

行政院所屬各機關因公出國人員出國報告書
(出國類別：會議)

赴菲律賓國際稻米研究所出席
「2016年第二次執行委員會議」出國報告

出國人員：	李栢淳	財團法人國際合作發展基金會	副秘書長
	呂秀英	行政院農業委員會苗栗區農業改良場	場長
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	李瓊妮	行政院農業委員會國際處	科長

出國地點：菲律賓

出國期間：2016年12月15日至17日

報告日期：2017年4月14日

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摘要

行政院農業委員會(以下簡稱農委會)自2012年度起，由農委會農業試驗所、相關農業改良場及接受計畫委託之研究機構等組成研究團隊，與國際稻米研究所(IRRI) 進行水稻抗耐逆境品種選育研究，第一期(2012年至2015年)針對我國水稻生產所面臨之重要生物性及非生物性逆境包含稻熱病、白葉枯病、耐旱及耐鹽等進行合作研究，藉由導入逆境耐受性／抵抗力基因以改良臺灣現行的水稻商業品種。第二期(2016年至2019年)合作計畫係依據2015年簽署之合作備忘錄，由農委會(含所屬試驗單位及接受計畫補助之研究機構)及外交部、財團法人國際合作發展基金會與IRRI共同研議及執行各項合作。2016年12月15日至17日於IRRI召開「2016年第二次執行委員會議」，檢討各工作項目進度，包含：耐熱及耐旱品種選育、低升糖指數(GI)稻米品種及米質研究、辦理「褐飛蟲研討會」、「稻作收穫後處理暨市場行銷研習班」、「稻種生產暨推廣訓練課程」等。2017年，農委會與IRRI之合作除延續2016年各項工作外，將新增抗飛蟲品種選育；國合會部分則預計與IRRI合作「海地強化稻種生產能力計畫」、另委託IRRI與International Center for Tropical Agriculture (CIAT) 規劃國合會拉丁美洲地區駐外技術人員客製化稻作訓練課程，並持續辦理與緬甸之稻作培訓課程。

壹、行程表

Program for Steering Committee Meeting December 15-17, 2016

Date	Activities	Remark	
12/15 (Thursday)	Flight PR895 (1040-1305) 5 delegates	Flight BR277 (1530-1750) 3 delegates (ICDF*2+COA*1)	All Taiwan delegation. Pick up by IRRI drivers
	To IRRI (2hrs)	To IRRI (2hrs)	Check in at IRRI Guest house
	Visit TTChang Genetic Research Center and SNP Seek database demonstration (For 5 delegates if time permit)		GRC, bioinformatics team
	Dinner (Guesthouse)		
12/16 (Friday)	IRRI Venue: IRRI Board Room Main agenda <ul style="list-style-type: none"> • Review of 2016 progress • 2017 workplan discussion • Steering Committee meeting • Tour of research activities 	*07:50 it will take 15 min from Guesthouse to Board Room by car	
0815-0830	Welcome and short speech on Taiwan-IRRI collaboration	IRRI Director General	
0830-0930	Review of Year 1 progress	Hei Leung	
	Discussion		
0930-1015	ICDF	Corinta Guerta	
	Discussion		
1015-1030	Coffee/Tea Break		
1030-1200	1. 2017 workplan 2. Discussion of Phase 2 collaboration; issues in project implementation	Taiwan team, Hei Leung, Corinta Guerta, Peter Brothers	
1200	Lunch at IDR		
1300-1500	Steering Committee meeting	Chair of SC	

1300-1320	<ul style="list-style-type: none"> • Change of Committee members • Recommend the meeting chairperson • Opening remarks and introducing delegations 	Members of SC Hei Leung Corinta Guerta
1320-1405	<ul style="list-style-type: none"> ■ Final report including latest progress and expected outcomes of 2016 projects, 15min for each report. (1)<u>NTU</u> (2)COA (3)ICDF 	
1405-1420	<ul style="list-style-type: none"> ■ Logistics of implementation ■ Discussion and suggestion including difficulty encountered (eg. budget allocation, report submission, etc.) 	
1420-1450	budget allocation report	
1450-1500	Conclusion and next meeting	
1500	Coffee/Tea Break	
1515-1600	Drone Phenotyping, demonstration over Long-term trial	Steve Klassen
1600-1645	Grain Quality and Nutrition Center (GQNC)	Nese Sreenivasulu
1830:21:00	Welcome Dinner (House #1)	Hosted by Matthew Morell
12/17 (Saturday)		
0830-0930	Complete paper work	Review team and Hei Leung
Departure		
<u>0830</u>	Leave from IRRI to airport for first group	B272 1250 departure
0930	Leave from IRRI to Alabang for lunch for second group	
1400	Leave from Alabang to airport	PR894 1755 departure

