出國報告（出國類別：國際會議）

第三屆生物技術世界會議

服務機關：行政院農委會高雄區農業改良場
姓名職稱：蔡奇助副研究員
派赴國家：杜拜
出國期間：**103** 年 **2** 月 **8~13** 日
報告日期：**103** 年 **4** 月 **28** 日

摘要

2014 年第三屆生物技術世界會議(3rd Biotechnology World Congress)在杜拜舉行，由尤里卡科學組織(Eureka Science)主辦，阿聯酋科技高等學院(Higher Colleges of Technology, UAE)協辦，由 1998 年諾貝爾獎生理學或醫學組得主 Ferid Murad 教授擔任主席。研討會成員來自世界 51 個國家總計約 400 位學者參與此會，其中台灣有 5 位學者參加。本會議題包含轉基因植物和作物、基因調控，生物復育和微生物多樣性、製藥方面的生物技術（例如疫苗，中樞神經系統癌症，抗體），醫療生物技術，工業生物技術，生物過程工程，蛋白質、工程設計、生物技術商業模式的發展、策略聯盟、合作的發展趨勢、產品的機會等研究主題。心得與建議包括：1. 國際研討會的價值：舉辦國際學術研討會是一個提升國際學術地位與國家形象的良好機會，政府應加以鼓勵與補助。2. 跨領域合作研究的重要性：生物技術使用的技術多且廣，唯有集合多人的力量與專長，方能有突破性的發展。3. 會議探討主題涵蓋廣泛：本次的國際生物技術世界會議幾乎涵蓋各個領域，因此可以藉此擴展參與者的視野，也可以激發新的研究主題，產生新的靈感，有助於未來的創新研發。4. 鼓勵研究人員積極參與國際活動：積極鼓勵研究人員從事國外短期研究、參與國際活動及國外修讀博士或博士後，不僅能增進研發人員的國際視野，也能提昇研發能量。

目錄

一、目的

2014 年第三屆生物技術世界會議(3rd Biotechnology World Congress)是生物技術領域的盛事，生物技術領域的研究人員能夠在此獲得生物技術最新的研究進展。會議議題包含轉基因植物和作物、基因調控、生物復育、微生物多樣性、製藥生物技術、醫療生物技術、工業生物技術、生物過程工程、蛋白質、工程設計等研究主題，以及生物技術商業模式的發展、合作的發展趨勢及產品的機會等。希望藉由參與此國際研討會，可以獲取目前農業生物技術發展的重點，並與相關領域的國外學者交流，藉此激發出新的研究方向，以進一步應用於蘭花生物技術研發，提升台灣蘭花產業競爭力。

二、行程表及研習內容

「第三屆生物技術世界會議」行程內容

8-13 Feb 2014

時間		地點	行程內容
2 月 8 日	（六）	高雄、香港	高雄小港機場->香港機場->夜宿飛機上
2 月 9 日	（日）	杜拜(住宿：杜拜)	抵達杜拜的杜拜國際機場->飯店->抵達會場及註冊
2 月 10 日	（一）		開幕式 專題演講 1: Dr. F. Murad (Nobel Laureate) 專題演講 2: Dr. J.-M. Lehn (Nobel Laureate) 專題演講 3: Dr. R. Kumar 分組研討 歡迎茶會
2 月 11 日	（二）		專題演講 1: Dr. E.H. Fischer (Nobel Laureate) 專題演講 2: Dr. J.-P. Stasch 專題演講 3: Dr. B.S. Moore 分組研討 海報展示簡報 晚餐
2 月 12 日	（三）	杜拜(住宿：夜宿飛機)	專題演講 1: Dr. R. Huber (Nobel Laureate) 專題演講 2: Dr. R.L. Atkinson 專題演講 3: Dr. M.I. Choudhary 分組研討 會場->杜拜國際機場->香港機場->夜宿飛機上
2 月 13 日	（四）	香港、高雄、屏東	飛抵香港機場->高雄小港機場->本場

研討會記要

第一屆～第三屆生物技術世界會議(3rd Biotechnology World Congress)都在杜拜舉辦，由於總能吸引國外學者踴躍的參與，因此，第四屆(2015 年)也預定在杜拜舉行。本國際會議由尤里卡科學組織(Eureka Science)主辦，阿聯酋科技高等學院(Higher Colleges of Technology, UAE)協辦，會場就在阿聯酋科技高等學院校區，藉由校區現有的國際會議廳舉行開、閉幕及專題演講，以及幾個小型會議室舉辦分組研討。本國際會議的特色是專題演講很多，計有 9 場，其中 4 場的講者爲諾貝爾獎得主，因此吸引來自 51 個國家，400 多位的學者參與，重要的會議行程如下：

