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肉雞飼料用乳酸菌株之篩選分離

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34. 肉雞飼料用乳酸菌株之篩選分離

陳若菁(1)、沈韶儀(1)、黃建榕(1)、林德育(1)、陳椒華(2)

(1)行政院農業委員會畜產試驗所 (2)嘉南藥理科技大學生物科技系

將1、2、4、7及28日齡的雞隻糞便培養在MRS培養基上，挑選631個單一菌落，經凝乳反應 (curdling reaction)、革蘭氏染色 (Gram stain) 及觸酶反應 (catalase test) 等特性試驗之初步篩選後，得到177株菌株。再以16S rDNA序列分析進行菌種鑑定，共鑑定出46株菌，分別屬於Uncultured bacterium、Enterococcus faecalis、Lactobacillus johnsonii、Lactobacillus reuteri 及Lactobacillus salivarius。對鑑定出之6株乳酸菌株 (Lactobacillus) 測定其產酸能力、生長速率及對酸與0.3%膽鹽的耐受性，其中以Lactobacillus salivarius 28DM-68的產酸能力最好，Lactobacillus johnsonii 4DM-45的耐酸及耐膽鹽能力較佳。大量培養這兩株菌後利用低溫冷凍乾燥方法，製成乾燥菌粉，其活菌存活率分別為10%及53%，將作為後續之肉雞飼料試驗的添加劑。

關鍵語：乳酸菌、益生菌、肉雞、篩選

ISOLATION OF POTENT LACTOBACILLUS STRAINS AS PROBIOTICS FOR THE BROILERS

J. C. Chen(1), S. Y. Sheen(1), C. J. Huang(1), D. Y. Lin(1) and J. H. Chen(2)

(1)Livestock Research Institute, Council of Agriculture, Executive Yuan

(2)Chia-Nan University of Pharmacy and Science

The feces from 1, 2, 4, 7 and 28 days old chickens are sampled and cultured on the MRS agar. Screening of the 631 single colonies by curdling reaction, Gram stain test and catalase test, we get 177 strains of lactic acid bacteria (LAB). These LABs are Uncultured bacteria, Enterococcus faecalis, Lactobacillus johnsonii, Lactobacillus reuteri and Lactobacillus salivarius as identified by the 16S rDNA sequencing. The six identified Lactobacillus strains are further studied for their acid productivities, growth rates and tolerance for acid and bile salts. Among them, the Lactobacillus salivarius 28DM-68 has the best acid productivity and Lactobacillus johnsonii 4DM-45 shows good performance on the tolerance for acid and bile salts. The viability of the freeze-dried culture for Lactobacillus salivarius 28DM-68 and Lactobacillus johnsonii 4DM-45 are 10% and 53%, respectively.

Key Words: Lactobacillus, Probiotics, Broiler, Isolation

蘭嶼豬粒線體細胞色素氧化酶基因第一次單元基因全長定序

44. 蘭嶼豬粒線體細胞色素氧化酶C1基因全長定序

陳佳萱(1) (3) 楊雅(1) 顏念慈(1) 朱賢斌(2) 陳坤照(2) 吳明哲(1) 黃木秋(3)

(1)行政院農業委員會畜產試驗所 (2)行政院農業委員會畜產試驗所台東種畜繁殖場 (3)國立中興大學動物科學系

粒線體DNA是一雙股構成的環狀分子，哺乳動物大約為15-17 Kb，胞器組成包括2個核糖體核糖核酸（ribosomal RNA, rRNA），22個轉譯核糖核酸（transfer RNA, tRNA），13個蛋白質基因（protein coding genes），與一段D環區（control region, D-loop）。粒線體細胞色素氧化酶C1基因（cytochrome c oxidase subunit 1, C01）已被列入物種基因條碼的重要標示區域，本試驗設計兩對引子成功完成蘭嶼豬C01基因核DNA序列，全長共1545 bp，以blast軟體與其他序列比較，發現蘭嶼豬C01基因與其他種豬間序列相似度高達99%，與其他物種序列歧異度分別為牛81%、山羊82%、梅花鹿81%、馬81%與雞77%。成功完成粒線體C01基因有助畜產應用在基因條碼編列與物種鑑定。

關鍵語：細胞色素氧化酶C1基因、粒線體DNA、蘭嶼豬

PRIMARY ANALYSIS OF MITOCHONDRIAL DNA CYTOCHROME C OXIDASE SUBUNIT I REGION SEQUENCE IN LANYU PIG

C. H. Chen(1) (3), H. Y. Yang(1), N. T. Yen(1), H. P. Chu(2), K. J. Chen (2), M. C. Wu(1) and M. C. Huang(3)

(1)Livestock Research Institute, Council of Agriculture, Executive Yuan

(2) Taitung Animal Propagation Station, Livestock Research Institute, Council of Agriculture, Executive Yuan