貳、會議紀錄

農委會及外交部、財團法人國際合作發展基金會與國際稻米研究所「2016年第二次執行委員會議」及「因應氣候變遷以生物遺傳資源平台建置抗耐逆境優質水稻研究計畫」105年度期末暨106年度期初審查會議紀錄

一、 時間：2016年12月16日上午8時

二、 地點：國際稻米研究所(IRRI)會議室(Los Bañols，菲律賓)

三、 出席單位及人員：(略)

四、 主席致詞：

(一) Dr. Bruce Tolentino (IRRI 副主任)表示，為因應糧食危機，雙方之合作具有重要意義，例如近年東南亞地區如越南、泰國均遭遇長時間乾旱，如何減緩氣候變遷對作物之影響並增加其適應能力，為研究人員急需進行的工作。IRRI 於 2016 年 11 月 29 日為紀念引起綠色革命的 IR8 高產水稻品種發表第 50 周年，特別舉辦 Partners' Day，並邀請我駐菲律賓代表處林大使松煥與會，以紀念來自臺灣品種低腳烏尖「DGWG」半矮性基因之貢獻，未來期待與臺灣持續合作。

(二) 行政院農業委員會(下稱農委會)國際處林副處長回應，氣候變遷已使國際社會增強對於糧食安全問題的重視，我國為減緩及調適氣候變遷對於作物如水稻的影響，積極與國際間合作，過去 4 年間已與 IRRI 建立密切的夥伴關係，共同分享及交換研究構想，未來仍將在此平台上持續與 IRRI 進行更具前瞻性之合作。

五、 2016 年合作計畫成果審查及 2017 年工作項目檢討紀錄

(一) 農委會(包含農委會所屬農業試驗所、改良場及臺灣大學)與 IRRI 2016 年合作計畫，經審查符合期末指標，成果摘要如下：

1. 應用 new reference genome 建立基因多樣性平台以支援氣候逆境高恢復能力的水稻選種，有關 3K genome 的 SNP (Single Nucleotide Polymorphism)資料已由 2000 萬筆增加至 4200 萬筆。
2. 有關耐旱及耐旱品種選育，已發現有高度相關之 reference genome 可應用(如 N22 及 Giza178 品系)，我方並要求 IRRI 提供該等品係之種子，以進一步評估及篩選。
3. 於田間進行高通量基因型分析(high throughput genotyping)，並應用無人機及固定感測器等工具進行資料蒐集分析，以分析性狀及估測產量等。
4. 持續建立多親本多世代互交水稻族群(Multi-parent Advanced Generation Inter-Cross, MAGIC)資料，已篩選具早熟、良好產量之品系，以利未來提供農民應用。
5. 已改善 genome editing 方法，應用突變技術開發所需農藝性狀，加速育種過程。
6. 有關抗白葉枯病及稻熱病品種選育，IRRI 於 2016 年派遣 2 位專家至臺灣與相關研究人員討論，並於試驗田觀察，就病原菌族群監測及基因體定序交換意見。
7. 低升糖指數(GI)稻米品種及米質研究，開發較低成本及更有效率之 genotyping 方法，應用 cooked grain amylolysis，已建立 GI 預估方法(*in vitro* GI prediction)，以從種原篩選具低 GI 之品種。
8. 於 2016 年 9 月 20-22 日在臺舉辦褐飛蝨研討會，雙方達成共識將於 2017 年新增有關抗飛蝨品種選育之工作項目。

9. 本計畫 2016 年執行成果如預期，在遺傳資源平台、生物性逆境、非生物性逆境及升醣指數四大研究目標均有適當產出，另審查委員建議，期末報告請補充有關耐旱育種概況。

