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豐輝牧場紅羽土雞選育族群母雞產蛋性能檢定

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豐輝牧場紅羽土雞選育族群母雞產蛋性能檢定

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為了解豐輝牧場紅羽土雞選育族群之產蛋性能，分析該族群 G8 世代候選種母雞之產第 1 個蛋的日齡、達 280 日齡之產蛋紀錄，A 品系、B 品系及 C 品系分別有 68 隻、50 隻及 168 隻母雞，共 266 隻。母雞產第 1 枚蛋的日齡從 150 日齡到 210 日齡，母雞產第 1 枚蛋的平均日齡為 185 ± 13 天；母雞達 280 日齡產蛋數最少為 22 枚，最多可達 125 枚，母雞達 280 日齡平均產蛋數與平均產蛋率為 70.2 ± 18.0 枚與 $73.6 \pm 15.4\%$ 。不同品系母雞產第 1 枚蛋的日齡與達 280 日齡產蛋數在品系間存在極顯著差異 (P

關鍵語：紅羽土雞、產蛋性能、檢定

Egg production performance test of red feather native chickens in Feng Hui breeding farm

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To understand the egg production performance of red feather chickens in Feng Hui breeding farm. Totally, 266 hens from 3 lines of current selection breeding flock including 68 hens of A line, 168 hens of C line and 50 hens of E line were carried out the age at first egg (AFE) and egg number up to 280 days of age (EN280) test. The AFE of hens was ranged from 150 to 210 days, and the average AFE of hens was 185 ± 13 days. The EN280 of hens was ranged from 22 to 125 eggs, and the average EN280 and egg production rate of hens were 70.2 ± 18.0 eggs and $73.6 \pm 15.4\%$, respectively. There were significant differences in the age at first egg(AFE) and egg number up to 40 weeks of age (EN40) were detected among the three lines (P

Key Words: Red feather native chicken, Egg production performance, Test

乳牛完全混合日糧飼料配方線性規劃系統 (LTMR)之研發

乳牛完全混合日糧飼料配方線性規劃系統 (LTMR)之研發

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應用電腦網路系統提供酪農進行乳牛營養配方試算，有利於乳牛群日糧平衡之精準管理，是酪農在牛群經營實務上重要的工具。新竹分所本著提昇產業生產技能，發展優質畜產生產資訊服務系統的原則，擴增原有「台灣乳牛雲端資訊 (TDC) 服務網」(網址：www.tlrihc.gov.tw) 網頁功能內容，開發「乳牛完全混合日糧飼料配方線性規劃系統」(簡稱：LTMR 系統)

(<http://tmrsite.com.salal.arvixe.com/>)，系統內容包含「簡易版」、「教學」、「乳牛」、「原料」及「配方」等 5 項模組，使用流程是酪農先依據牛群產能狀況，進入「乳牛」功能選項，將牛隻性能設定適當分群作為配方計算之前置檔案，再以系統新增或自建原料等方式，建立屬於自己的原料資料庫，系統的原料關聯檔案係依據 NRC 乳牛營養需要量建議設計，內置達 72 種成分欄位，可供選擇的常用原料種類則內建有 226 種。在營養配方計算上，本系統提供 3 種配方試算 (1)「常用配方」選項，收集 25 種台灣酪農最常使用之飼糧配方，提供初學者進行套餐式選擇，作為乳牛場進行飼料配方調製之參考 (2)「最小成本配方試算」功能選項，採用線性規劃模式中之修正單純法 (Revised simplex method) 作為最小成本飼料配方規劃求解，兼顧乳牛營養需求與最小成本利益考量之平衡，適合乳牛場經營之精準管理 (3)「原料營養成份試算」選項，以營養需求為考量原則，對於選定的原料分別進行用量的設定後，由系統計算原料營養成分需求比例。