2 月 9 日：下午註冊報到。

2 月 10 日：開幕酒會後，第一節是由諾貝爾獎得主 E.H. Fisher 主持，有兩場專題演講，第一場是諾貝爾獎得主 Ferid Murad 教授的專題演講，題目：Application of nitric oxide research to drug development and disease。另一場是另一位諾貝爾獎得主 J.-M. Lehn 教授的專題演講，題目：Supramolecular and adaptive chemistry bioorganic and drug discovery aspects-recent advances。中午午休用餐後，第二節是由 D. K. Lahiri 教授主持，由 R. Kumar 教授進行專題演講，題目：Targeting PAK1 kinase in human cancer。第三節爲分組研討，主要分三組，第一組爲醫藥生物技術組、第二組製藥生物技術組及第三組爲其他領域組，筆者主要參與其他領域組。

2月11日：早上第一節是由諾貝爾獎得主 Ferid Murad 教授主持，有兩場專題演講，是由諾貝爾獎得主E.H. Fisher 授的專題演講，題目：Cell signaling by protein phosphorylation。另一場是由 J.-P. Stasch 教授的專題演講，題目：Targeting soluble guanylate cyclase for the treatment of cardiopulmonary disease。第二節是由

M.I. Choudhary 教授主持，由 B.S. Moore 教授進行專題演講，題目：Rewriting natural product drug discovery through synthetic biology。中午用餐後爲分組研討。

2月12日：早上第一節是由諾貝爾獎得主 J.-M. Lehn 教授主持，有兩場專題演講，第一場是諾貝爾獎得主 R. Huber教授的專題演講，題目：Biological basic research and its translation into practice and business, my business, my experience。另一場是由 R.L. Atkinson 教授的專題演講，題目：Current and future drug treatment of obesity。第二節是由 W.J. Rowe 教授主持，由 M.I. Choudhary 教授進行專題演講，題目：Natural-product based drug discovery—Can we afford to ignore chemical diversity of nature。中午用餐後爲分組研討，然後進行閉幕式。

四、心得及建議

1. 國際研討會的價值：

本國際研討會在杜拜舉行，借用阿聯酋科技高等學院(Higher Colleges of Technology, UAE)的綜合大樓場地，主場地不僅具有氣派的場地與豪華的設備，分組研討分成好幾個場地同時進行，由於議題多元且資料充足，每一個與會者皆能依照各自的專長與興趣，參與不同的主題研討。最特別的是邀請多位諾貝爾獎得主進行專題演講，讓整個研討會的號召力大大的提升，因此能吸引很多學者參與。

2. 跨領域合作研究的重要性：

由諾貝爾獎得主的專題演講中發現，都是跨領域的合作所獲得的成果，現今生物技術使用的技術多且廣，重要發現的研究都需要集合多人的力量與專長方能有所得。因此有必要透過計畫研提管道，鼓勵學、研機構研提跨領域的研究計畫，提升台灣生物技術的研究水平。

3. 會議探討主題涵蓋廣泛：

大部分的國際會議都僅針對某一領域或議題，而本國際會議探討的議題涵蓋甚廣，舉凡醫學、藥學、農學、食品及環保、生態等，幾乎涵蓋生物技術所能應用的各個領域，因此可以藉此擴展參與者的視野，也可以激發新的研究主題，產生新的靈感，有助於未來的創新研發。值得台灣未來在舉辦國際會議時參考。

4. 鼓勵研究人員積極參與國際活動：

近年來中國大陸學者參與國際研討會相當踴躍，本次國際研討會參與的人數約 400 人，中國大陸參加 24 人，僅次於主辦國，可見中國大陸現在不僅經濟實力強，在科學研究的軟實力也很積極，不僅鼓勵出國進修，也鼓勵積極參與國際活動，未來的科學研發將無可限量。建議台灣應該提供多元管道，鼓勵研究人員從事國外短期研究、參與國際活動及國外修讀博士或博士後，這樣不僅能提昇研究水準，也能增進研發人員的國際視野及國際觀。

五、附件

1. 發表論文內容

Comparative transcriptome analysis of *Gastrodia elata* (Orchidaceae) in response to fungus symbiosis