(3)Department of Animal Science, National Chung- Hsing University

Mitochondrial DNA is a circular structure of double strand nucleotide, about 15-17 Kb in mammals. There are 2 ribosomal RNA, 22 transfer RNA, 13 protein coding gene and 1 D-loop region in mitochondrion. Mitochondrial cytochrome c oxidase subunit I (C01) has become an important marker region for species barcode. Two pair of primers, a total length of 1545 bp, were designed in this trial to sequence C01 nucleotide in Lanyu pig. Comparing with the sequence of other species by blast software, the similarity of C01 between Lanyu and other pig breeds reached a high level of 99 %; while the divergence among Lanyu and other species were 81 % in cow, 82 % in goat, 81 % in Sika deer, 81 % in horse and 77 % in chicken. The results implicated that mitochondrial C01 was applicable for barcode editing and species identity in farm animals.

Key Word : Cytochrome c oxidase subunit 1, Mitochondrial DNA, Lanyu pig

豬種的粒線體細胞色素b基因序列鑑定及親緣關係

45. 豬種的粒線體細胞色素b基因序列鑑定及親緣關係

陳佳萱(1) (3) 楊雅(1) 顏念慈(1) 朱賢斌(2) 陳坤照(2) 吳明哲(1) 黃木秋(3)

(1)行政院農業委員會畜產試驗所 (2)行政院農業委員會畜產試驗所台東種畜繁殖場 (3)國立中興大學動物科學系

粒線體具有母系遺傳、單倍體、無重組、高突變率、缺乏修補系統、演化速度比核內DNA快十倍、分子量小而成族群結構、演化、基因交流、生物地理與親緣關係分析的有利工具。粒線體共有37個基因，目前粒線體DNA除D-loop高變異區被研究外，有越來越多粒線體基因被重視，細胞色素b (Cytochrome b, Cyt b)已被列入對物種鑑別與親緣關係演化的重要區域。本試驗設計二對引子分別定序出蘭嶼豬NADH6 (NADH dehydrogenase subunit 6)、tRNA-Glu與Cyt b基因，全長共1737 bp，並以MEGA3.1軟體分析蘭嶼豬Cyt b基因與歐洲豬種間親緣關係。研究結果發現蘭嶼豬種屬於獨立的分支，而杜洛克、漢布夏與藍瑞斯屬於歐洲型，支持度可達100%，盤克夏與大白豬則屬於亞洲型，支持度達96%。

關鍵語：細胞色素b、粒線體DNA、蘭嶼豬

IDENTIFICATION AND PHYLOGENETIC ANALYSIS OF MITOCHONDRIAL CYTOCHROME b OF PIG

C. H. Chen(1) (3), H. Y. Yang(1), N. T. Yen(1), H. P. Chu(2), K. J. Chen (2), M. C. Wu(1) and M. C. Huang(3)

(1)Livestock Research Institute, Council of Agriculture, Executive Yuan

(2) Taitung Animal Propagation Station, Livestock Research Institute, Council of Agriculture, Executive Yuan

(3)Department of Animal Science, National Chung- Hsing University

Mitochondrion has the characteristics of maternal inheritance, haploid, non-recombination, high mutation rate, lack an effective mismatch repair system, evolution of ten-times faster than nuclear DNA, and group-structured due to small molecular weight, which has become a powerful tool for the analysis of evolution, gene exchange, and phylogeographic and phylogenetic study. Pig mitochondrial DNA, contains 37 genes. The importance of gene variations existed not only the well studied high mutation region of D-loop but also in other regions. Among these genes, cytochrome b (cyt b) has been considered as an important region in species identity and phylogenetic evolution. Two pair of primers, a total length of 1737 bp, were designed in this study to sequence dehydrogenase subunit 6 (NADH 6), tRNA-Glu and cytochrome b in Lanyu pig. Phylogenetic relations between Lanyu and European pigs were analyzed through cyt b by MEGA 3.1 software. The results indicated that Lanyu pig belongs to an independent clade; while Duroc, Hampshire and Landrace belong to the European clade with a bootstrapping of 100 %, but Berkshire and Large White belong to Asian clade with a bootstrapping of 96 %.

