Yim, A. K.-Y. Leung, S. K.-W. Tsui, <b>T.-F. Chan</b> and T. C.-K. Lau*	Organism-specific rRNA capture system for application in next-generation sequencing. <i>PLoS ONE</i> <b>8</b> : e74286.	2013	Yes	Yes	No
2013				(#4) Y.-S. Ku, W.-K. Au-Yeung, Y.-L. Yung, M.-W. Li,	Drought stress and tolerance in soybean. In: "A Comprehensive Survey of	2013	Yes	Yes	No

				C.-Q. Wen, X. Liu and <b>H.-M. Lam*</b> .	<i>International Soybean Research - Genetics, Physiology, Agronomy and Nitrogen Relationships</i> ". J.E. Board (ed.). InTech Education and Publishing, Austria. pp209-237.				
2013				(#5) T.-H. Wong, M.-W. Li, X.-Q. Yao and <b>H.-M. Lam*</b>	The GmCLC1 protein from soybean functions as a chloride ion transporter. <i>J. Plant Physiol.</i> <b>170</b> :101-104.	2013	Yes	Yes	No
2013				(#6) M.-W. Li, X. Qi, M. Ni and <b>H.-M. Lam*</b>	Silicon era of carbon-based life: application of genomics and bioinformatics in crop stress research. <i>Int. J. Mol. Sci.</i> <b>14</b> :11444-11483.	2013	Yes	Yes	No
2013				(#7) <b>H.-M. Lam</b> , J. Remais, M.-C. Fung, L. Xu and S.S.-M. Sun*	Food supply and food safety issues in China. <i>Lancet</i> <b>381</b> :2044-2053.	2013	Yes	Yes	No
2013				(#8) Y. Lu, <b>H.-M. Lam</b> , E. Pi, Q. Zhan, S. Tsai, C. Wang, Y. Kwan and <b>S.-M. Ngai*</b>	Comparative metabolomics in <i>Glycine max</i> and <i>Glycine soja</i> under salt stress To reveal the phenotypes of their offspring. <i>J. Agric. Food Chem.</i> <b>61</b> :8711–8721.	2014	Yes	Yes	No
2014				(#9) L.X. Deng, F. Chen, L. Jiang, <b>H.-M. Lam</b> and G. Xiao*	Ectopic expression of <i>GmPAP3</i> enhances salt tolerance in rice by alleviating oxidative damage. <i>Plant Breed.</i> <b>133</b> :348–355.	2014	Yes	Yes	No



2014				(#10) C. Chan and <b>H.-M. Lam*</b>	A putative lambda class glutathione S-transferase enhances plant survival under salinity stress. <i>Plant Cell Physiol.</i> <b>55</b> :570-579.	2014	Yes	Yes	No
2014				(#11) X. Qi, M.-W. Li, M. Xie, X. Liu, M. Ni, G. Shao, C. Song, A.K.-Y. Yim, Y. Tao, F.-L. Wong, S. Isobe, C.-F. Wong, K.-S. Wong, C. Xu, C. Li, Y. Wang, R. Guan, F. Sun, G. Fan, Z. Xiao, F. Zhou, T.-H. Phang, X. Liu, S.-W. Tong, T.-F. Chan, S.-M. Yiu, S. Tabata. J. Wang, X. Xu* and <b>H.-M. Lam*</b>	Identification of a novel salt tolerance gene in wild soybean by whole-genome sequencing. <i>Nat. Commun.</i> <b>5</b> :4340.	2014	Yes	Yes	No
2013				(#12) A.N.M.R. Bin Rahman and <b>J. Zhang*</b>	Rayada specialty: the forgotten resource of elite features of rice. <i>Rice</i> <b>6</b> : 41.	2016	Yes	Yes	No
2014				(#13) N. Ye, H. Li, G. Zhu, Y. Liu, R. Liu, W. Xu, Y. Jing, X. Peng and <b>J. Zhang*</b>	Copper Suppresses Abscisic Acid Catabolism and Catalase Activity, and Inhibits Seed Germination of Rice. <i>Plant Cell Physiol.</i> <b>55</b> : 2008–2016.	2016	Yes	Yes	No
2015				(#14) R. Liu, Y. Liu, N. Ye, G. Zhu, M. Chen, L. Jia, Y. Xia, L. Shi, W. Jia and <b>J. Zhang*</b>	AtDsPPT1 acts as a negative regulator in osmotic stress signalling during <i>Arabidopsis</i> seed germination and seedling establishment. <i>J</i>	2016	Yes	Yes	No