(二) 農委會(包含農委會所屬農業試驗所、改良場及臺灣大學)與 IRRI 2017 年工作項目：

由於抗耐逆境品種選育為一持續性之工作，2017 年除將延續 2016 年各項工作外，並將新增有關抗飛蟲品種選育，進行以下工作：1.於屏東/高雄、嘉義、臺中/彰化及花蓮等四個地區進行臺灣褐飛蟲族群分佈調查及抗蟲基因之研究；2.由 IRRI 提供功能性分子標誌資料(specific functional markers)以進行回交試驗，由臺灣水稻品種中篩選具抗性之品種；3.舉辦工作坊一場次，應用生態農業工程(agricultural eco-engineering)以控制褐飛蟲族群。

(三) 財團法人國際合作發展基金會(下稱國合會)與 IRRI 2016 年合作成果：

1. 國合會與 IRRI 於 5 月 16 至 27 日合作辦理「稻作收穫後處理暨市場行銷研習班」，計有 10 國(汶萊、印尼、菲律賓、韓國、索羅門群島、奈及利亞、巴布亞紐幾內亞、緬甸、海地、臺灣等)17 名學員參訓。
2. 國合會與 IRRI 於 8 月 15 日至 9 月 2 日合作辦理「稻種生產暨推廣訓練課程」，計有 10 名派駐於海地、尼加拉瓜、聖多美、索羅門群島等國合會農藝技術人員參加。
3. 國合會原訂與 IRRI 於緬甸辦理研討會，因緬方因素取消辦理。

(四) 國合會 2017 年預計與 IRRI 合作項目：

1. 「海地強化稻種生產能力計畫」—IRRI 專家派遣任務，透過 IRRI 專家檢驗國合會海地稻作技術合作計畫成效。

2. 委託 IRRI 與 International Center for Tropical Agriculture(CIAT) 規劃國合會拉丁美洲地區駐外技術人員客製化稻作訓練課程 (希望透過 IRRI 建立與 CIAT 之合作管道)。
3. 持續辦理與緬甸之稻作培訓課程。

六、 有關執委會未來辦理形式：

雙方同意現行一年兩次執委會會議改為一年一次，在年中輪流於臺灣及 IRRI 辦理，以檢討未來工作規劃及相關行政事項之溝通，下次執委會會議將於 2017 年第 3 季在臺灣舉辦；另有關年底計畫期末審查併工作會議，則均於臺灣舉辦。

參、參訪摘要

一、無人載具於品種選育之應用

為配合有關本計畫品種選育之性狀外表型性大量篩選需要，IRRI 利用無人機(載具)掛載多種感測器進行預設性狀(如病害、蟲害、耐旱、耐熱等)之外表徵狀偵測與分析，俾協助進行種原雜交、回交世代之篩選，如此可降低人力、物力及時間上的花費。同時，此一方法亦可減少約一個栽培世代的篩檢需求，因而可以加速品種選育過程。未來本會所屬各試驗改良場所也可嘗試採用此一方式，從事國內農作物品種選育，成為育種選拔之有利與有效的篩選工具，提高性狀選育的效率。然而，此種外表性狀的篩選方式，相關選育性狀與偵測參數之間的關係，乃最重要的基礎研究工作。必須先行建立各別性狀與其相關參數之間的關係模式或模組，才能據以利用作為性狀篩選的判別工具，進行田間栽培大量種原和中間品系之有效篩檢。

二、參訪米質研究室

亞洲地區以稻米為主食，無論開發中國家或已開發國家因罹患糖尿病人數逐年增加，鑒於營養均衡問題，爰開發低升糖指數(GI)稻米品種及米質研究，也逐漸受重視。惟現有具低 GI 之品種，因具高直鏈澱粉或抗性澱粉，米質硬、適口性不佳，故 IRRI 之米質研究室透過基因體(genomics)、代謝體學(metabolomics)及蛋白質體學(proteomics)等研究，以篩選更符合消費喜好之低升糖指數品種。

肆、建議事項

- 一、有關 2016 年度與 IRRI 合作之各項計畫均已順利完成，2017 年度除延續性工作外將新增抗飛蝨品種選育工作項目，於屏東/高雄、嘉義、臺中/彰化及花蓮等四個地區進行調查研究，並舉辦工作坊，研討應用生態農業工程(agricultural eco-engineering)以控制褐飛蝨族群。關於引進耐熱及耐旱水稻品系之種子，將由農委會農業試驗所續與 IRRI 聯繫引種事宜。
- 二、2017 年國合會將與 IRRI 進行「海地強化稻種生產能力計畫」，透過 IRRI 專家檢驗國合會海地稻作技術合作計畫成效，另委託 IRRI 與 International Center for Tropical Agriculture (CIAT) 規劃國合會拉丁美洲地區駐外技術人員客製化稻作訓練課程，並持續辦理與緬甸之稻作培訓課程。
- 三、有關未來執委會辦理形式，依雙方決議改為一年一次於年中辦理，輪流於臺灣及 IRRI 召開，有關年底之計畫期末審查併工作會議則均於臺灣舉辦。