Key Words : Cytochrome b, Mitochondrial DNA, Lanyu pig

畜試土雞原原種異地繁殖三代之性能

54. 畜試土雞原原種異地繁殖三代之性能

鍾秀枝(1) 林宗貴(1) 王治華(1) 張秀鑾(2) 吳明哲(1) 鄭裕信(1) 王政騰(1)

(1)行政院農業委員會畜產試驗所 (2) 屏東科技大學畜產系

畜試所除了進行土雞品系選育工作外，為因應降低禽流感之風險管理，於2004年開始進行畜試土雞分散種原工作，將L7、L9、L11及 L12等四個近親品系之種蛋共計998個，送往高雄種畜繁殖場進行孵化飼養，作異地活體保種，共孵出465隻雛雞，四個品系之16週齡育成率為95.7 %，並於17週齡後選留具品種特徵之種原作小族群之保種，選留數目為每個品系各選公雞10隻母雞40隻，並於26週齡時進行配種，進行下一世代之繁殖，目前已繁殖三個世代，L7、L9、L11及 L12等四個品系之G1、G2及G3各世代達16週齡體重±標準機差分別為1485 ± 24公克、1384 ± 17公克、1406 ± 22公克及1552 ± 24公克；1484 ± 19公克、L9、1491 ± 21公克、1530 ± 17公克及1552 ± 24公克；1507 ± 24公克、1461 ± 20公克、1438 ± 20公克及1512 ± 19公克，世代與品系間皆具顯著差異 (P

關鍵語：畜試土雞、原原種、繁殖

THE PERFORMANCE OF LRI NATIVE CHICKEN IN THREE GENERATION EX-SITU CONSERVATION

H. C. Chung(1), T. K. LIN(1), C. H. WANG(1), H. L. Chang(2) , M. C. Wu(1) , Y. S. CHENG(1) AND C. T. WANG(1)

(1)Livestock Research Institute(LRI), Council of Agriculture

(2)National Pingtung University of Science and Technology

In order to reduce the risk of Avian influenza, a sub-population of LRI native chicken migrated from core population in Tainan to Kaohsiung animal propagation station. In 2004, 998 fertilized eggs of four inbred lines, L7, L9, L11 and L12 LRI native chicken, were shipped cross Kaohsiung county to the destination station in Pingtung, for the ex-situ conservation. There were 465 chicks hatched in the destination and Survival rate at 16-week of age was 95.7%. Breeding candidates, 10 males and 40 females for each line, were selected at 17-week of age, and inseminated at 26-week of age. Three generations were propagated, G1, G2 and G3, and the body weights at 16 weeks of L7, L9, L11 and L12 were 1485 ± 24g, 1384 ± 17g, 1406 ± 22g and 1552 ± 24g at G1, 1484 ± 19g, 1491 ± 21g, 1530 ± 17g and 1552 ± 24g at G2, and 1507 ± 24g, 1461 ± 20g, 1438 ± 20g and 1512 ± 19g at G3. Differences existed among generations and lines (P

Key Words: LRI Native Chicken, GGP, Reproduction

家禽性染色體上的紡錘蛋白基因分析

57. 家禽性染色體上的紡錘蛋白基因分析

楊琇雅 林德育 陳若菁 鍾秀枝 吳明哲
行政院農業委員會畜產試驗所

應用性別鑑定技術來有效繁殖及管理家禽具有極重要的經濟價值，並有助於畜產種原的保存及利用。以土雞、褐色萊鴨、番鴨、白羅曼鵝、青銅火雞、澳洲黑天鵝、鶉鶉(*Coturnix coturnix*)、環頸雉(*Phasianus colchicus*)各5公5母個體 DNA作為模版，應用SPIN12及SPIN13引子組進行聚合酶連鎖反應(PCR)後，由電泳分析結果顯示所有受檢物種之雄性與雌性均呈現不同樣態，且與實際性別吻合，證實此引子組可成功鑑別雞、鴨、番鴨、鵝、火雞之性別外，亦可作為黑天鵝、鶉鶉、環頸雉等鳥類的性別遺傳標記，從不同物種所呈現的DNA片段亦有變異存在。本研究以PCR檢測家禽Z與W性染色體中之紡錘體蛋白(Spindlin)基因intron序列，以其長度的差異來鑑定家禽性別，可避免僅檢測W染色體性別鑑定標記的誤判，且不需再搭配內部對照(internal control)，更不需結合限制酶切割法(RFLP)即進行家禽性別鑑定。

關鍵語：家禽、紡錘體蛋白基因、性別鑑定

ANALYSIS OF SPINDLIN GENE IN POULTRY

H. Y. Yang, D. Y. Lin, J. C. Chen, H. C. Chung and M. C. Wu
Livestock Research Institute, Council of Agriculture, Executive Yuan