關鍵語：試算系統、乳牛、飼料配方

Online linear programming of total mixed ration (LTMR) for dairy cattle

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It was beneficial to precision management of the total mixed ration for dairy cattle, if the dairy farmer using network system to calculate the feed formulation of dairy cow, it was also an important tool in management of the dairy cows. In order to promote the production technology in dairy industry and develop high quality information service system for animal products in the Hsin-Chu Branch, Livestock Research Institute. A system of the 'Online linear programming of total mixed ration (LTMR) for dairy cattle' was developed in the dairy cloud information service in Taiwan (TDC) (<http://tmrsite.com.salal.arvixe.com/>) of the Hsin-Chu Branch, Livestock Research Institute website. There were five module included 'Easy version', 'Teaching', 'Dairy cow', 'Raw Material' and 'Formula' in the LTMR system. The process of apply was basic on the production performance of dairy cow to adapt grouping on the 'Dairy cow' functional options, then a front file was formed prior to calculate feed formula, then we could establish a raw material file by system increased or creation voluntarily manner. The raw material relation file was designed that basic on 'Nutrient Requirement Council' suggestion, there were 72 ingredient field included and 226 raw species available choice. The methods of the feed formulation calculator were available in this system (1) 'Common formula' - there were 25 species usually used feed formula for farmer in Taiwan, it could be as reference at feed modulation. (2) 'Floor coast feed formulation calculator' - The 'Revised simplex method' in the Linear program was used to plan solving, both nutrition demand of dairy cow and smallest coast benefit were balance considerable, that was suitable for precision management of cows for dairy farmer. (3) 'Raw nutrition calculator' - The nutrition demand was main considered in principle, we could set up variable raw apply quantity, then the nutrition demand ratio was calculated by computer.

Key Words: Calculator system, Dairy cow, Feed formula

種豬全胎檢定測重性狀生物機電模組之研發

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種豬全胎檢定工作係應用產業技術發展台灣種豬產業的重要精進策略之一，本研究著重於種豬全胎檢定測重性狀檢測機具之研發，期藉由自動傳輸功能精準收集全胎檢定資料，來探討雄親遺傳穩定度與整齊度之育種優勢。種豬全胎檢定生物機電模組係透過 Arduino Mega 2560 (核心機板)、PT580 Handheld Reader (手持讀取器)、Load Cell (荷重元件)與RTC (Real time clock,時間記錄器)等電子模組，取得種豬之耳號、體重、與時間等測量資料加以整合，顯示於LCD (液晶螢幕)上，並儲存於SD卡 (Secure Digital Memory Card,安全數位卡)中，當測重資料紀錄於SD卡後，即由機板內建動物重量管理程式，透過無線網路，快速上傳至畜產種原資料庫的對應儲存區，以利後續資料運算與應用。本模組與目前新型的德國BOSCHE (編號 101-001型)豬隻電子秤相較，兩者荷重元承重範圍同為100至300kg，均配備有30cm的液晶顯示器，然而模組還具有藍芽連線及無線傳輸功能模組，可支援雲端物聯資料庫傳輸應用，亦附加SD卡備援儲存及鍵盤輔助輸入等功能，價格僅約BOSCHE電子秤10萬元的1/3；另以Handheld Reader讀取豬隻134.2KHz電子耳標後進行資料儲存測試，最高儲存量可達7000張，實測讀取距離有效範圍為9至22cm，本模組可改善傳統人工紀錄費力耗時的缺點，有效提升種豬場管理者的工作效率。

關鍵語：種豬、全胎檢定、測重性狀

The development of the bio-mechatronic module for the weighting traits of swine litter test

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The breeding pigs litter test work was an important progress strategy for developing the industry breeding pigs by production technology. It was emphasized that development of tool module of weight tested for the full parity tested work of breeding pigs in this study. We could probe the stable degree of genetic and neat degree for boar by precision data collected from automatic transmission function. There were the Arduino Mega 2560 motherboard, the PT580 handheld reader, the load cell and the real time clock (RTC) chipset be included in the bio-mechatronic module for the weighting traits of breeding pigs litter test, when the ear tag of , body weight and time data be obtain, all of that data would displayed on LCD and the saved in SD card, then be transported to the "Animal Genetic Resources Information Network in Taiwan" website, it was favorable to application of data. Compared the Arduino module with the BOSCHE (101-001style) Electronic scales in Germany system, the same range of bear weight were 100 to 300kg and 30cm LCD attached , but this Arduino module still had Bluetooth connection and transmission automatically, the application of cloud database was supported, there were

backup and key in additional function, however the price of this Arduino module was 1/3 of the BOSCHE. We tested the save capacity of the Handheld Reader read 134.2KHz for the ear tag of breeding pigs, the effective range of reading distance was 9 to 22cm. The transitional artificial data recorded defect could be improve by using the Arduino module, and elevated work effectiveness of the Supervisor for management breeding pigs.

