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樂高模組化圖形應用於親屬關係之標示

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動物親屬關係之文字敘述表達困難，儲存個別的親屬關係圖時又需龐大的儲存空間或資料運算時間，為使親屬關係更簡易表達、快速讀取及網際網路化，本研究把兩代關係(雄—父，雌—父，雄—母，雌—母等四種)、三代關係(雄—祖父，雄—祖母，雄—外祖父，雄—外祖母，雌—祖父，雌—祖母，雌—外祖父，雌—外祖母等八種)、以及四代關係(雄—曾祖父，雄—曾祖母，雄—曾外祖父，雄—曾外祖母，雄—外曾祖父，雄—外曾祖母，雄—外曾外祖父，雄—外曾外祖母，雌—曾祖父，雌—曾祖母，雌—曾外祖父，雌—曾外祖母，雌—外曾祖父，雌—外曾祖母，雌—外曾外祖父，雌—外曾外祖母等十六種)，以樂高模組化圖形檔來表達個體與祖先的關係。應用方形圖表示雄性個體，圓形圖表示雌性個體。被查詢的兩個體以藍色圖形標示，其餘親屬個體標以綠色圖形。每個模組化圖形檔約為 1 K (1024位元組)大小。樂高模組化之親屬關係圖等28個圖形檔，目前已應用在畜產種原資訊網 www.angrin.tlri.gov.tw 的登錄種豬系譜查詢系統。網路網頁呈現種豬基本資訊外，藉助本研究模組化圖形的排序與堆疊，改善了系譜資訊表達的視覺效果。

關鍵語：樂高模組、系譜、網際網路

GRAPHIC LEGO MODULES APPLIED IN RELATIONSHIP BETWEEN RELATIVES

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Relative relationship described in words is not easy but also tedious in animal population, which requires identification of all relationship graphics among individuals involved and thus huge memory for storage and tremendous time are needed for graphic computation. In this study, male (M) and female (F) animals were represented in square and circle, respectively, in the graphic Lego modules. Graphic Lego modules used to represent parentage of M and F to its parents were M-Sire, M-Dam, F-Sire and F-Dam four modules. Following the rules for presentation, eight modules (M-SS, M-SD, M-DS, M-DD, F-SS, F-SD, F-DS and F-DD) were involved with SS and SD standing for grandsire and grandam of sire, respectively when three generations considered. Therefore, sixteen modules, M-SSS, M-SSD, M-SDS, M-SDD, M-DSS, M-DSD, M-DDS, M-DDD, F-SSS, F-SSD, F-SDS, F-SDD, F-DSS, F-DSD, F-DDS and F-DDD, were used in parentage identification involving four generations. The application of graphic Lego pedigree chart was not only useful in

transition of web information but also had benefits on easy reading and display in the Internet. Two inquired individuals were highlighted in blue color along with other relatives in green ones. In general, each Lego file of 28 pedigree Legos accounts for 1 Kb (1024 bytes) of storage size. The graphic Lego modules is currently applied to pedigree inquiring system of registered stocks for Formosa pigs which can be accessed in internet (http://www.angrin.tlri.gov.tw). On the web page, the browser presents the lineage data of the inquired pig with the corresponding graphic Lego modules in pedigree order. In addition, the visualization efficacy of pedigree inquiry can be significantly improved by Lego modules' stacking and sorting functions.

Key Words: Lego modules, Pedigree, Internet.