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					<i>Exp. Bot.</i> <b>66</b> : 1339–1353.				
2014				(#15) Md.M. Hossain, X. Liu, X. Qi, <b>H.-M. Lam</b> and <b>J. Zhang*</b>	Differences between soybean genotypes in physiological response to sequential soil drying and rewetting. <i>Crop J.</i> <b>2</b> :366-380.	2016	Yes	Yes	No
2015				(#16) S. Zhao, F. Zheng, W. He, H. Wu, S. Pan and <b>H.-M. Lam*</b>	Impacts of nucleotide fixation during soybean domestication and improvement. <i>BMC Plant Biol.</i> <b>15</b> :81.	2016	Yes	Yes	No
2015				(#17) C. Ju, R. J. Buresh, Z. Wang, H. Zhang, L. Liu, J. Yang* and <b>J. Zhang*</b>	Root and shoot traits for rice varieties with higher grain yield and higher nitrogen use efficiency at lower nitrogen rates application. <i>Field Crop Res.</i> <b>175</b> : 47–55.	2016	Yes	Yes	No
2015				(#18) H. Yang, C. Li, <b>H.-M. Lam</b> , J. Clements, G. Yan and S. Zhao*	Sequencing consolidates molecular markers with plant breeding practice. <i>Theor. Appl. Genet.</i> <b>128</b> :779-795.	2016	Yes	Yes	No
2015				(#19) A.K.-Y. Yim, J.W.-H. Wong, Y.-S. Ku, H. Qin, <b>T.-F. Chan</b> and <b>H.-M. Lam*</b>	Using RNA-seq data to evaluate reference genes suitable for gene expression studies in soybean. <i>PLoS ONE</i> <b>10</b> :e0136343.	2016	Yes	Yes	No
2015				(#20) Y.S. Ku, J.W.-H. Wong, Z. Mui, X. Liu, J.H.-L. Hui, <b>T.-F. Chan</b> and <b>H.-M. Lam*</b>	Small RNAs in plant responses to abiotic stresses: regulatory roles and study methods. <i>Int. J. Mol. Sci.</i> <b>16</b> : 24532-24554.	2016	Yes	Yes	No

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2015				(#21) Md. M. Hossain, <b>H.-M. Lam</b> and <b>J. Zhang*</b>	Responses in gas exchange and water status between drought-tolerant and -susceptible soybean genotypes with ABA application. <i>Crop J.</i> <b>3</b> : 500-506.	2016	Yes	Yes	No
2015				(#22) E. Pi*, L. Qu, J. Hu, Y. Huang, L. Qiu, H. Lu, B. Jiang, C. Liu, T. Peng, Y. Zhao, H. Wang, S.-N. Tsai, <b>S.-M. Ngai*</b> and L. Du*	Mechanisms of Soybean Roots' Tolerances to Salinity Revealed by Proteomic and Phosphoproteomic Comparisons Between Two Cultivars. <i>Mol. Cell. Proteomics</i> : <b>15</b> :266-288.	2016	Yes	Yes	No
2016				(#23) G. Chu, Z. Wang, H. Zhang, J. Yang* and <b>J. Zhang*</b>	Agronomic and Physiological Performance of Rice under Integrative Crop Management. <i>Agron. J.</i> <b>108</b> :1-12.	2016	Yes	Yes	No
2016				(#24) N. Munoz, M.-W. Li, <b>S.-M. Ngai</b> , and <b>H.-M. Lam*</b>	Use of proteomics to evaluate soybean response under abiotic stresses. In "Abiotic and Biotic Stresses in Soybean Production". M. Miransari (ed.). Academic Press, Oxford. pp79-105.	2016	Yes	Yes	No
2016				(#25) M.-W. Li, N. B. Munoz, C.-F. Wong, F.-L. Wong, K.-S. Wong, J.W.-H. Wong, X. Qi, K.-P. Li, M.-S. Ng and <b>H.-M. Lam*</b>	QTLs regulating the contents of antioxidants, phenolics and flavonoids in soybean seeds share a common genomic region. <i>Front. Plant Sci.</i> <b>7</b> :854.	2016	Yes	Yes	No