The importance of sex determination for farm animal production is well known. To search for DNA-based sex identification candidate marker of poultry, whole blood DNAs from each five males and five females of Native Chicken(*Gallus domesticus*), Brown Tsaiya(*Anas platyrhynchos*), Muscovy(*Cairina moschata*), White Roman Goose(*Anser cygnoides*), Bronze Turkey(*Meleagris gallopavo*), Australian Black Swan(*Cygnus atratus*), Quail(*Coturnix coturnix*) and Ring-necked Pheasant(*Phasianus colchicus*) were analyzed by spindlin gene. PCR products were amplified by SPIN12 and SPIN13 primer kits. Different electrophoresis patterns showed correct gender for each bird species. The accuracy of sex identification was 100%. Furthermore, the PCR DNA fragments of the same gender were different among bird species. Based on different DNA fragments between Z and W chromosome, the developed PCR method has no risk of the mistrial of those sex identification markers depended on W chromosome, and can omit extra internal control or restriction enzyme digestion. The DNA-based spindlin gene approach can provide a rapid, exact and low cost method for sex identification in poultry.

Key Words: Poultry, Spindlin gene, Sex identification

乳牛瘤胃微生物多樣性分析

59. 乳牛瘤胃微生物多樣性分析

廖仁寶(1)、江家豐(1)、黃文瑛(1)、謝昌賢(1)、蕭宗法(1)、吳明哲(1)、李佳音(2)
行政院農業委員會畜產試驗所(1) 國立台灣大學農業化學系(2)

瘤胃為一特殊複雜的厭氧環境含之微生物包括細菌、古細菌、真菌、原蟲，且85-95%尚未能以人工分離培養。本研究採集之乳牛瘤胃液樣品，其pH值約為6.8，於顯微鏡下觀察，可發現原蟲與格蘭氏陰性和陽性的細菌。使用商業核酸萃取套組直接萃取瘤胃液中之微生物核酸。其後分別以細菌與真菌小單位核糖體核酸基因專一性之引子進行PCR增幅放大，並將增幅片段選殖於TA選殖套組，進行DNA定序與瘤胃微生物多樣性分析。其結果顯示在細菌多樣性分析中，52個株系中有521個是屬於未被分離培養或未被鑑定者，僅一株屬於 *Fibrobacter succinogenes* (相同度為96%)，而所屬菌門則有bacteroidetes(32/52)，Fibrobacteres (1/52)，Firmicutes (18/52)及unclassified Bacteria(1/52)。在真菌多樣性分析中，75個株系中有74個屬於*Neocallimastix* sp.，另僅一株屬於*Trichosporon jirovecii*。由以上得知，瘤胃中細菌之多樣性較為豐富，應該可從其中藉由多源基因體學方式找到新穎之水解酶基因。

關鍵語：瘤胃、微生物、多樣性

Rumen is a special, complicated, and anaerobic environment consisting of different microorganisms such as bacteria, archaea, fungi, and protozoa, and 85% to 95% of these

microbes are very hard to cultivate individually and artificially. In this study, the pH value of the rumen fluid from dairy cow was about 6.8. Protozoa and Gram positive and negative bacteria were found under microscopic investigation. The microbial DNAs of rumen samples were extracted directly using a commercial kit. Further, the small subunit ribosomal RNA genes of bacteria and fungi were amplified with bacterial and fungal specific sets of primers by PCR, respectively. Then the amplicons were ligated into TA cloning vector for DNA sequencing and microbial diversity analyses. The results indicated that 51 of 52 clones were classified as uncultured or unidentified bacteria in bacterial diversity analysis and only one was *Fibrobacter succinogenes* (identities: 96%). And they belonged to bacterial phyla of Bacteroidetes (32/52), Fibrobacteres (1/52), Firmicutes, and unclassified Bacteria (1/52). In fungal diversity analysis, 74 of 75 clones were identified as *Neocallimastix* sp. and only one as *Trichosporon jirovecii*. Based upon the results above, the bacterial diversity of rumen was more abundant than that of fungi. Therefore, it is possible to discover some novel hydrolase genes from such a sample through metagenomic approach.

Key Words: Rumen, Microorganism, Diversity

努比亞山羊黏多醣症(G6S)基因致死效應之驗證

61. 努比亞山羊黏多醣症(G6S)基因致死效應之驗證

林德育 陳坤照 張溪泉 王炳煌 黃鈺嘉 吳明哲
行政院農業委員會畜產試驗所

山羊黏多醣症(G6S)為努比亞山羊之一重要遺傳缺陷，它是由於乙醯醯胺氨基硫酸³⁷²³⁸基因單點核³³⁵²⁷酸突變所導致的隱性遺傳之代謝異常疾病。為驗證此不良基因對努比亞山羊生產之影響，選用1頭帶有山羊黏多醣症基因雜合型的公羊與配12頭雜合型母羊，經配種繁殖後有8頭母羊受孕，共產出17頭仔羊，受孕率。所有仔羊經G6S基因型檢測結果，有6頭為正常型(TG)、7頭為雜合型(CG)，4頭為有病型(G6S)。有病型仔羊育生長至2月齡前即有75%(3/4)頭死亡，顯示山羊黏多醣症確實會造成仔羊生長早期死亡，而影響仔羊育成率。