新引進美國盤克夏豬種之屠體性能

新引進美國盤克夏豬種之屠體性能

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美國盤克夏豬種於1996年被引種到台灣，進行純種繁殖，產下的第一代豬中，計有30頭公豬和50頭母豬被用來進行屠體分切。公母豬屠體重(含頭、皮、腳、尾及板油)分別為81.6±2.0和82.4±1.7kg；屠體長(第一肋骨前緣至恥骨前端的直線長)分別為77.8±1.1和80.8±0.9 cm；背脂厚度(剝皮後的第一肋、最後肋和最後腰椎處的背脂厚度平均)分別為2.69±0.07和2.50±0.06 cm；腹脂厚度(剝皮後的胸部肋骨後緣、肚臍和鼠蹊處腹脂厚度平均)分別為3.85±0.07和4.07±0.06 cm；第十肋腰眼面積分別為34.39±1.31和39.79±1.12㎝2；瘦肉量分別為42.22±1.22和45.16±1.04 kg；瘦肉率分別為52.48±0.63和55.10±0.54 %。同場同期台灣藍瑞斯、約克夏與杜洛克品種公豬之瘦肉率則分別為58.42±0.47 (N=42)、57.21±0.51 (N=36)和57.74±0.52% (N=29)；又前述三個品種母豬的瘦肉率分別為58.70±0.36 (N=81)、57.98±0.37 (N=72)和58.15±0.39% (N=62)。試驗結果發現美國盤克夏豬種的瘦肉率顯著地低於台灣藍瑞斯、約克夏與杜洛克品種。

關鍵語：豬、品種、屠體性狀。

CARCASS PERFORMANCE OF BERKSHIRE PIGS IMPORTED FROM USA

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American Berkshire pigs were imported in Taiwan for purebred production in 1996. F1 progeny was used to evaluate the carcass performance. Average carcass weights (containing head, skin, feet, tail and leaf fat) of 30 boars and 50 gilts were 81.6±2.0 and 82.4 ±1.7kg, respectively. The rest carcass traits for the males and females were as follows:

length measured on the chilled carcass from the fore edge of the first rib to the fore tip of the pubic bone being 77.8±1.1 and 80.8±0.9 cm; skinless backfat thickness (mean thickness measured at first rib, last rib and last lumbar vertebra) being 2.69±0.07 and 2.50±0.06 cm; skinless bellyfat thickness (mean thickness measured at sternum, belly button and groin) being 3.85±0.07 and 4.07±0.06 cm; loin muscle area measured at the tenth rib being 34.39±1.31 and 39.79±1.12cm2 , carcass lean meat being 42.22±1.22 and 45.16±1.04 kg; carcass lean percent being 52.48±0.63 and 55.10±0.54 %. However, when comparisons were made between breeds within herd, the carcass lean percents in Formosa Landrace, Yorkshire and Duroc boars were 58.42±0.47% (N=42), 57.21±0.51% (N=36) and 57.74±0.52% (N=29), respectively. Also, the corresponding trait in gilts were 58.70 ±0.36 (N=81), 57.98±0.37 (N=72) and 58.15±0.39% (N=62), respectively. Results showed that American Berkshire pigs had a lower carcass lean percent than those of Formosa Landrace, Yorkshire and Duroc breeds.

Key Words: Pig, Breed, Carcass trait.

盤克夏豬與藍瑞斯豬雜交一代之生長性能

盤克夏豬與藍瑞斯豬雜交一代之生長性能

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盤克夏豬種以肉質聞名，自美進口的盤克夏豬種之生長性能不及台灣育成的藍瑞斯、約克夏和杜洛克等豬種，因此考量做為雜交肉豬肉質改良用終端公豬。本研究以盤克夏(B)與藍瑞斯(L)豬種進行雜交，生產雜交一代LB (L母畜×B公畜)與BL (B母畜×L公畜)，雜交一代豬採固定日齡(自70日齡至150日齡)生長性能檢定。LB公豬5頭和女豬6頭於70、120、135 與150日齡之體重分別為 (31.8±4.6和27.8 ±4.4kg)、(69.0±9.2和58.8±8.3kg)、(89.0±11.9和75.8±8.1kg) 與 (104.4±14.4和89.3 ±8.2kg)。同時，150日齡活體超音波即時顯像掃瞄公豬和女豬之第十肋骨處腰眼面積與背脂厚度分別為(32.26±6.07和30.30±2.78cm2) 與 (1.61±0.24和1.39±0.30cm)，而公豬飼料效率則為2.81 ±0.18。又BL公豬8頭和女豬6頭於70、120、135 與150日齡之體重分別為 (28.9±3.0和30.1±2.7kg)、(79.9±5.4和77.3±5.0kg)、(93.3±5.0和90.5±6.6kg) 與 (110.3±8.4和105.0±7.0kg)；且150日齡活體超音波即時顯像掃瞄之第十肋骨處腰眼面積與背脂厚度分別為 (29.23±1.41和30.22 ±2.48cm2) 與 (1.41±0.17和1.38±0.26cm)。至於公豬飼料效率則為2.29±0.09。此外，同場同期純種藍瑞斯和盤克夏公豬之150日齡體重分別102.4±1.7和93.5±3.3公斤；而女豬則分別92.0±1.8和80.3±2.6公斤。試驗結果顯示：150日齡之B公豬顯著地重於同品種女豬，且雜交一代公豬與女豬的生長性能均具雜交優勢。