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2016				(#26) P. Wei, L. Wang, A. Liu, B. Yu* and <b>H.-M. Lam*</b>	GmCLC1 confers enhanced salt tolerance through regulating chloride accumulation in soybean. <i>Front. Plant Sci.</i> <b>7</b> :1082.	2016	Yes	Yes	No
2016				(#27) C. H. Foyer*, <b>H.-M. Lam</b> , H. T. Nguyen, K. H. M. Siddique, R. K. Varshney, T. D. Colmer, W. Cowling, H. Bramley, T. A. Mori, J. M. Hodgson, J. W. Cooper, A. J. Miller, K. Kunert, J. Vorster, C. Cullis, J. A. Ozga, M. L. Wahlqvist, Y. Liang, H. Shou, K. Shi, J. Yu, N. Fodor, B. N. Kaiser, F.-L. Wong, B. Valliyodan, and M. J. Considine	Neglecting legumes has compromised human health and sustainable food production. <i>Nat. Plants</i> <b>2</b> : 16112.	2016	Yes	Yes	No
		2016		(#28) Y. Sun, Z. Mui, X. Liu, A. K.-Y. Yim, H. Qin, F.-L. Wong, T.-F. Chan, S.-M. Yiu, <b>H.-M. Lam</b> *, B. L. Lim *	Comparison of small RNA profiles of <i>Glycine max</i> and <i>Glycine soja</i> at early developmental stages. <i>Int. J. Mol. Sci.</i>	2016	Yes	Yes	No

**9. Recognized international conference(s) in which paper(s) related to this research project was/were delivered** *(Please attach a copy of each conference abstract)*

Month/Year/ Place	Title	Conference Name	Submitted to RGC ( <i>indicate the year ending of the relevant progress report</i> )	Attached to this report ( <i>Yes or No</i> )	Acknowledged the support of RGC ( <i>Yes or No</i> )	Accessible from the institutional repository ( <i>Yes or No</i> )
June 2012; Hong Kong -C01	Whole-genome-sequencing assisted genetic studies to identify salinity stress tolerance genes/alleles from wild soybean.	Gordon Research Conference: Salt and Water Stress in Plants.	2013	Yes	Yes	No
August 2012, Shihezi, PRC-C02	Whole-genome-sequencing assisted genetic studies of soybean.	The 10 <sup>th</sup> Cross-Strait Symposium on Plant Molecular Biology and Biotechnology.	2013	Yes	Yes	No
November 2012, Hong Kong-C03	Whole-genome-sequencing assisted genetic studies of wild soybean.	The 7th International Conference on Genomics & Bio-IT APAC.	2013	Yes	Yes	No
December 2012, Shenzhen, PRC-C04	Soybean genetic research in the era of genomics.	Shenzhen International Biotech Innovation Forum & Exhibition.	2013	Yes	Yes	No
February 2013, Durban, South Africa-C05	Applying a whole-genome-sequencing strategy to study the wild soybean genome.	World Soybean Research Conference 2013	2013	Yes	Yes	No
February 2013, Durban, South Africa-C06	Identification of small RNA genes in the wild soybean ( <i>Glycine soja</i> ) with a salt-tolerant phenotype.	World Soybean Research Conference 2013	2013	Yes	Yes	No
February 2013, Durban, South Africa-C07	Understanding of histone H3 phosphorylation and acetylation on enhancement of the soybean tolerance to salinity via proteomic profile.	World Soybean Research Conference 2013	2013	Yes	Yes	No
February 2013, Durban, South Africa-C08	Comparative metabolomics analysis of seedling leaves from ten different salt-tolerant soybean varieties under normal and salt stress conditions.	World Soybean Research Conference 2013	2013	Yes	Yes	No

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April 2013, Nanjing, PRC-C09	Genomic studies to identify important loci in wild soybean.	WDD 2013 - BIT's 4th Annual World DNA and Genome Day.	2013	Yes	Yes	No
July 2013, Vancouver, Canada-C10	A putative lambda class glutathione-S-transferase gene in the wild soybean interacts with polyphenolic metabolites which promote plant growth and enhance survival under salinity stress.	Annual Meeting of Plant Signaling and Behavior	2013	Yes	Yes	No
November 2013, Hong Kong-C11	Soybean genetic research in the era of genomics.	The 4 <sup>th</sup> Symposium on Systems and Synthetic Biology	2013	Yes	Yes	No
July 2014, Portland, Oregon-C12	Identification of a putative causal gene of salinity tolerance in soybean.	Plant Biology 2014 Annual Scientific Meeting of the American Society of Plant Biologists	2014	Yes	Yes	No
April 2015, Shenzhen, China-C13	Genomic and molecular studies of salt tolerance in soybean	The Biennial Conference and the 15th Congress of the Chinese Society for Cell Biology. Organizer: Chinese Society for Cell Biology	2016	Yes	Yes	No
November 2015, Shenzhen, China-C14	Exploring wild soybean using a genomic approach.	Nature Conference – Agricultural Genomics 2015: From Variation to Improved Production	2016	Yes	Yes	No
November 2015, Hangzhou, China-C15	Genomic and molecular studies of stress tolerance in soybean.	Legumes2020	2016	Yes	Yes	No