伍、附錄

附錄 1、IRRI 背景資料

附錄 2、Activity by Team and Progress indicator in 2017

附錄 3、A genetic diversity platform to enhance development of climate resilient and nutritious rice, year 1 reported by IRRI

附錄 4、COA-IRRI collaboration program, reported by COA

附錄 5、Development of rice production model in response to global weather change and breeding of high night temperature tolerant rice cultivars with superior grain quality, reported by NTU

附錄 6、ICDF training at IRRI, 2016 workshop on rice post-production and marketing, reported by IRRI

附錄 7、Outcome review of cooperation between TaiwanICDF and IRRI in 2016, reported by TaiwanICDF

附錄 1、IRRI 背景資料

IRRI (International Rice Research Institute, 國際稻米研究所)。創建於 1960 年的 IRRI 位於菲律賓北部內湖省洛斯巴洛斯，是國際農業研究諮商組織 (CGIAR) 下屬 15 個國際農業研究中心之一，與菲律賓大學洛斯巴羅斯分校 (相當於農業大學) 比鄰而居。IRRI 使命是：「為了減少貧困和饑餓、改善種植水稻的農民和消費者的健康，並通過合作研究、合作夥伴關係，加強國家農業研究和推廣體系，確保環境的可持續性」。

來自臺灣的科學家張德慈院士對 IRRI 的貢獻；1927 年出生的張德慈院士，於 1961 年赴菲律賓參與 IRRI 工作，任遺傳學家職。他首將臺中在來一號引入印度試種，因其具有耐肥高產之特性，在該地適應極佳，迅即大規模推廣栽培，為熱帶地區增產糧食，創綠色革命之先聲，此亦為臺中在來一號揚名國際之濫觴。

張德慈院士更進一步與 IRRI 育種家利用臺灣之低腳烏尖、矮子尖等帶有半矮生習性 (sd1) 之親本與熱帶高桿低產品種雜交，育成多個性能優異、國際馳名之優良品種，其表現更超越臺中在來一號，在東南亞迅速傳播，成就非凡，創較原有品種增加三倍之高產紀錄。

現在 IRRI 保存有八萬五千份稻種，已成為全球最大作物種源。供給全球稻作人員暨稻農之稻種已逾七十萬份。世界水稻改良品種近九成以上親本均利用 IRRI 種源，作為增產、早熟、抗病、抗蟲與品質改良之用。由張德慈院士所領導推動之國際水稻種源交換與合作研究數量，已高佔全世界各種作物之首位。

我國政府與 IRRI 自 2015 年 1 月 26 日簽署合作備忘錄，未來 4 年 (2016 至 2019 年) 係新階段合作的開始，各項目的工作內容計 7 項，包

括「能力建構及人力資源發展」、「種源多樣性平臺」、「生物性抗逆境育種」、「非生物性抗逆境育種—耐熱育種」、「水稻功能性育種—低升糖指數 Glycemic Index,GI)之選種改良」、「種源交換」、「加強國際合作」。

IRRI 和農委會分別指定梁曦博士(Dr. Hei Leung)及農試所楊純明組長擔任本合作計畫的統籌人(coordinator)，另各細部計畫均將指定執行專家 (principle investigator) 及訂定預期效益指標(progress indicator)。

附錄 2. Activity by Team and Progress indicator in 2017

Topic	Activity by IRRI	% Project activities	Progress indicator (2017) by IRRI		Activity by TARI/NTU
			Jan-June	July-Dec	
1. Genetic diversity platform to support development of climate resilient rice	1.1 Conduct comparative genomics using high quality reference genomes	10%	Assembly of new reference genomes to improved quality of SNP calling	Reference genomes compared to identify unique features for the main rice subtypes	Fixed introduction lines of back Taiwan and evaluated yield potential as well as biotic stress tolerance
	Identify structural variations			Cases of association between structural variations and agronomic traits identified	<ul style="list-style-type: none"> ◆ Plants with better performance will be selected from BC3F2 generation. The number of lines are expected to increase in 2017. ◆ Plants will be more uniform in BC3F3 generation and more seeds will be produced to evaluate yield potential in 2017.
	Detect SNP correlation				
	Expand SNP-Seek database		Allele miming performed for several target	New functional tools incorporated	