關鍵語：豬、雜交優勢、生長性能。

GROWTH PERFORMANCE OF F1 HYBRIDS BETWEEN BERKSHIRE AND LANDRACE BREEDS OF PIGS

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Berkshire (B) breed is in famous of meat quality among breeds of the pig. Berkshire pigs imported from USA did not perform well in growth performance when compared to those of Formosa Landrace (L), Yorkshire and Duroc breeds. Therefore, it is considered to serve as one of the terminal sire breeds for pork quality improvement purpose in hog production. In this study, F1 hybrid pigs, LB (L dam X B sire) and BL (B dam X L sire) from B and L crosses were produced and tested at fixed ages (from 70 to 150 days of age) for growth performance. The body weights of 5 boars and 6 gilts in LB cross at 70, 120, 135 and 150 days of age were 31.8±4.6 and 27.8±4.4kg, 69.0±9.2 and 58.8±8.3kg, 89.0±11.9 and 75.8±8.1kg, 104.4±14.4 and 89.3±8.2kg, respectively. Both loin muscle area and backfat thickness of live animals measured at the tenth rib using SSD-500 B-mode real-time ultrasound scanner for boars and gilts at 150 days of age were (32.26±6.07 and 30.30 ±2.78cm2) and (1.61±0.24 and 1.39±0.30cm), respectively. Feed efficiency of LB boars during tested period was 2.81±0.18. Also, body weights of 8 boars and 6 gilts in BL cross at the corresponding ages were 28.9±3.0 and 30.1±2.7kg, 79.9±5.4 and 77.3 ±5.0kg, 93.3±5.0 and 90.5±6.6kg, 110.3±8.4 and 105.0±7.0kg, respectively. And the corresponding loin muscle area and backfat thickness at the tenth rib for boars and gilts were (29.23±1.41 and 30.22±2.48cm2) and (1.41±0.17 and 1.38±0.26cm). Feed efficiency of BL boars was 2.29±0.09. Results indicated that boars weighed significantly heavier than gilts at 150 days of age in B breed. In addition, when comparison was made between breeds within herd for body weight at 150 days of age, both LB and BL boars showed significant heterosis with corresponding weights for L and B being 102.4±1.7kg and 93.5 ±3.3kg, respectively. Similar trend was also observed in F1 gilts.

Key Words: Pig, Heterosis, Growth performance.

種公豬性能檢定資料庫網際網路化之研究

種公豬性能檢定資料庫網際網路化之研究

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種豬場登錄豬的後裔公豬在位於台南新化的畜產試驗所檢定站進行生長性能檢定，自1989年9月起至1999年8月止完成40期公豬檢定，計有3796頭公豬參檢，完檢率為82.8%。1989年至1995年間檢定公豬之開檢體重為30公斤，而於1996年後因配合全國性豬瘟撲滅計畫，而改為40公斤開檢，且均以110公斤為完檢體重。公豬檢定期間之日增重、飼料效率及達110公斤體重的日齡和背脂厚度，以及依同期檢定平均計算離均差而評估之種豬選拔指數，均逐項予以網際網路化。該資料庫可查詢每一期之任何完檢豬資料，包括原場耳號、出生日期、同窩仔豬數、父畜登錄名號、母畜登錄名號、日增重、飼料效率、背脂厚度、選拔指數、送檢場及緊迫基因型等。歷年來檢定公豬達110kg體重之最小日齡在藍瑞斯、約克夏與杜洛克分別為128 (199905期)，134 (199609期)與131 (199905期)日齡。