Key Words: Breeding pigs, Litter test, Weighting traits

自活性污泥篩選具脂解活性之細菌

自活性污泥篩選具脂解活性之細菌

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本研究目的為自畜產廢水處理設施中之活性污泥樣品，篩選能產生胞外脂解酵素的細菌，期能應用於生物產業。以傳統菌株分離篩選方式，將活性污泥樣品溶於無菌水中，序列稀釋後塗抹於選擇性培養基上，分別在 37 °C 與 55 °C 下過夜培養。在選擇性培養基上可發現一些藍色菌落與其周圍有透明圈，此為能產生胞外脂解酵素之菌株，進一步將此等菌株純化培養與冷凍保存。總共篩選出 9 株具脂解活性菌株，其中於 37 °C 培養條件下篩得 5 株；在 55 °C 培養條件下則篩得 4 株。進一步培養這 9 株菌，並萃取其 DNA 以進行分子鑑定。由 16S rRNA 基因序列分析得知，此 9 株菌中，5 株為 *Bacillus licheniformis*、2 株為 *Bacillus pumilus*、1 株為 *Bacillus subtilis* 及另 1 株為 *Bacillus mojavensis*。其中 *B. mojavensis* 為較特殊的菌株，將列為進一步研究的對象。

關鍵語：活性污泥、脂解活性、選擇性培養基

Isolation of lipolytic enzyme producing bacteria from activated sludge

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The purpose of this study was to screen for lipolytic enzyme producing bacteria from activated sludge samples of livestock wastewater treatment facility, and these isolates were expected for application in bioindustry. By conventional isolating protocol, the activated sludge samples were diluted in series in sterile water and smeared on selective media. The media were grown at 37 °C and 55 °C, respectively, overnight. Some isolates showed lipolytic activities with clear zones around their colonies on the selective media, and these isolates were purified and preserved in a freezer. A total of nine isolates were obtained, 5 isolates cultured at 37 °C and 4 isolates cultured at 55 °C. Furthermore, the nine isolates were cultured for DNA extraction and molecular identification. Based on the analysis of 16S rRNA gene sequences, 5 isolates were identified as *Bacillus licheniformis*, 2 isolates as *Bacillus pumilus*, others as *Bacillus subtilis* and *Bacillus mojavensis*, respectively. Because *B. mojavensis* was a special one among these isolates, it was the first target for future study.

Key Words: Activated sludge, Lipolytic activity, Selective medium

畜試紅豬夏季公豬精子體能表現

畜試紅豬夏季公豬精子體能表現

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公豬精液品質定期的鏡檢評估，可提前預測公豬精液的品質，以提高母豬受孕的機率。傳統精液品質評估的項目有精液濃度、精子活力、可生育精蟲百分比，以及異常精子型態等，但這些評估項目對於預測公豬生育力仍顯貧乏不足，並無法精準預測精蟲的表現。本試驗選擇3頭平均2歲齡R6代畜試紅豬針對臺灣夏季7~9月精子體能性狀進行檢測，試驗分析項目與結果分別為精液量 240.00 ± 66.55 、 182.50 ± 38.41 與 177.58 ± 61.71 毫升、平均精液濃度 3.93 ± 9.2 、 3.24 ± 8.89 與 3.43 ± 1.45 億/毫升、平均總精子數 897 ± 164 、 571 ± 133 與 608 ± 216 億、活精子 89.67 ± 4.30 、 85.52 ± 10.08 、 75.51 ± 22.00 %、活精子且頭帽完整性 76.85 ± 6.14 、 69.86 ± 14.37 與 60.64 ± 20.82 %、活精子中粒線體破損率 17.33 ± 2.79 、 21.81 ± 19.68 與 19.29 ± 13.86 % 與活精子中染色體完整 93.48 ± 2.05 、 96.23 ± 1.58 與 87.28 ± 27.37 %。畜試紅豬未飼養於水簾式豬舍，總體而言，精子體能表現優異，並未受夏季熱緊迫影響。