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ABSTRACT

Gastrodin, a pharmacologically active constituent, are the major phenolic components of gastrodia (*Gastrodia elata*). Under symbiotic with unique fungus *Armillaria mellea*, gastrodia will switch on the biosynthesis of gastrodin and develop from small protocorms to tubers. To understand the gene regulation in gastrodin biosynthesis in gastrodia, we conducted comparative transcriptome analysis for *Armillaria mellea*, small protocorms, and tubers of gastrodia. Transcriptome comparison between tubers and small protocorms of gastrodia revealed 1070 differentially expressed unigenes, of which 491 were up-regulated in tubers whereas 579 were down-regulated. KEGG pathway analyses were conducted for the up- and down regulated unigenes. Forty-nine up-regulated unigenes were assigned to 116 different pathways, and 55 down-regulated unigenes were assigned to 200 different pathways. Inspection of aforementioned up- and down-regulated pathways, two unigenes named locus 25051 and locus 22288 which may participate in the hydroxylation and glucosylation of gastrodin biosynthesis pathway were focused. Real-time PCR analysis for the two unigenes was conducted to confirm the differential expression between tubers and small protocorms. As the result, gene expression of unigene locus 25051 in tubers are higher than that in small protocorms about 3.6 fold, and gene expression of unigene locus 22288 are about 6.5 fold.

Keywords: *Gastrodia elata*; *Armillaria mellea*; gastrodin biosynthesis; comparative transcriptome; symbiosis.

INTRODUCTION

Gastrodia elata, one of an achlorophyllous orchid plant, which without root and green leaf and grows in a complex relationship with two compatible mycorrhizal fungi *Mycena* spp. and *Armillaria mellea*, establishes symbiotic associations with compatible mycorrhizal fungi of *Mycena spp*. (Figure 1) at seed germination to form small protocorms, and with compatible mycorrhizal fungi of *Armillaria mellea* (Figure 1) during vegetative growth (tuber stage) (Huang *et al*., 2004 ; Zhou *et al*., 1987). In vegetative growth, *Armillaria mellea* provides nutrition and energy for *Gastrodia elata* to grow immature tubes, and its quality and grow situation influence the grows of *Gastrodia elata* tuber significantly (Zhou *et al*., 1987; Zou *et al*., 2010). Gastrodin, a simple glycoside consisting of glucose and 4-hydroxybenzyl alcohol, are the major phenolic components of *Gastrodia elata* and have been used to treat many human illnesses (Chen and Sheen, 2011). To understand the gene regulation in gastrodin biosynthesis in gastrodia, we conducted comparative transcriptome analysis for *Armillaria mellea*, small protocorms, and tubers of gastrodia.

MATERALS AND METHODS

We performed the sequencing and *de novo* transcriptome assembly for small protocorm and tuber (Figure 2) of *Gastrodia elata* by next-generation sequencing (Illumina HiSeqTM 2000 platform) and analyzed the unigenes for Gene Ontology (GO) annotation, Enzyme Commission (EC) and KEGG pathway analyses. Further, we examined the differential expression of target unigenes between small corm and tuber of *Gastrodia elata* by Real-time PCR analysis.

RESULTS AND DISCUSSION

Gastrodin, a pharmacologically active constituent, are the major phenolic components of gastrodia (*Gastrodia elata*). Under symbiotic with unique fungus *Armillaria mellea*, gastrodia will switch on the biosynthesis of gastrodin (Figure 3) and develop from small protocorms to tubers. Comparative transcriptome analysis for small protocorms and tubers of gastrodia revealed 1070 differentially expressed unigenes, of which 491 were up-regulated in tubers whereas 579 were down-regulated. Forty-nine up-regulated unigenes were assigned to 116 different pathways, and 55 down-regulated unigenes were assigned to 200 different pathways. Inspection of aforementioned up- and down-regulated pathways, two unigenes named locus 25051 and locus 22288 (Table. 1) which may participate in the hydroxylation (Figure 4) and glucosylation (Figure 5) of gastrodin biosynthesis pathway were focused. Real-time

PCR analysis for the two unigenes was conducted to confirm the differential expression between tubers and small protocorms. As the result, gene expression of unigene locus 25051 in tubers are higher than that in small protocorms about 3.6 fold, and gene expression of unigene locus 22288 are about 6.5 fold (Figure 6).

CONCLUSION

After germination, *Gastrodia elata* varied into vegetative growth to form tubers by the symbiotic with *Armillaria mellea*, which turn on the biosynthesis pathway of gastrodin and accumulate the gastrodin in rhizome tubers.

ACKNOWLEDGEMENTS

This research was supported by funding from the National Science Council, Executive Yuan, Taiwan, R.O.C.

Literature Cited

Chen, P. and L. Sheen (2011) Gastrodiae Rhizoma: a review of biological activity and antidepressant mechanisms. Journal of Traditional and Complementary Medicine 1: 31-40.

Huang, H., Z. Liang and W. Wang (2004) Review of nutrient source studies on *Gastrodia elata* Bl growth up. Journal of Northwest Science Tech University of Agriculture and Forrest 32: 145-153.