**10. Student(s) trained** (please attach a copy of the title page of the thesis)

Name	Degree registered for	Date of registration	Date of thesis submission/ graduation
Pan, Shengkai	M.Phil. (Analysis of fixed SNP reveals insight of morphology differences between wild and cultivated soybeans)	2010	2013
Chan Ching	Ph.D. (Biochemical and functional study of a putative Lambda class	2010	2013

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	glutathione-S-transferase gene in the wild soybean)		
Li, Man-Wah	Ph.D. (Identification of a putative causal gene of salinity tolerance in soybean)	2011	2014
Qi, Xinpeng	Ph.D. (Quantitative trait locus (QTL) mapping of important agronomic traits using soybean genomic information)	2010	2014
Zhao, Shancen	Ph.D. (Impacts of nucleotide fixation during soybean domestication and intensive breeding)	2010	2015

**11. Other impact** (*e.g. award of patents or prizes, collaboration with other research institutions, technology transfer, etc.*)

## a. Award of patents:

There are 3 China Patents and 3 Hong Kong Patents approved within the period of this project (see Patents).

## China patents:

- GMRD22-樣基因及其保護抵禦非生物應激的應用 (GmRD22-like genes and use thereof to protect against abiotic stress) (Patent No. CN101548013B) (March 21, 2012)
- 減輕植物非生物脅迫的方法 (Method to alleviate abiotic stress in plants) (Patent No. CN101541165B) (May 15, 2013)
- 含 J- 結構域蛋白質賦予的非生物應激耐受 (Abiotic stress tolerance conferred by J-domain-containing proteins) (Patent No. CN101553569B) (June 12, 2013)

## Hong Kong Patents:

- GmRD22-like genes and use thereof to protect against abiotic stress (Patent No. 1137776) (December 7, 2012)
- Method to alleviate abiotic stress in plants (Patent No. HK1132878) (September 19, 2013)
- Abiotic stress tolerance conferred by J-domain-containing proteins (Patent No. HK1138033) (March 14, 2014)

## b. Generation of new soybean lines:

One indirect output of this research is the production of various soybean lines that are stress tolerance and the accumulation of a large volume of genetic information. Based on these indirect outputs and through collaborations with agricultural scientists in Mainland China, we generated two new soybean lines that have been approved by the Gansu Province in 2016 to release to farmers for cultivation use (see Certificates).

## c. Public education

As a technology transfer activity to the public, our soybean research was selected for exhibition by the Hong Kong Science Museum at their Science News Corner from April 13 to July 31, 2013. In conjunction to this exhibition, the project coordinator also gave two educational seminars organized by the Education Bureau (June 26, 2013; attended by ~600 high school teachers and students) and one popular science lecture hosted by the HKSM (June 29, 2013; attend by ~100 general public). A video recording a snapshot of the soybean research is being shown in the exhibition room. This video

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produced by the Education Bureau has won an award of excellence in the Indie Fest, an award of merit in the in Accolade File, Television, New Media and Videography Competition, and an award of merit in the Chicago International Film Festival TV Award. The video is also available in a public education website:

[http://minisite.proj.hkedcity.net/stds\\_sci/cht/Video\\_of\\_Scientist/soybean\\_homecoming.html](http://minisite.proj.hkedcity.net/stds_sci/cht/Video_of_Scientist/soybean_homecoming.html)

### d. Team building in Hong Kong

Expanding from the core CRF team, we have established the Center for Soybean Research at CUHK (see CRF team). This Center consisted of 13 PIs from CUHK, 2 PIs from HKU and 1 PI from HKBU. New members have given additional inputs to optimize our research strategies.

## **Project Coordinator**

Contact Information: honming@cuhk.edu.hk