關鍵語：努比亞山羊、山羊黏多醣症、致死效應。

AN EXPERIMENTAL INVESTIGATION ON lethal effect of CAPRINE MUCOPOLYSACCHARIDOSIS IIID Gene in Nubian GOAT

D. Y. Lin, K. J. Chen, H. C. Chang, P. H. Wang, Y. C. Huang and M. C. Wu
Livestock Research Institute, Council of Agriculture, Executive Yuan

Caprine Mucopolysaccharidosis IIID is an important inherited deficiency in Nubian goat. It was caused by a point mutation of N-acetylglucosamine 6-sulfatase(G6S) gene. To verified the caprine mucopolysaccharidosis IIID gene effect on surviving rate of Nubian kids, one heterozygote buck of G6S were mated with 12 heterozygote nanny goats in mating season. Eight nannies were pregnant and produced seventeen kids. The pregnant rate and kidding rate were 67%(8/12) and 213%(17/8), respectively. All of these kids were

genotyped for G6S. Six kids are normal (TG, test free of G6S), 7 kids are heterozygote (GC, G6S carrier) and 4 kids are affected (G6S). Three of the four affected kids died within two months after birth. Results showed that caprine mucopolysaccharidosis IIID could cause kid died at early stage, and affected the rearing rate of kids.

Key Words: Nubian goat, Caprine Mucopolysaccharidosis, Lethal effect

利用累加性親屬係數圖形以探掘族群中的重要種畜禽

63. 利用累加性親屬係數圖形以探掘族群中的重要種畜禽

黃鈺嘉、顏念慈、鍾秀枝、廖仁寶、吳明哲
行政院農業委員會畜產試驗所

利用陣列形態呈現的累加性親屬係數，除可用於行列運算、轉置或分割為不同群組的子矩陣等多形態之資訊整理外，尚可藉由圖形形態呈現親屬關係矩陣，以展示個體彼此間的複雜關係，並於座標軸中對有興趣的個體標以性別、基因型及親代來源等不同的遺傳資訊。因此，開發不同類型的累加性親屬係數圖形可以協助探掘重要的個體。遺傳學的研究與育種計畫的執行常需數個世代之龐大系譜資料。然而，迄今面對龐大的不同群組之系譜資料，可用於協助找尋重要種畜禽之有效率的工具仍然十分有限。試驗取自不同世代(出生時間區段)的133選育個體系譜，依世代別分割為累加性親屬係數矩陣，繪製親屬關係矩陣圖形，再經子矩陣的行、列加總，繪製加總共親條型圖，可以有效地協助找出不同世代中對現有族群較具影響力的重要祖先，並探討不同世代間的共親關係，如重要共同祖先。由繪製的累加性親屬係數圖形可提供進階遺傳研究或選育方向的修正參考。

關鍵語：圖形、累加性親屬係數、親屬關係

PLOT ADDITIVE RELATIONSHIPS BETWEEN ANIMALS TO DETECT THE RELEVANT IMPORTANT INDIVIDUALS IN GROUPS

Y. C. Huang, N. T. Yen, H. C. Chung, R. B. Liaw and M. C. Wu
Livestock Research Institute, Council of Agriculture, Executive Yuan

The additive relationship matrix can produce useful information after matrix operations, such as addition, multiplication, transposition and partition, and can help in detecting the relevant important individuals in different groups. The new developed kinship matrix chart with statistics can simplify the complex relations between animals. Gender, genotype or parents' ID were marked along axis for the selected individuals. Due to genetic study or breeding program requires large numbers of individuals. The useful pedigree analysis tools for large pedigree are very limited. Graphics derived from the additive relationship matrix can provide as a new tool for genetic researchers. In this study, additive relationship matrix of 133 animals are partitioned by generations. One generation is classed as one group. Graphics show partitioned kinship matrix by groups. The histogram of row summation of the sub-matrix can help in detecting the important common ancestors. The distinct coancestry information from graphics of additive relationship matrix is useful for adjusting the further genetic practices.

