

國立成功大學課程採彈性密集授課

教學單位名稱	熱帶植物與微生物科學研究所		填表日期	111 年 5 月 30 日
課程名稱	智慧農業 R 軟體在作物性狀改良之應用	學分數	1 學分	<input type="checkbox"/> 必修 V 選修
開課學年學期	112 學年 第 1 學期	授課教師	李瑞花、蔣鎮宇、謝羅倫	
彈性密集授課時間及地點	詳如課程時程規劃表附件 授課時間合計 <u>18</u> 小時			

附件一、課程時程規劃表

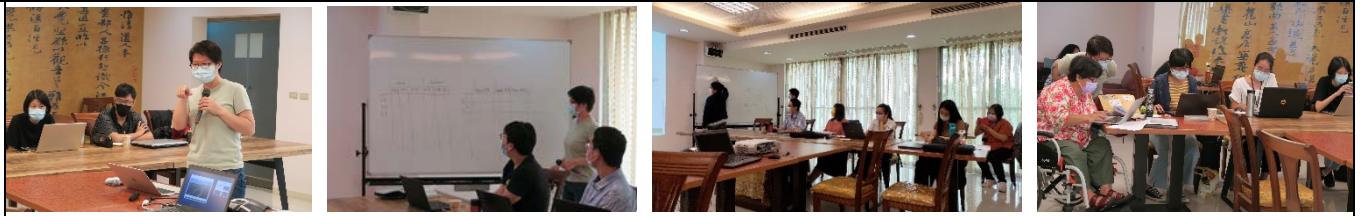
Date	Time	Topic	Lecturer	Location
7/10 Mon. (6h)	08:10 – 10:00	Introduction to phenotyping and genotyping	Roland Schafleitner	WorldVeg Center
	10:00 – 11:00	Phenotyping – Use of sensors and cameras to measure plant traits	Roland Schafleitner	WorldVeg Center
	11:00 – 12:00	Experimental design I	Ya-ping Lin	WorldVeg Center
	13:10 – 14:00	Experimental design II	Ya-ping Lin	WorldVeg Center
	14:00 – 15:00	R for beginners I	Ya-ping Lin	WorldVeg Center
7/11 Tue. (7h)	08:10 – 09:00	Crop phenotyping	Derek Barchenger	WorldVeg Center
	09:00 – 11:00	Crop phenotyping and data analysis (hands-on exercise)	Roland Schafleitner Ya-ping Lin	WorldVeg Center
	11:00 – 12:00	R for beginners II	Ya-ping Lin	WorldVeg Center
	13:10 – 15:30	Phenotyping data analysis	Ya-ping Lin	WorldVeg Center
	15:30 – 16:00	Wrap up and Q&A	Roland Schafleitner	WorldVeg Center
7/12 Wed. (6h)	09:10 – 12:00	Plant genotyping in Lab	Ruey-Hua Lee	NCKU
	13:10 – 16:00	Plant phenotyping in Lab	Ruey-Hua Lee	NCKU

附件二、外國學者名單及簡歷

	姓名/國籍	產業別	服務單位及其所在地	職稱	學歷/經歷	專長資格 (專長領域應與系科專業實務技能相關)	所屬企業是否提供實習機會
1	Roland Schafleitner 謝羅倫 / 奧地利	國際研究中心	亞蔬-世界蔬菜中心/ 台灣台南	Flagship Leader, Vegetable Diversity & Improvement	PhD in Biochemical Technology, Vienna University of Technology, Austria August 2018 to present: 熱帶植物科學與微生物研究所合聘老師 October 2017 to present: Flagship program leader Vegetable Diversity and Improvement, World Vegetable Center, Taiwan Aug. 2010-present: Head, Molecular Genetics, World Vegetable Center, Taiwan 2003 –July 2010: Plant Biotechnology Research Scientist and Project Manager, Germplasm Enhancement and Crop Improvement Division, International Potato Center (CIP), Lima, Peru. 2002-2003: Postdoctoral Researcher, INRA, Centre de Recherche de Bordeaux, France 1996-2002: Biotechnology Research Scientist, Austrian Research Centers Seibersdorf, Austria 1993-1996: Research Associate, Austrian Research Centers, Seibersdorf, Austria 1995: Research Assistant, International Atomic Energy Agency, Vienna, Austria 1991-1993: Research Technician, Vienna General Hospital, Austria	分子遺傳	是
2	Derek Barchenger 德瑞克/美國	國際研究中心	亞蔬-世界蔬菜中心/ 台灣台南	育種科學家	PhD in Plant Breeding, New Mexico State University USA 2016-2017, Norman Borlaug Research fellow, AVRDC-World Vegetable Center 2017-till now, Breeding Scientist, AVRDC-World Vegetable Center	蔬菜育種	是

附件三、課程實作內容及結合工作坊

實作內涵說明	<p>With the availability of next generation sequencing and modern automated genotyping technologies, generating accurate genotypic data for a large set of germplasm and breeding population has become easier. This training aims to impart training on recent development in high throughput phenotyping of crops. In the first part of the course, the student will learn about trial design and phenotyping methods and collect phenomic data using a high throughput field phenotyping device. In the second part of the course, the students will work with the instructors to analyze large phenomic datasets and tentatively map traits in a vegetable crop using R program. The last part of the course allows students to practice genotyping and phenotyping on lab scale that are important for forward and reverse genetics in studying gene function.</p>
其他補充資料 圖為前期智慧農業R軟體在作物性狀改良之應用實作照片	<p>9/1</p>     <p>Roland taught phenotyping and genotyping,</p>     <p>Roland taught phenotyping – Use of sensors and cameras to measure plant traits</p>     <p>Students ask questions</p>     <p>Students ask questions</p>     <p>Coffee break Visit Gene Bank Visit Demo Garden</p>  <p>Install R package</p>



Dr. Lin, Ya-pin taught "Experimental design using R package"



Learning experimental design using R



Students ask questions



Students doing exercises

9/2



Dr. Derek Barchenger taught Crop Phenotyping on line



Visit high throughput phenotyping facility in the field





Dr. Lin, Ya-pin taught “Phenotyping data analysis”

9/3 Genotyping and Phenotyping in Lab scale