關鍵語：資料庫、生長、全球資訊網。

DEVELOPMENT OF INTERNET-BASED DATABASE FOR GROWTH PERFORMANCE TESTED YOUNG BOARS

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Young boars with registered parent(s) were performance tested in Taiwan Livestock Research Institute, COA since September 1989. There were 40 contemporary groups finishing the growth performance tests in the station by August 1999. In total, there were 3796 boars in attendance, and 82.8% completed the tests. Starting weight was set around 30 kg during 1989 and 1995, and then increased to 40 kg in accordance with the requirements of national hog cholera free project since then. End weight was set as 110 kg during all testing periods mentioned. Average daily gain, feed efficiency and backfat thickness were recorded and evaluated as a contemporary group deviation form for selection index calculation purpose. Furthermore, all the informative information from original data and evaluated results were stored in an internet-based database. The performance tested data and related information can be inquired easily in anywhere of World Wide Web accessible. In addition, the economic important traits such as genotype of PSS, lineage information such as registration information, and performance of parents tested can be also hyper linked recursively through web. Minimum ages of tested boars at 110 kgbody weight were 128, 134 and 131 days of age in L (199905 tested group), Y (199609 tested group) and D (199905 tested group), respectively.

Key words: Database, Growth, World Wide Web.

豬肋骨數基因座定位於第一號染色體短臂上

豬肋骨數基因座定位於第一號染色體短臂上

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豬的脊椎分為頸椎、胸椎、腰椎、薦椎和尾椎，肋骨對數取決於胸椎數。本研究首先初步調查肉用豬種之肋骨數，發現逢機檢視之121頭肉用豬種之左右側肋骨數型式為14/14、14/15、15/14、15/15、15/16、16/15、16/16、16/17、17/16與17/17者分別佔有14.0、2.5、0.0、46.3、2.5、1.7、30.6、0.8、0.8和1.7%；故左右側肋骨數不等的豬隻佔8.3%（10/121）。因此，試驗係先檢視肉豬屠體的肋骨對數，若為14對肋骨或17對肋骨者，再取其肌肉樣材萃取DNA，共計取得肋骨對數為14對者39頭與

肋骨對數為17對者34頭。應用在第1號染色體上的SW373、SW705、SW1515、SW1514和ESR，以及第6號染色體上的Hal-1843和第8號染色體上的OPN等7個遺傳標記，鑑別具14對肋骨數與17對肋骨數者的基因型。經肋骨對數與個別遺傳標記基因型之卡方分析後，結果顯示肋骨對數與第1號染色體短臂上的ESR（P＜0.036）和SW1514（P＜0.023）有顯著的連鎖關係。根據已知的豬基因圖譜，初步推定豬肋骨數基因位於第1號染色體的短臂1p2.4-2.5區。

關鍵語：豬、肋骨數、基因定位。

THE RIB LOCUS MAPPED ON THE CHROMOSOME 1p IN PIG

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Vertebrae of pigs consist of cervical, thoracic, lumbar, sacral and coccygeal vertebra. Number of rib pairs depends on the number of thoracic vertebrae. In the preliminary study, 121 hog carcasses were randomly sampled and examined to count ribs in left and right sides. Percentages of pigs with 14/14, 14/15, 15/14, 15/15, 15/16, 16/15, 16/16, 16/17, 17/16 and 17/17 ribs in left and right side were 14.0, 2.5, 0.0, 46.3, 2.5, 1.7, 30.6, 0.8, 0.8 and 1.7%, respectively. Hence, there were 8.3%(10/121) pigs with an asymmetric number of ribs in left and right sides. In this study, only hogs with 14 or 17 pairs of symmetric number of ribs were muscles sampled and identified for genotypes. Muscle samples for DNA purification were then collected from 39 and 34 heads of carcasses with 14 and 17 pairs of ribs, respectively. SW373, SW705, SW1515, SW1514 and ESR on chromosome 1, Hal-1843 on chromosome 6, and OPN on chromosome 8, were used as genetic markers for genotyping. Chi-square statistics were then used to detect the relationship between the number of rib pairs (named as the rib locus) and alleles of seven marker loci used in this study Results indicated that the rib locus was associated with ESR (P＜0.036) and SW1514 (P＜0.023) markers. According to the linkage map established, the rib locus was then mapped on chromosome 1p2.4-2.5.