關鍵語：畜試紅豬、精子、夏季

Sperm quality of LRI Duroc boar in summer season

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An early prediction of semen quality by regular microscopic examination would help predicting donor sperm fertility ability thereby elevating the pregnancy rate of sows. It is not enough to accurately predict fertility ability of boar via the traditional semen assessment includes sperm concentration, vitality and morphology, and etc. Three R6 LRI Duroc boars at age of 2 years old (on average) were used in this study for assessment of semen quality in summer season (July, August, and September). All boars were not raised in wet pad and forced ventilation house. The results showed that respectively, in July, August and September, the semen volume was 240.00 ± 66.55 , 182.50 ± 38.41 and 177.58 ± 61.71 mL; average semen density was 3.93 ± 9.2 , 3.24 ± 8.89 , $3.43 \pm 1.45 \times 10^8$ /mL; average sperm count was 897 ± 164 , 571 ± 133 and $608 \pm 216 \times 10^8$; percentage of live sperm was 89.67 ± 4.30 , 85.52 ± 10.08 and 75.51 ± 22.00 %; percentage of live sperm with acrosome intact was 76.85 ± 6.14 , 69.86 ± 14.37 and 60.64 ± 20.82 %; percentage of mitochondrial status was 17.33 ± 2.79 , 21.81 ± 19.68 and 19.29 ± 13.86 %; and percentage of live sperm with normal structural chromosome was 93.48 ± 2.05 , 96.23 ± 1.58 and 87.28 ± 27.37 %. These finding demonstrated that sperm quality of LRI Duroc boar not only did not influenced by summer heat stress, but even at high quality.

Key Words: LRI Duroc Pig, Sperm, Summer

應用多源基因體學方法自乳牛瘤胃篩選脂解酵素基因

應用多源基因體學方法自乳牛瘤胃篩選脂解酵素基因

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本研究目的在建立乳牛瘤胃微生物多源基因庫，並以功能導向方式篩選脂解酵素基因。乳牛 瘤胃內容物以磁珠震盪方式萃取多源基因體 DNA，利用質體建構多源基因庫。結果篩選出 2 株具脂解活性的株系，經 DNA 定序、ORF 分析及序列比對後發現，此 2 株系的插入片段 具有 2 個完整脂解酵素基因 (LipoR1、LipoR2)。LipoR1 基因長 1,155 bp，可轉譯出 384-aa 蛋白質；LipoR2 基因長 960 bp，可轉譯出 319-aa 蛋白質。2 個預測的脂解酵素胺基酸序列 經與資料庫比對分析後，發現與現有蛋白質比對最高分數者之相同性百分比分別為 39% 與 86%。依據 Arpigny & Jaeger 之細菌脂解酵素分類，其中 LipoR1 屬於第一類，而 LipoR2 則 可能成為新的類別。

關鍵語：脂解酵素基因、多源基因體學、瘤胃

Use of metagenomic approach to screen for lipolytic genes from dairy cattle rumen

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The purpose of this study was to construct a metagenomic library from dairy cattle rumen microorganisms, and to screen for lipolytic genes using function-driven approach. The metagenomic DNA was extracted from dairy cattle rumen contents using bead-beating method. Then the metagenomic library was built with a plasmid system. As a result, two clones with lipolytic activity were obtained. By DNA sequencing, ORF finding, and sequence comparing, a total of 2 lipolytic genes (LipoR1 and LipoR2) were found. The lipoR1 gene was 1,155 bp, encoding 384-aa protein; the lipoR2 gene was 960 bp, encoding 319-aa protein. Both proteins showed 39% and 86% identity with the highest score to the closest in the protein database. Based on the lipolytic enzyme classification proposed by Arpigny & Jaeger, LipoR1 was affiliated to Family 1, and LipoR2 maybe belonged to the new family.

Key Words: Lipolytic gene, Metagenomics, Rumen

候選小公牛遺傳缺陷基因型分析

候選小公牛遺傳缺陷基因型分析

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本研究目的在探討候選小公牛常見遺傳缺陷基因型頻率，包括牛淋巴球黏力缺失症、瓜胺酸血症、單譜症、脊椎畸形複合症及短脊椎綜合症。本研究自全國種牛場收集 28 頭候選小公牛血樣，經 DNA 萃取與 5 項遺傳缺陷基因型檢測後發現，所有候選小公牛除 BS 基因型 有雜合型外，其餘 4 項遺傳缺陷基因型皆屬正常型，而 BS 雜合型的頻率則高達 10.71%。藉由篩除攜帶有不良遺傳缺陷基因的候選小公牛，將來可避免把此等公牛不良基因經由人工 授精而散布於乳牛族群中，造成產業之潛在損失。

關鍵語：遺傳缺陷、基因型、候選小公牛

Genotyping of genetic defects for young bull candidates

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This study was conducted to genotype frequencies of bovine genetic defects, including Bovine Leukocyte Adhesion Deficiency (BLAD), Deficiency of Uridine Monophosphate Synthase (DUMPS), Citrullinemia (CITL), Complex Vertebral Malformation (CVM), and Brachyspina Syndrome (BS), for young bull candidates. A total of 28 blood samples of young bull candidates were obtained from breeding farms in Taiwan. The cattle DNA was extracted and tested for 5 genetic defects. The results showed that all the genotypes except BS were normal, and the BS carrier frequency was as high as 10.71%. Through eliminating those bulls with genetic defects the recessive lethal genes can be avoided transmitting to cattle population by AI with the semen produced from those defective bulls. Therefore, the potential financial loss due to genetic defects could be prevented for dairy industry.