Key Words: Graphs, additive relationship, Kinship

台灣家畜禽育種知識資料庫整合與應用

73.台灣家畜禽育種知識資料庫整合與應用

賴永裕 李世昌 翁書穎 蔡秀容 黃鈺嘉 吳明哲
行政院農業委員會畜產試驗所

台灣畜產種原知識庫 agrkb.angrin.tlri.gov.tw 採用新一代網站內容管理XOOPS (eXtended Object-Oriented Portal System)系統透過PHP模組程式將資料儲存於資料庫供維護與管理之用，知識資料庫定期重建檢索，提高育種資料之利用效率。整理已建置於畜產種原資訊網內 www.angrin.tlri.gov.tw 之畜禽育種相關文件、畜產相關期刊及雜誌等資料，依其不同特性之知識資料種類分類整理，並完成文件物件化之架構與資料庫系統分析等工作，將蒐集的畜禽育種相關文件，依知識資料種類的內容分類整理與建立電子檔案，並完成知識資料交換、排序、搜尋與重新輸出各式文件或報表。共計7大項分類中有18種專輯、9種雜誌、20種書刊及手冊、8種法規、13種會議資料、6種多媒體、27種其他資料等次分類。本知識資料庫是一個高度可擴充、具物件導向，導入知識管理為核心，經由網路的連結，使用者可以迅速、便捷的獲取家畜育種資訊，提高育種資料之利用效率。

關鍵語：資料庫、網路、育種

KNOWLEDGE DATABASE FOR ANIMAL BREEDING IN TAIWAN

Y. Y. Lai, S. C. Lee, S. Y. Weng, S. R. Tsai, Y. C. Huang and M. C. Wu
Livestock Research Institute, Council of Agriculture

Based on the XOOPS system (eXtensible Object Oriented Portal System project, a Discoverable Knowledge Database), agrkb.angrin.tlri.gov.tw, was developed for animal breeding in Taiwan. XOOPS uses a relational database to store data required for running a web-based content management system by PHP programming language which can effectively set-up and maintain a comprehensive website for working group. The database is re-indexed routinely; therefore users can approach the newest data efficiently. The established knowledge data records were from documents of www.angrin.tlri.gov.tw. Documents were sorted, classified analysis and re-edited before integrated into the database. Seven categories were available now which included special albums (18 books), magazine (9 kinds), digital books (20 books), rules(8 items),meeting documents(13 sorts),multimedia (6 groups) and breeding research reports. The developed AGRKB system is an extensible, object oriented, and easy to use dynamic web content management system. Farmers or general public can search the data or knowledge at farm/home by the on-line browse system. Efficient data and knowledge gathering and utilization will not only profit livestock producers but also can cumulate a heritage property for people of Taiwan, Republic of China.

Key words: Database, World web, Breeding

台灣土雞粒線體DNA全長定序及變異分析

75. 台灣土雞粒線體DNA全長定序及變異分析

林德育(1) 楊琇雅(1) 江家豐(1) 黃文瑛(1) 鍾秀枝(1) 張秀鑾(2) 吳明哲(1)

(1)行政院農業委員會畜產試驗所 (2)國立屏東科技大學畜產學系

為建立台灣土雞粒線體DNA遺傳資訊，已完成16個台灣土雞品系(包括12個選育品系與4個保種品系)之雞隻粒線體DNA全長定序(16,785-16,788 bp)。經DNA序列比對分析發現共有56個變異位點，其中有30個變異位點發生在11個蛋白質編碼基因中，產生的12個非同義置換與18個同義置換的位點；6個單點突變的位點發生在轉運RNA(tRNA)；1個單點突變發生在12S 核糖體核酸(rRNA)；14個單點突變的位點發生在D-loop調控區域以及2個單點突變與3個插入或缺失的位點發生在16S rRNA。粒線體DNA已普遍應用在物種鑑別、演化、保育及疾病的研究，這些資料除了可作為台灣土雞進行保種與選育的參考外，更可結合核內DNA提供新的動物模式之重要資訊。

關鍵語：土雞、粒線體DNA、序列變異

Complete Sequences of Mitochondrial DNA of Taiwan Native chicken

D. Y. Lin(1), H. Y. Yang(1), C. F. Chiang(1), W. Y. Huang(1), H. C. Chung(1), H. L. Chang(2) and M. C. Wu(1)

(1)Livestock Research Institute, Council of Agriculture, Executive Yuan

(2)Department of Animal Science, National Pingtung University of Science and Technology

In order to explore the mitochondrial DNA information of Taiwan native chicken, we sequenced the entire mitochondrial genomes (16,785-16,788 bp) from sixteen lines of indigenous chicken included twelve selection lines and four conservation lines. A total of fifty-six variant sites were found. Thirty variant sites includes twelve non-synonymous substitutions and eighteen synonymous substitutions in eleven protein coding genes. There were six single nucleotide polymorphisms (SNPs) within the transfer RNA (tRNA) and one SNP in the 12S ribosomal RNA (rRNA) and fourteen single nucleotide polymorphisms in the D-loop. In 16S rRNA, two SNPs and three insertions/deletions were detected. Mitochondrial genome has been widely used for study of species identification, evolution, conservation and disease researches. The integrated Mitochondrial genome data of Taiwan native chicken will be informative in future breeding and conservation studies. These data may also combine with other information from nuclear genomes to create the new animal models.