Topic	Activity by IRR	% Project activities	Progress indicator (2017) by IRR		Activity by TARI/NTU
			Jan-June	July-Dec	
			traits. Accessions identified for phenotyping	into database	
	Develop Galaxy			IRRI galaxy pipeline tools available to public and include genome selection tools.	
	1.2 Bioinformatics and genome analysis to expand SNP database for allele mining	10%	Number of SNP in SNP SEEK database increased	New analytical tools deployed for allele mining	
	1.3 Create and use new genetic resources for discovering new gene combinations, including characterization of genetic populations such as 3K accessions and MAGIC	20%	High performing lines from MAGIC japonica and Heat MAGIC identified	Date collected in wet season Yield data of two seasons available for identification of major yield QTL and its interaction with	

Topic	Activity by IRRRI	% Project activities	Progress indicator (2017) by IRRRI		Activity by TARI/NTU
			Jan-June	July-Dec	
				season.	
			High performing lines from 2016 evaluated for Initial Yield Trial (IYT) in 2017 dry season.	Data from high performing lines analyzed to identify yield QTL	
	1.4 HTP phenotyping of targeted traits	10%	Field evaluation of 1196 MAGIC Global lines under drought stress and well-watered condition established.	HTP data on relative performance of MAGIC-global lines based on drones and tractor phenotyping	
			Different subtypes of 3K sequenced accessions phenotyped	Gene-phenotype relationships determined by genome wide association analysis	
	1.5 Genome editing	10%	CRISPR delivery	Genetic variants	

Topic	Activity by IRRI	% Project activities	Progress indicator (2017) by IRRI		Activity by TARI/NTU
			Jan-June	July-Dec	
	for validating function of candidate genes for tolerance of biotic and abiotic stresses		systems improved in efficiency	created in at least two traits	

Topic	Activity by IRRI	% of Project activity	Progress Indicator		Activity by TARI/NTU
			Jan-June	July-Dec	
2. Biotic stresses (bacterial blight and blast)	2.1 New resistance genes introduced into elite germplasm	10% for diseases	New crosses initiated	BC1F2 progeny produced	<p>◆ More basic data about local rice blast and bacterial blight will be added to database in 2017. With the needed information and technical assistance provided from IRRI, it will further strengthen research power of Taiwan's young scientists and contribute to the sustainable development of agriculture in Taiwan.</p> <p>◆ Exchange new selected bred lines between COA and IRRI to verify their resistance against <i>Xoo</i> populations in hotspots of Taiwan</p>

					and Philippines.
	2.2 Monitoring pathogen populations and evaluation of host resistance to achieve stable and effective resistance to rice bacterial blight and blast disease.		Representative isolates of blast and BLB pathogens sequenced and Arv genes available	Pilot pathogen diagnostics markers tested	<ul style="list-style-type: none"> ◆ Hotspots will be selected and be suggested as experimental sites. ◆ Continue monitoring of <i>Xoo</i> populations in Taiwan.
	2.3 Molecular epidemiology—assess and analyze pathogen populations by genomic tools to guide deployment of resistance.		Reference collection of pathogen isolates established	Sequencing strategies for both pathogens evaluated	

Topic	Activity by IRRI	% Project activity	Progress indicator		Activity by TARI/NTU
			Jan-June	July-Dec	
3. Heat-tolerance	3.1 Introduce heat tolerance QTL and early morning flowering QTL (heat avoidance) into drought tolerant germplasm (produced in phase 1)	15% for heat and drought	Continue crossing	BC2F2 population produced	<ul style="list-style-type: none"> ◆ Seeds of C3F5 generation will be transplanted in well-watered and drought for yield comparison. ◆ Evaluation of spikelet fertility and grain quality of near isogenic lines derived from 'N22' with higher heat tolerance
	3.2 Allele mining for heat and drought tolerance using the 3K genomes.		Accessions with potential for heat tolerance predicted from 3K genomes data	Accessions grown out to observe phenotypes and seed increase	<ul style="list-style-type: none"> ◆ Build up recombinations of crossing between NILs of heat tolerance and tolerance of high night temperatures
	3.3 Apply heat MAGIC to generate breeding-ready heat tolerant lines		Subset of heat MAGIC lines phenotyped	Increased heat tolerance observed in segregating population	<ul style="list-style-type: none"> ◆ Evaluation of grain quality of MAGIC lines under high night temperature