Key Words: Genetic defect, Genotype, Young bull candidate

模擬選配結合進口乳牛冷凍精液挑選適配公牛之應用

模擬選配結合進口乳牛冷凍精液挑選適配公牛之應用

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應用台灣荷蘭乳牛模擬選配系統挑選適配公牛冷凍精液，作為乳牛性能遺傳改進或矯正配種，是DHI酪農戶的重要育種策略之一，從研究所獲得適配公牛群之遺傳性能資訊，可結合國內乳牛冷凍精液資料庫得知是否曾經進口等相關訊息。以DHI乳牛統一編號「99060201」為例，自台灣乳牛雲端資訊服務網（網址：www.tlri.gov.tw）的乳品質檢驗及近10個月乳量體細胞變化等數位報表得知，該乳牛為第4胎次，其近6次測乳平均305-2X-ME乳量（305MY）為 8362 ± 194 kg，體細胞分數（SCS）平均為 5.67 ± 0.94 分，屬於高產泌乳性能卻有潛在性乳房炎之困擾情形，若應用模擬選配系統，挑選SCS前20%及305MY前50%選拔強度的公牛等級，經電腦資料庫運算後，約有15,439頭適配公牛可供選擇，若再考量該乳牛體型中醫的角度（RA）性狀為低斜之因素，則曾進口之國家動物育種碼（NAAB）編號「007H008778」的公牛為可能適合的選擇，經連結公牛遺傳評估模組查詢，該公牛乳產量預測傳遞能力（PTAM）為352.9 kg，SCS為2.7分，RA之標準傳遞能力為-1.7%，顯示選擇該精液配種可對乳母牛後裔在305MY之同期場平均多增加352.9 kg，SCS下降2.7分，同時矯正低斜臀角之同期平均約1.7%的預估遺傳改進量，透過模擬選配系統的應用，有利乳牛場對不同牛隻性能表現採取相對應的育種措施。

關鍵語：模擬選配、冷凍精液、公牛

Application of mating simulation system by linking the imported frozen semen database for

selection of candidate dairy bulls

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It was important breeding strategy for dairy farmer by mating simulation system to choose adapted breeding bull and improve dairy production, these genetic information of the candidate dairy bulls from data editing would link the imported frozen semen database, then we could know more imported data. Took the DHI cow NO. of '99060201' for instance, which was the fourth lactation and the latest six tested milk data, the mean of the 305-2X-ME milk yield (305MY) was 8362 ± 194 kg and the somatic cell count score was 5.67 ± 0.94 , and the data source from 'Dairy cloud information service in Taiwan' web site (www.tlri.gov.tw). This dairy cow was likely some problem with high production milk yield with subclinical mastitis. If we used mating simulation system to choose 20% bull select intensity grade for the SCS and 50% for the MY, after the computer calculation, there were 15,439 bull were choose and we further assessed the cow with slope rump angle (RA), the '007H008778' bull of the NAAB code was considerable. We could find the 'Predicted Transmitting Abilities' for Milk yield (PTAM), the 'Predicted Transmitting Abilities' for SCS and the 'Standard Transmitting Abilities' for RA were 352.9 kg, 2.7 and -1.7% for this bull, respectively. That means we could predict the genetic improved volume were increase 352.9 kg, reduced 2.7 score for the SCS and then corrected 1.7% of the RA mean of same period for the offspring dairy cows, respectively. It was favorable for us to take corresponded breeding method for the different performance of dairy cattle by using the mating simulation system.