Key Words: Native chicken, Mitochondrial DNA, Sequence variation

天鵝乳牛產乳性狀與繁殖性狀之選拔

77. 天鵝乳牛產乳性狀與繁殖性狀之選拔

吳明哲(1)、黃鈺嘉(1)、張菊犁(1)、李素珍(1)、曾青雲(1)、陳志毅(1)、陳榮泰(2)

(1)行政院農業委員會畜產試驗所 (2)中華民國乳業協會

天噸乳牛是指一頭泌乳牛在台灣濕熱氣候下，自開始測乳後的平均每一個泌乳期(305-2X-ME)就能夠生產牛奶超過10,000公斤以上的乳量，亦就是年產乳量有10公噸以上，10公噸的英文是Ten Tons，取其音取其義，我們稱這種乳牛為天噸乳牛(Ten Tons Cow)。台灣乳牛育種策略上，期望以乳量、乳質及繁殖性狀兼顧的選拔為主，來培育台灣乳牛具有適應濕熱環境的特色，成為熱帶品系，並出口東南亞國家。自2001年完檢的天噸乳牛頭數32頭(僅為該年28,381頭測乳牛之0.1%)，增加至2002年的103頭，至2003年的146頭，至2004年的254頭，至2005年的312頭(為該年37,820頭測乳牛之0.8%)，五年來，天噸乳牛頭數成長率達9倍(312/32)。從2001至2005年完檢的天噸乳牛月齡平均分別為52、57、50、56、55月；乳量育種價分別為+1113、+988、+1051、+960、+949 kg；脂肪量育種價分別為+41、+32、+40、+34、+35 kg。2006年測乳中的33,064頭牛有1,135頭(佔3.4%)天噸乳牛，其乳量育種價為+894 kg及脂肪量育種價為+33 kg，分散在150戶(佔測乳戶293戶之51.2%)；其中擁有10頭以上的戶數有40戶(佔測乳戶293戶之13.7%)，合計有797頭，佔70.22%。再分析2006年測乳達12公噸以上乳量的牛隻有44頭，其平均月齡為44月，平均測乳次數12次(等同於第二胎)；其中有8頭是三胎以上的牛。因此，應用超高乳量的天噸乳牛來進行乳量、乳質及繁殖性狀兼顧的選拔，將有利於牛群性能之改進。

關鍵語：乳牛、選育、乳量

SELECTION ON REPRODUCTIVE PERFORMANCE ASSOCIATED WITH MILK YIELD OF TEN TONS COW

M. C. Wu(1), Y. C. Huang(1), C. L. Chang(1), S. J. Lee(1), C. Y. Tseng(1), J. Y. Chen(1) and L. T. Chen(2)

(1)Livestock Research Institute, Council of Agriculture, Executive Yuan; (2)Dairy Association of ROC

Ten Tons Cow is designated as milk yield of 305-2X-ME greater than 10,000 kg for hot and humid environment in Taiwan. For breeding scheme of dairy cattle, selection on milk yield and quality associated with reproductive performance is essential to the hot and humid weather, and therefore selected cows will become a heat-tolerance line for exportation to Southeast Asia. In 2001, there were 32 test-off Ten Tons Cow (0.1% to 28,381 cows for milk test), and then number of cows up to 103 head in 2002, 146 head in 2003, 254 head in 2004, and 312 head (0.8% to 37,820 cows for milk test) in 2005. An increment of 9 times (312/32) for the number of ten tons cows for the past five years. From 2001 to 2005, age of test-off Ten Tons Cow were 52, 57, 50, 56, and 55 months old, respectively; along with breeding value on milk yield (BVM) of +1113, +988, +1051, +960, +949 kg; and on fat yield (BVF) of +41, +32, +40, +34, +35 kg, respectively. In 2006, there were 1,135 head of Ten Tons Cow (3.4% to 33,064 cows for milk test) with BVM of +894 kg and BVF of +33 kg. Those of Ten Tons Cow were raised in 150 farms (51.2% to 293 testing farms) and among of 40 farms (40/293=13.7%) having more than 10 cows with a total of 797 head (70.22% to 1135 head). A total of 44 cows was selected with more than 12-tons milk yield with a mean of 44 months of age after 12 times of milk test in average, based upon number of milk test equivalent to their second lactation, in 2006. Among of them, 8 out of 44 had more than three lactations. In conclusion, application of milk yield and quality associated with reproductive performance would be feasible to improve herd performance in dairy cattle.