	3.4 Rice grain quality (in particular eating and cooking quality) of MAGIC rice populations under high night temperature stress (NTU)		Phenotyping for heat stress tolerance in grain quality of HEAT MAGIC, Global Magic and Magic Japonica	Phenotyping for heat stress tolerance in grain quality of HEAT MAGIC, Global Magic and Magic Japonica	Grain quality analysis of MAGIC rice populations (NTU)
	3.5 Establishment of GWAS analysis platform for heat and other agronomical traits related QTL identification (NTU)		genotyping-by-sequencing (GBS) analysis of MAGIC japonica and parental rice lines and collect SNP data	Set up MySQL data manage system for storage of SNP genotyping data	Establish different QTL statistical analysis model such as GLM, MLM, interval mapping (NTU) (Using Apache HTTP server for building graphical user platform)
	3.6 Identification the parameters and build up the crop model for adaption to high temperature stress (NTU)		Analysis of the parameters related to yield and physiological traits and molecular markers of major rice cultivars in Taiwan.	Analysis of the parameters related to yield and physiological traits and molecular markers of major	Estimation of the parameters of the major rice cultivars and using the estimation for crop model establishment. (NTU)

				rice cultivars in Taiwan.	
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Topic	Activity by IRRI	% Project activity	Progress indicator		Activity by TARI/NTU/ICDF
			Jan-Jun	July-Dec	
4. Development of low glycemic index (GI) rice varieties	4.1 Establish reliable and cost-effective phenotyping methods for low GI traits	15% for low glycemic rice	New phenotyping methods including starch hydrolysis applied to screening germplasm.	Phenotyping experiments become routine for screening	
	4.2 Survey low GI traits in traditional germplasm and 250 breeding lines and identify QTLs through genome wide association studies			10 low GI accessions identified	◆ At least 10 germplasm accessions with low GI will be identified
	4.3 Generate mapping populations conferring low GI traits		Potential parental lines with low GI identified	Crossing between low GI rice lines and elite lines initiated	

Topic	Activity	% Project activity	Progress indicator		Activity by TARI/NTU/ICDF
			Jan-Jun	July-Dec	
<p>NEW TOPIC</p> <p>5. Developing an integrative strategy for sustainable management of BPH</p>	<p>5.1 Selecting four hot areas/spots (Pingtung + Kaohsiung, Chiayi, Taichung + Changhua, and Taitung + Hualien) in Taiwan to identify BPH populations and the effective R genes against respective populations using NILs. (budget estimate 10K USD)</p> <p>5.2 Establishing a regional research network on BPH. It is suggested to be formed by related countries across Northeast, East and Southeast Asia or through a coordination program sponsored by IRRI. (budget estimate</p>				<ul style="list-style-type: none"> ◆ For the genetic approach to study BPH, four hot areas (Pingtung + Kaohsiung, Chiayi, Taichung + Changhua, and Taitung + Hualien) in Taiwan will be selected to identify BPH populations and the effective R genes against respective populations using NILs. ◆ In considering their current responsibilities and load capacity, topic selection for BPH is based on research priority and demands. ◆ The donor information for resistance to BPH is very important. It is hoped that the information of specific functional markers provided by IRRI can be used to generate BC2F1 lines from crossing BPH resistance donor with Taiwan elite rice varieties. TARI will monitor and ascertain the introgression of effective R gene(s) into backcross progenies.

	<p>10K USD)</p> <p>5.3 Implementing donor information for resistance to BPH. It is hoped that the information of specific functional markers provided by IRRI can be used to generate BC2F1 lines from crossing BPH resistance donor with Taiwan elite rice varieties. COA/TARI will monitor and ascertain the introgression of effective R gene(s) into backcross progenies. (budget estimate 10K USD)</p>				
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Topic	Activity by IRRI/TaiwanICDF	% Project activity	Progress indicator
			Jan-Dec
6. Capacity building and development of human resources	Training program(s) for TaiwanICDF staff		<ul style="list-style-type: none"> ● Seek cooperation possibilities with CIAT and AfricaRice via IRRI ● Initiate the development of the syllabus for training program(s) with IRRI ● Finalize the syllabus of training program(s) ● Dispatch TaiwanICDF staff to participate in training program(s)