Key Words: Mating simulation, Frozen semen, Bull

豐輝牧場紅羽土雞選育族群近親係數分析

豐輝牧場紅羽土雞選育族群近親係數分析

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豐輝牧場紅羽土雞選育族群係該場為進行種原固定，於 2010 年從原有紅羽土雞族群中以每個品系 1 公 40 母進行人工授精系譜繁殖來更新下一代所建立之 4 個品系的閉鎖族群。選育過程中 B 品系與 D 品系因外觀與性能表現不佳分別於 2012 年與 2013 年與予全數淘汰。2014 年再從自家紅羽土雞族群中選留一批種雞建立 E 品系，同時引進 C 品系純系 31 隻母雞進入選育族群中。為瞭解該族群經 9 個世代選育後之各世代雞隻之近親係數，以 SAS 統計分析軟體來分析 2010 年至 2016 年的 13,690 筆雞隻系譜資料，其中 A 品系、C 品系及 E 品系分別有 4,453 筆、5,782 筆及 3,454 筆。A 個品系與 C 品系選育族群雞隻於 G2、G3、G4、G5、G6、G7、G8、G9 世代之近親係數平均與標準差分別為 0.1367 ± 0.0106 與 0.1391 ± 0.0396 、 0.2229 ± 0.0367 與 0.2213 ± 0.0927 、 0.3096 ± 0.0118 與 0.3121 ± 0.0220 、 0.3471 ± 0.0474 與 0.3857 ± 0.0154 、 0.4175 ± 0.0123 與 0.4517 ± 0.0515 、 0.4801 ± 0.0106 與 0.5142 ± 0.2482 、 0.5370 ± 0.0113 與 0.1974 ± 0.2482 及

0.5842 ± 0.0171 與 0.2735 ± 0.0243。E 品系選育族群雞隻於 G2、G3 及 G4 世代之近親係數平均與標準差分別為 0.1250 ± 0.0178、0.1250 ± 0 及 0.2496 ± 0.0235。目前選育族群 2,331 隻雞隻之近親係數為 0.3755 ± 0.1536。以半同胞配種進行種原固定，C 品系選育族群 G7 世代雞隻與 A 品系選育族群 G8 世代雞隻之平均近親係數皆達 0.5 以上。

關鍵語：近親係數、紅羽土雞、選育

Inbreeding coefficients of red feather native chicken selection flock in Feng Hui breeding farm

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Feng Hui red feather native chicken selection flock was established from the original flock. One roaster mating 40 hens per line to breeding next generation by AI pedigree reproduction. There were four lines in the selection flock. The B line and D line were eliminated for appearance and performance consideration in 2012 and 2013, respectively. A new E line was established from the original flock and 31 hen from C line pure line expansion flock were added into C line selection flock in 2014. We analyzed 13,690 records pedigree data including 4,453 records of A line, 5,782 records of C line and 3,454 records of E line collected from 2010 to 2016 by SAS statistical software. It shows the inbreeding coefficients of G2, G3, G4, G5, G6, G7, G8 and G9 generations in A line and C line were 0.1367 ± 0.0106 and 0.1391 ± 0.0396, 0.2229 ± 0.0367 and 0.2213 ± 0.0927, 0.3096 ± 0.0118 and 0.3121 ± 0.0220, 0.3471 ± 0.0474 and 0.3857 ± 0.0154, 0.4175 ± 0.0123 and 0.4517 ± 0.0515, 0.4801 ± 0.0106 and 0.5142 ± 0.2482, 0.5370 ± 0.0113 and 0.1974 ± 0.2482, and 0.5842 ± 0.0171 and 0.2735 ± 0.0243, respectively. The inbreeding coefficients of G2, G3 and G4 generations in E line were 0.1250 ± 0.0178, 0.1250 ± 0 and 0.2496 ± 0.0235. The inbreeding coefficient of current flock with 2,331 birds was 0.3755 ± 0.1536. Results showed the inbreeding coefficients of G7 in C line and G8 in A line reached more than 0.5 in the selection flock.

Key Words: Inbreeding coefficient, Red feather native chicken, Selection

豐輝牧場紅羽土雞選育族群種蛋受精率與孵化率檢定

豐輝牧場紅羽土雞選育族群種蛋受精率與孵化率檢定

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為了解豐輝牧場紅羽土雞選育族群之種蛋受精率與孵化率，以該族群 G8 世代 3 個品系 152 隻 7 月齡種雞進行配種試驗。選用 54 隻 A 品系母雞、57 隻 C 品系母雞及 41 隻 E 品系母雞與同一品系 1 隻公雞以人工授精進行純品系配種，每 5 天進行人工授精一次，種蛋於配種後第 3 天開始收集，種蛋每天收集一次，置於 16-17 °C 貯蛋室。每收集 10 天的種蛋回溫後進行入孵一批，連續 3

批。入孵後第 8 天進行驗蛋，第 18 天移入發生機，第 21 天出雛。孵化機與發生機溫度分別為 100 與 99 。A、C 及 E 品系之平均種蛋受精率與 受精蛋孵化率分別為 92.8% (956/1,036)與 86.6% (828/956)、91.0% (1,238/1,360)與 79.1% (979/ 1,238)及 90.2% (753/835)與 76.4% (575/753)。選育族群 3 個批次所有種蛋之平均 種蛋受精率與受精蛋孵化率分別為 91.2% (2,947/3,231)與 80.8% (2,382/2,947)。比較種蛋 受精率與受精蛋孵化率在批次間皆無顯著差異 ($P > 0.05$)，種蛋受精率在品系間亦無顯著差 異 ($P = 0.088$)，然而受精蛋孵化率則在品系間存在 顯著差異 (P)