Key Words: Dairy cattle, Selection, Milk yield

畜試土雞近親品系九與來亨雞正反雜交後裔之生長與繁殖性能

88. 畜試土雞近親品系九與來亨雞正反雜交後裔之生長與繁殖性能

鍾秀枝(1)、林德育(1)、黃祥吉(1)、林義福(1)、張秀鑾(2)、吳明哲(1)

行政院農業委員會畜產試驗所(1) 國立屏東科技大學(2)

為建立土雞基因定位研究之參考族群，利用畜試土雞近親品系九(L9)與來亨雞(P)進行正反雜交產生雜交一代後，在以全同胞配種生產雜交二代，雜交組合為P9(來亨雞P × L9)與9P(L9 × 來亨雞P)。比較不同雜交組合之雜交一代與雜交二代雞隻之生長與繁殖性能之表現。結果顯示雜交一代之9P達16週齡之體重雄雞與雌雞皆較P9重(P

關鍵語：畜試土雞、來亨雞、雜交

In order to set up reference family for gene mapping, the F1 hybrid progenies were produced from reciprocal crosses between LRI native chicken inbred line 9(L9) and Leghorn(P), and F2 were produced by F1 full-sib mating. The hybrid P9 was produced by L9 hen mated with P cock, and 9P was produced by P hen mated with L9 cock. The growth and reproduction traits of F1 and F2 from different mating designs were examined. Results showed the body weights at 16 weeks of 9P were heavier than P9 in both genders of F1, and the cockerels of 9P are also heavier than those of P9 (P

key Words: LRI Native Chicken, Leghorn, hybrid

種豬飼料效率遺傳標記選拔族群建立

97. 種豬飼料效率遺傳標記選拔族群建立

顏念慈(1)、陳裕琪(1)、楊琇雅(1)、朱賢斌(1)、陳佳萱(1)、張秀鑾(2)、陳坤照(1)、吳明哲(1)

行政院農業委員會畜產試驗所(1) 國立屏東科技大學(2)

台灣豬隻飼料原料大多仰賴進口，故長期以來豬隻飼料效率被列為種豬群生長性能選拔的重要性狀之一。遺傳標記輔助選拔技術的應用，可加速豬飼料效率性狀之改良。選留中央檢定站北站92-2期飼料效率第一名之藍瑞斯公豬，藍瑞斯女豬選留具飼料效率多樣性之臉豬群；飼料效率較差之賓朗豬則選留一公及四母為飼料效率遺傳標記選拔豬。源自中央檢定站瑞斯公豬L727-11飼料效率為1.48，試驗場之藍瑞斯族群飼料效率平均為2.7，選留藍瑞斯女豬飼料效率分布範圍介於2.26~3.22間，而賓朗豬平均飼料效率為3.6。所有參試種公與母豬之緊迫基因皆為CC正常型、多產基因僅少數為B產型，而肉質基因之組點基因型則為LL2，HL3與HL4基因型。此外，進行50組分布於各染色體之微衛星型遺傳標記的檢測；基定位出豬飼料效率基因，並進一步開發相關重要基因標記供豬種改良用。

關鍵語：飼料效率、遺傳標記、豬

CONSTRUCTION OF REFERENCE POPULATION FOR MAPPING FEED EFFICIENCY RELATED GENE(S) IN PIG

In taiwan, most of feed ingredients for pig production are imported and thus feed efficiency (FE) is one of the most important traits in swine selection program. The marker-assisted selection (MAS) not only provides an opportunity but also accelerates the

genetic progress of FE in pig production. To map the feed efficiency related gene(s), Landrace and Peinan breeds were used to establish the reference population. Landrace boar, ear notch being 727-11, with the best feed efficiency (FE=1.48) among pigs tested in the 92-2 term at the north central test station was selected and served as founder sire. Furthermore, the average and range of FE in Landrace gilts used in founder population were 2.7 and 2.26~3.22, respectively. for reciprocal cross purpose, one Peinan boar and for Peinan gilts were used in the study. Peinan pigs had poor FE as usual with the average FE being 3.6. All the founder animals were stress free (CC type), but only few pigs with BB genotype was observed when estrogen receptor was genotyped. The combined genotypes of heart fatty acid binding protein found in founders were LL2, HL3 and HL4. In addition, fifty microsatellites spread around 19 pairs of chromosomes were also screened for FE related gene mapping and exploration of the important flanking marker(s) for breeding program.

Key Words: Feed efficiency, Genetic marker, Swine