Zhou, J., Y. Yang, H. Liang and C. Liu (1987) Morphology of *Gastrodia elata*. Science Publish Center, Peijin, China. 1-122.

Zou, N., X. Bai, J. Lu, J. Yang, G. Xu and D. Sun (2010) Study on symbiotic mechanism between *Gastrodia elata* Blume and *Armillaria mellea* in tissue culture system. Medicinal plant 1:91-92.

Figures

Figure 1. *Mycena dendrobii* (left) and *Armillaria mellea* (right).

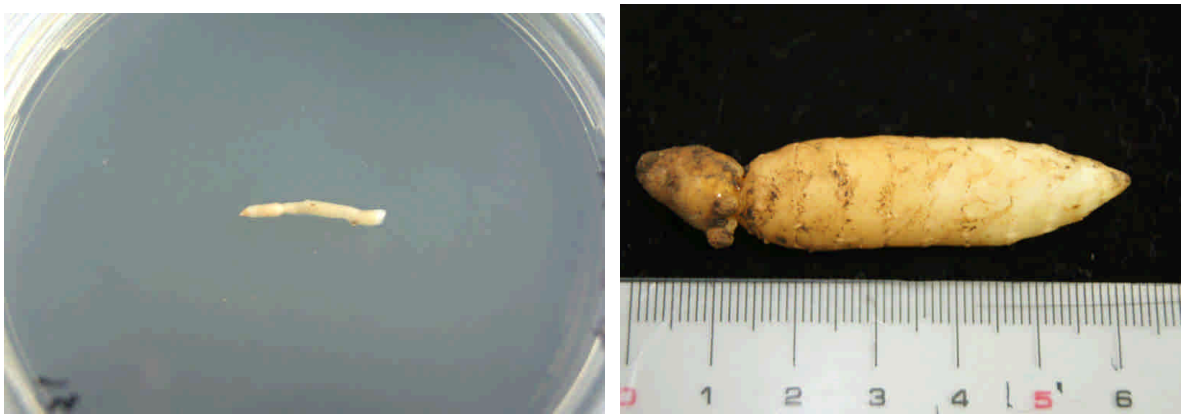

Figure 2. Small protocorm (left, germinated by the symbiotic with *Mycena dendrobii*) and tuber (right, symbiotic with *Armillaria mellea*) of *Gastrodia elata*.

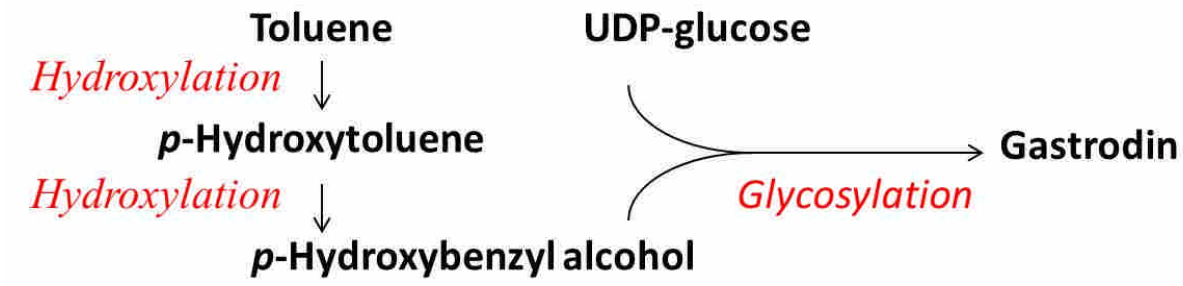

Figure 3. Hypothetical biosynthetic pathway of gastrodin.