關鍵語：受精率、孵化率、紅羽土雞

Fertility and hatchability test of red feathered chicken selection flock in Feng Hui breeding farm

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To understand the fertility and hatchability of red feathered chickens selection flock in Feng Hui breeding farm. One hundred and fifty two hens including 54 hens of A line, 57 hens of C line and 41 hens of E line were used for fertility and hatchability test. All hens of each line were mated with 1 roaster of each line by pure line artificial insemination every 5-day. The hatching eggs were collected daily and stored at 16 for 10 days per batch before setting in incubator. Three continued batches of hatching eggs were carried out for this trial. The average fertility and hatchability of fertilized eggs were 92.8% (956/1,036) and 86.6% (828/956) in A line, 91.0% (1,238/1,360) and 79.1% (979/ 1,238) in C line, and 90.2% (753/835) and 76.4% (575/753) in E line, respectively. The average fertility and hatchability of fertilized eggs of all hatching eggs in this trial were 91.2% (2,947/3,231) and 80.8% (2,382/2,947). There were none significant differences in fertility and hatchability of fertilized eggs detected among the three batches and fertility detected among the three lines($P > 0.05$). However, There was significant difference in the hatchability of fertilized eggs detected among the three lines ($P > 0.05$). The hatchability of fertilized eggs of A line was better than that of E line. Result shows the average fertility of the selection flock reached more than 90%, and the hatchability of fertilized eggs of the selection flock could reach more than 80% in Feng Hui breeding farm.

Key Words: Fertility, Hatchability, Red feather native chicken

臺灣努比亞山羊腦下垂體特異性轉錄因子與鈣蛋白?抑制蛋白基因DNA 序列多態性分析

臺灣努比亞山羊腦下垂體特異性轉錄因子與鈣蛋白?抑制蛋白基因DNA 序列多態性分析

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本研究目的主要探討努比亞山羊腦下垂體特異性轉錄因子 (pituitary specific transcription

factor, POU1f1)與鈣蛋白抑制蛋白基因 (Calpastatin, CAST)DNA 序列多態性, 試驗設計兩組引子對可以增殖出 DNA 片段, 再應用兩組適當引子進行定序。將試驗所得 POU1f1 之序列與 GenBank 編號 DQ826413 序列比對, 結果發現 91 頭努比亞山羊之腦下垂體特異性轉錄因子基因位置 10-446 之序列共有 8 個位置發生變異, 在序列位置 18-19 有 CT 置換成 TC。在位置 45-370 之間與比對序列有 3 處位置不同, 在位置 48、102 及 365 處核酸分別有 T、G 及 T/G 型、G、T 及 G/T 型及 C、T 及 C/T 型。在位置 437-439 之間序列有 6 型序列。將試驗所得 CAST 之序列與 DQ414516 序列比對, 結果發現 (1)174 頭努比亞山羊 CAST 基因位置 1-254 之序列共有 18 個位置發生變異, 有 6 處同類置換, 其中全部山羊 CAST 基因位置 157 有 G-A 同類置換。(2)在序列位置 60 後有 5'-GT 2 bp 的重複序列 0-6 個。(3)在位置 63 有 T 與 G 及 T/G 型。綜合以上結果顯示努比亞山羊 POU1f1 與 CAST 基因 DNA 序列分析可產生較多之多態性, 可進一步應用於其經濟性能相關研究。

關鍵語：努比亞山羊、鈣蛋白抑制蛋白、腦下垂體特異性轉錄因子

Sequence polymorphism of pituitary specific transcription factor and calpastatin genes in Taiwan Nubian goat

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The aim of this study was to investigate the DNA sequence polymorphism of pituitary specific transcription factor (POU1f1) and Calpastatin (CAST) in Nubian goat. Two groups of primers were designed to amplify DNA fragments of Nubian goat and then applied two groups of appropriate primers to sequence. The sequence of POU1f1 was compared with the sequence of DQ826413 in GenBank. It was found that there were 8 site substitutions between positions 10-446 of the pituitary-specific transcription factor gene in 91 Nubian goats. And CT was replaced with TC at position 18-19. Three positions differed from the alignment sequence between positions 45-370. There were T, G, T/G; G, T, G/T and C, T, C/T nucleotide type at positions 48, 102 and 365, respectively. There were 6 sequence types at positions 437-439. The sequence of the CAST obtained was compared with the sequence of DQ414516, showed that (1) there were 18 site substitutions in the 254 bp fragment of CAST gene of 174 Nubian goats, six nucleotide variations were transition substitution, and position 157 of all goat CAST gene had G-A transition substitution. (2) There were 0-6 repeats of 5'-GT 2 bp after position 60. (3) At position 63, there were T, G and T / G nucleotide types. Based on the above results, it was found that the DNA sequence analysis of POU1f1 and CAST gene in Nubian goat could produce more polymorphism, which would be applied to Nubian goat economic performance related research.

Key Words: Calpastatin, Nubian goat, Pituitary specific transcription factor

生長性能檢定合格種豬之體型評級與XY 染色體之骨架基因關係研究

生長性能檢定合格種豬之體型評級與XY 染色體之骨架基因關係研究

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杜洛克(D)、藍瑞斯(L)及約克夏(Y)豬種於新化檢定站進行生長性能檢定至體重110Kg(母 100Kg)或160+7 日齡。本研究利用201101 期至201604 期等42 期檢定豬隻，總計4,713 頭血 樣，包括D 公2,482 頭、D 母201 頭、L 公1,154 頭、L 母313 頭、Y 公466 頭與Y 母97 頭。分析微衛星標記SY11(骨架基因)在X 染色體73cM 位置交替基因型，骨架基因之交替基因間 鹼基數長短(bp)依序有161~177bp 等9 個交替基因。品種及性別差異上，使用拍賣成交頭數 最多的兩種基因型(鹼基數)來標示，在D 公是175+0 及171+0、D 母是171+4 及175+0、L 公 是171+0 及167+0、L 母是167+4 及171+0、Y 公是171+0 及169+0 與Y 母是171+0 及169+2。不分性別，骨架基因的交替基因在D 品種以175、171 及167bp 居多；L 品種以171 及167bp 居多；Y 品種以171 及169bp 居多。每期檢定合格種豬經體型評級，取各品種各性別之體型 高大冠軍豬各一頭，總計204 頭。體型高大冠軍豬性染色體的骨架基因交替基因型在D、L、 Y 品種分別為175+0、171+0、171+0 居多，因此，應用基因條碼及體型資料作為品種內高大 體型選拔品系選育用，有利於高大型種豬經濟性狀基因標記建置及選種。

關鍵語：種豬、遺傳標記、體型評級

Association analysis of conformation contest to skeletal integrity gene on chromosome X and Y from purebred pigs under growth performance test

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Duroc (D), Yorkshire (Y) and Landrace (L) pigs were tested for growth performance at Hsinhua Station. The off-tested age was on the weight of 110kg (100kg for gilt) or by 160+7 days of age. A total of 4,713 pig blood samples was collected during the sum of 42 classes from class 201101 to class 201604, in which were 2,482 D boars, 201 D gilts, 1,154 L boars, 313 L gilts, 466 Y boars and 97 Y gilts. Genetic marker of SY11 on chromosome X located at 73cM was designated as the skeletal integrity gene. The variation of DNA fragment size of 9 fragments were 161~177bp with a 2bp difference in size. Analysis on allelic variants in various breed and gender by using a higher pig head sold in auction, there were 175+0 and 171+0 genotypes in D boars, 171+4 and 175+0 genotypes in D gilts, 171+0 and 167+0 genotypes in L boars, 167+4 and 171+0 genotypes in L gilts, 171+0 and 169+0 genotypes in Y boars, 171+0 and 169+2 genotypes in Y gilts. Major allelic variants of skeletal integrity gene regardless of gender were 175, 171 and 167bp in D, 171 and 167bp in L, and 171 and 169bp in Y, respectively. Conformation contest was carried out in each class to select objectively a champion of tall pig in each breed and each gender, hence, a total of 204 head of champion pig with a tall conformation was selected. The major allelic genotype for those of tall champion pigs were shown as 175+0, 171+0 and 171+0 in D, L and Y, respectively. Utilization of allelic variants of the skeletal integrity gene on sexual chromosome as gene barcodes with conformation data to select tall pig lines within breed, it could be beneficial to establish genomic databank on gene-linked economic trait for conformation selection of tall pig breeds.

Key Words: Breeding pig, Genetic marker, Conformation contest