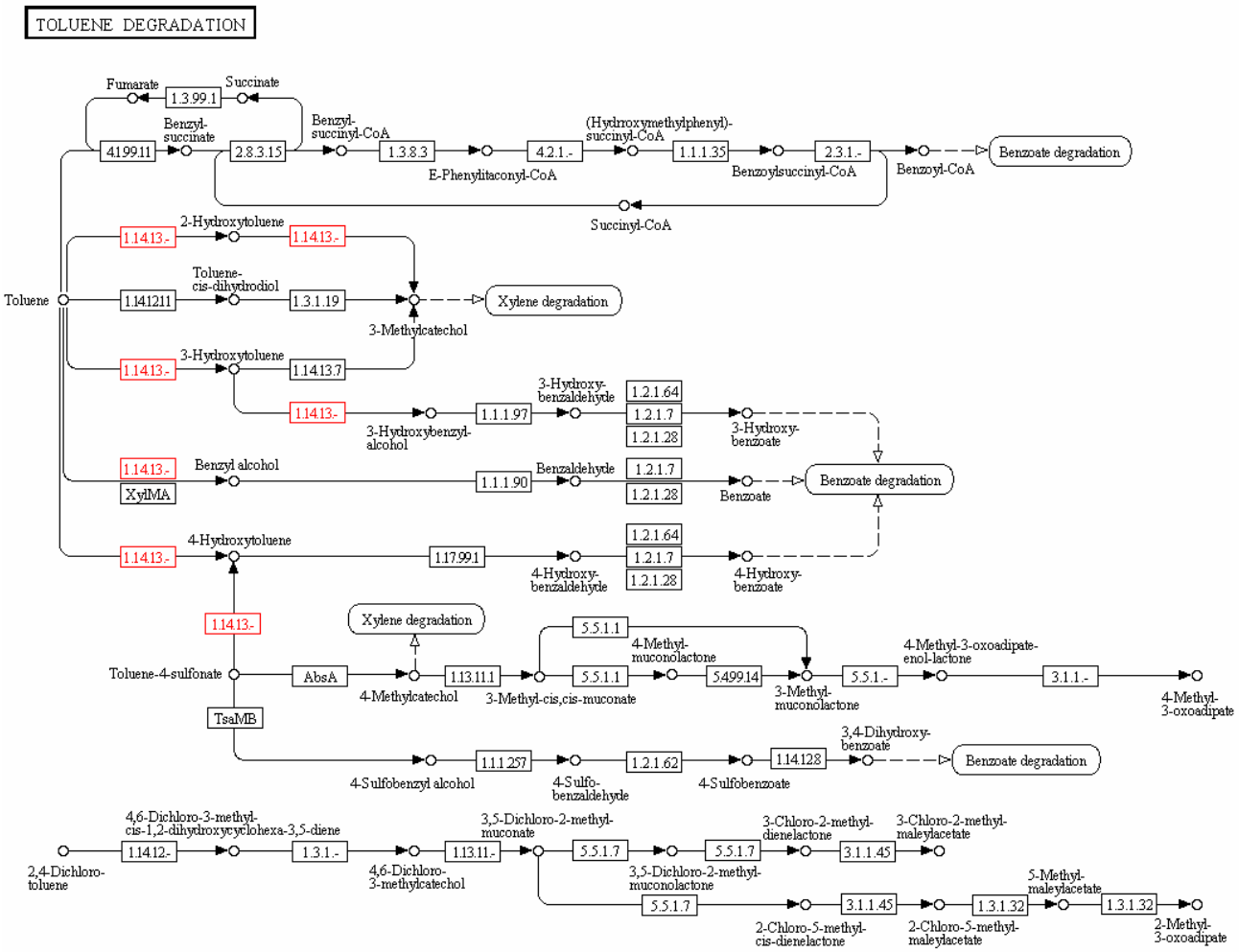

Figure 4. Hydroxylation by *monooxygenase* (EC:1.14.13.-) in toluene degradation.

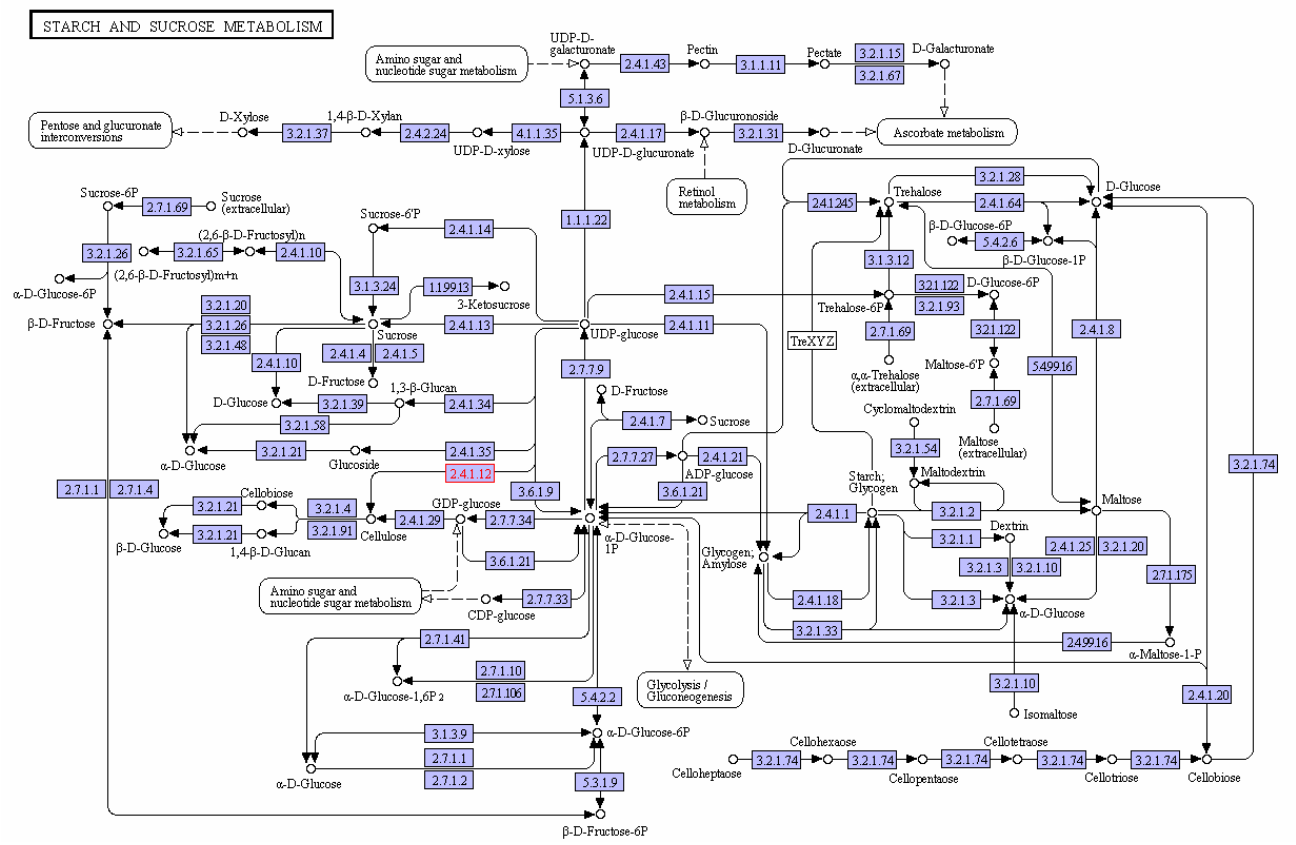

Figure 5. Glucosylation by *beta-1,4-glucosyltransferase* (EC:2.4.1.12) in starch and sucrose metabolism.

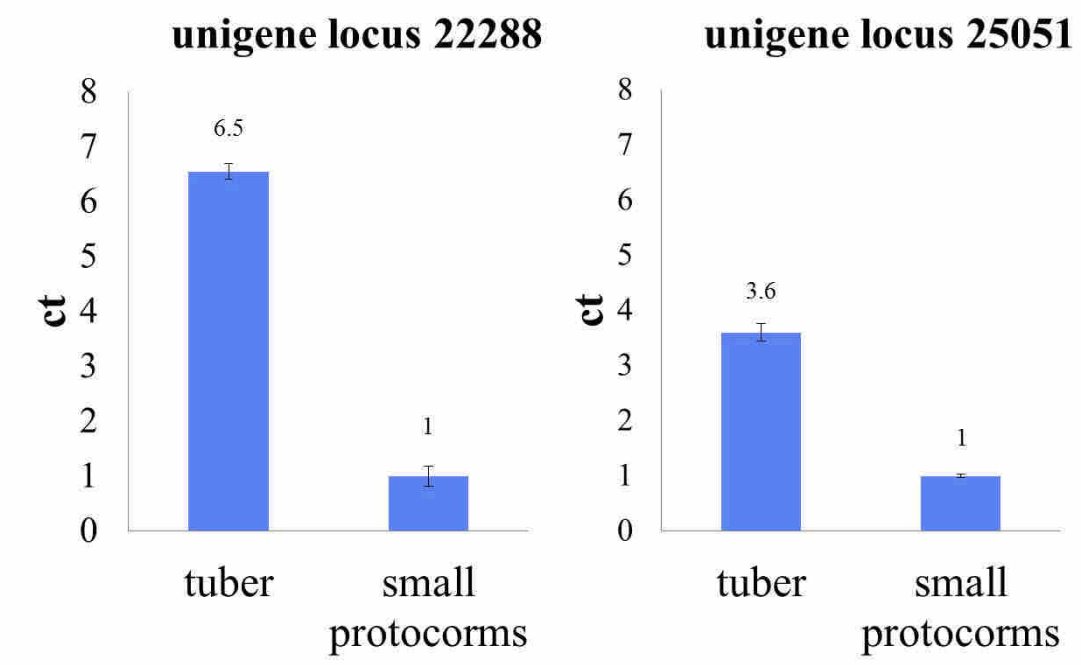

Figure 6. Real-time PCR analysis of unigenes locus 22288 and locus 25051 expression between tubers and small protocorms of *Gastrodia elata* .

2. 研討會摘要專書內容

Track: *Other areas/System Biology*

COMPARATIVE TRANSCRIPTOME ANALYSIS OF *GASTRODIA ELATA* (ORCHIDACEAE) IN RESPONSE TO FUNGUS SYMBIOSIS

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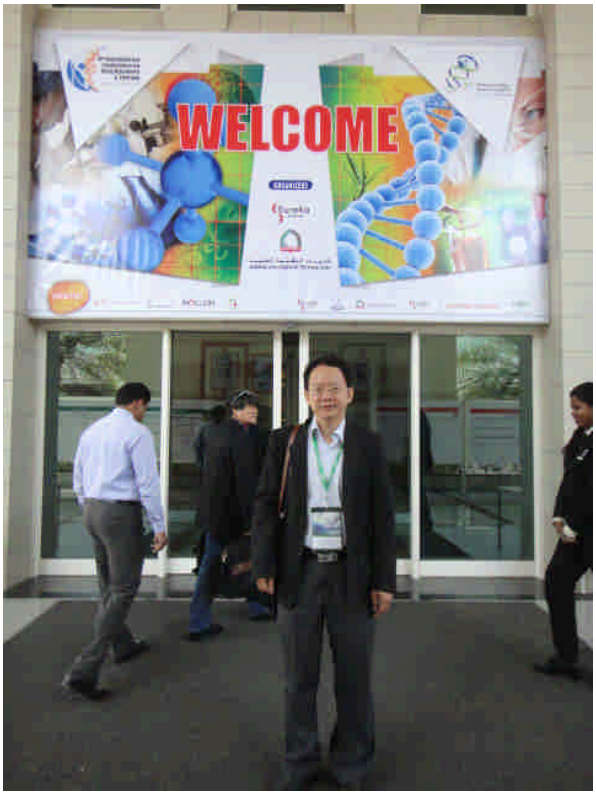
Gastrodin, a pharmacologically active constituent, are the major phenolic components of gastrodia (*Gastrodia elata*). Under symbiotic with unique fungus *Armillaria mellea*, gastrodia will switch on the biosynthesis of gastrodin and develop from small protocorms to tubers. To understand the gene regulation in gastrodin biosynthesis in gastrodia, we conducted comparative transcriptome analysis for *Armillaria mellea*, small protocorms, and tubers of gastrodia. Transcriptome comparison between tubers and small protocorms of gastrodia revealed 1070 differentially expressed unigenes, of which 491 were up-regulated in tubers whereas 579 were down-regulated. KEGG pathway analyses were conducted for the up- and down regulated unigenes. Forty-nine up-regulated unigenes were assigned to 116 different pathways, and 55 down-regulated unigenes were assigned to 200 different pathways. Inspection of aforementioned up- and down-regulated pathways, two unigenes named locus 25051 and locus 22288 which may participate in the hydroxylation and glucosylation of gastrodin biosynthesis pathway were focused. Real-time PCR analysis for the two unigenes was conducted to confirm the differential expression between tubers and small protocorms. As the result, gene expression of unigene locus 25051 in tubers are higher than that in small protocorms about 3.6 fold, and gene expression of unigene locus 22288 are about 6.5 fold.

Keywords: *Gastrodia elata*, *Armillaria mellea*, gastrodin biosynthesis, comparative transcriptome, symbiosis.

3. 本次國際研討會相關照片

大會主席 Ferid Murad 教授



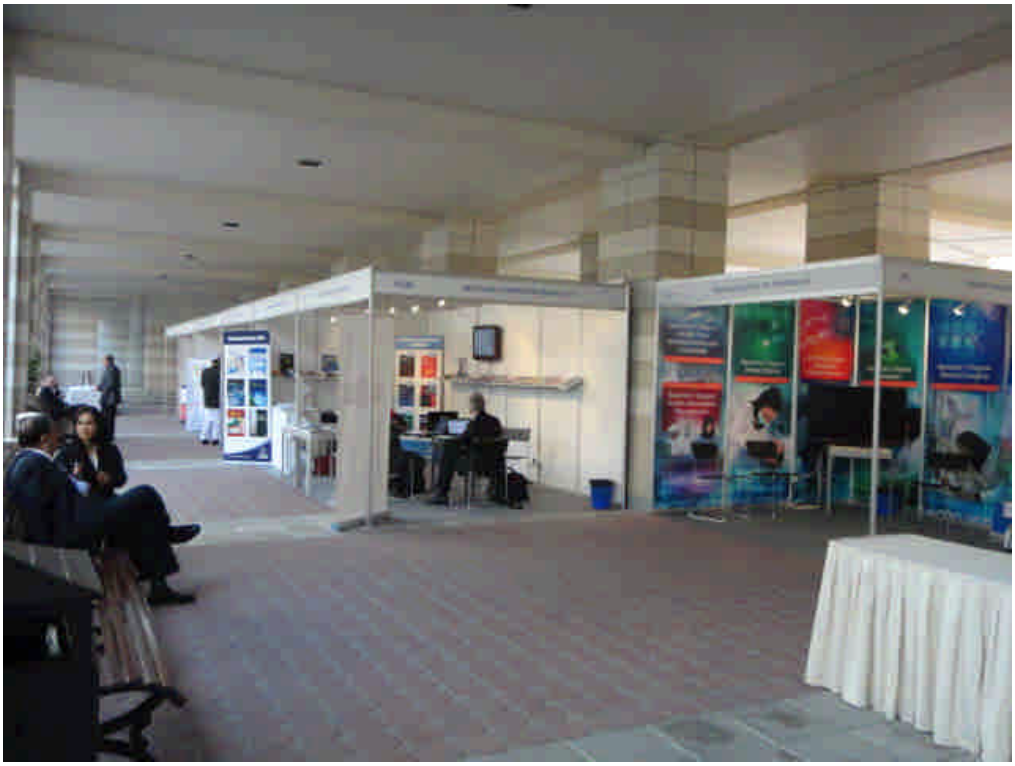
國際研討會會場~阿聯酋科技高等學院綜合大樓

國際研討會主會場

研究海報展示區

大會主席諾貝爾獎得主 Ferid Murad 教授的專題演講

分組研討情形

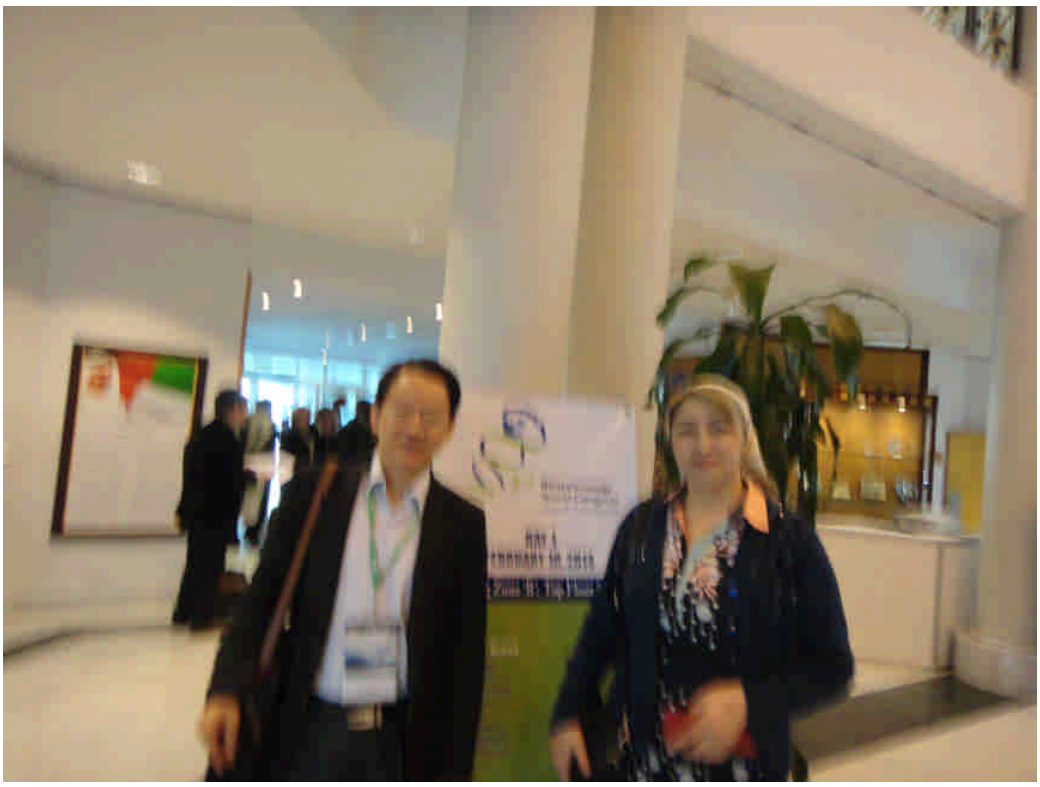


商業洽談區

筆者與台灣友人合影

筆者與澳洲華裔友人合影

筆者與韓國友人合影



筆者與美國友人合影