Key Words: Swine, Ribs, Gene mapping.

種豬多產基因之檢測

種豬多產基因之檢測

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種豬多產基因是指動情素接受器基因座的B對偶基因，而具BB型的母豬較AA型者每胎可多生1.5~2.3頭活仔豬。本研究利用A和B對偶基因的突變點差異，設計專一的引子，可直接由PCR產物來鑑別受檢個體

的基因型。本研究首先檢測多產品種梅山豬59頭，有94.9％(56/59)為BB型，其餘均為AB型。再檢測檢定站受檢的種公豬176頭，具BB、AB和AA型者分別為1.1、9.7和89.2％，絕大多數豬隻為AA型。依品種區分時，藍瑞斯和杜洛克均未有BB型者，而AB型者比率分別為13.6％(9/66)和3.4％(3/89)；但約克夏種則有9.5％(2/21)為BB型和23.8％(5/21)為AB型。而檢測民間種豬場在養種公豬235頭，藍瑞斯、約克夏和杜洛克種分別為24.2(24/99)、66.0(31/47)和5.6％(5/89)是具有B對偶基因者。檢測本所Hal-1843為CC型母豬群67頭中，母豬具BB、AB和AA型的比率分別為25.4、53.7和20.7％。整體而言，國內的約克夏種具有多產基因的頻率(66.0％)遠高於藍瑞斯種(24.2％)，而杜洛克種則僅有5.6％。篩檢具多產基因之種豬為目前協助民間豬場進行豬基選計畫之一項重點。

關鍵語：動情素接受器、基因型、品種。

DETECTION OF PROLIFICACY GENE IN PIGS

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The B allele in the estrogen receptor locus (ESR) is regarded as prolificacy gene in the study. Sows with BB genotype in ESR can produce 1.5~2.3 live piglets more per litter. The difference of mutation points between A and B alleles was used to design a specific primer which was then used directly to genotype tested animals via PCR. A total of 59 Meishan pigs were genotyped in the preliminary study and results showed 94.9％(56/59) pigs with BB genotype and the rests with AB genotype. The percentages of BB, AB and AA genotypes in 176 tested boars from Boar Test Station were 1.1, 9.7 and 89.2％, respectively. When comparison was made within breed, 13.6％(9/66) and 3.4％(3/89) tested boars with AB genotype were detected in Landrace (L) or Duroc (D) breeds, respectively but none of pigs with BB type was observed in the corresponding breeds. However, there were 9.5％(2/21) and 23.8％(5/21) of tested boars with BB and AB genotypes, respectively in Yorkshire (Y) breed. Also, when the technique was applied to 235 boars of private breeding farms for detection, results indicated that there were 24.2(24/99), 66.0(31/47) and 5.6％(5/89) boars with ESR B allele in L, Y and D breeds, respectively. Furthermore, results obtained from 67 sows of Hal-1843 CC-genotype herd in the institute showed that the frequencies of ESR-BB, -AB and -AA were 25.4, 53.7 and 20.7％, respectively in the stress-free herd. In general, the frequency of Y pigs with ESR-B allele (66.0％) was much high that of L pigs (24.2％), nevertheless the corresponding frequency was even lower in Duroc breed (5.6％). Therefore, identification of pigs with ESR B allele is one of major goals in marker assisted selection (MAS) program currently conducted in private breeding swine farms.

Key Words: Estrogen receptor, Genotype, Breed.

早熟母豬的女兒豬為早熟母豬的機率

早熟母豬的女兒豬為早熟母豬的機率

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在一歲齡前能產下女兒豬的母豬視為早熟母豬。本研究應用種豬登錄資料庫的種母豬資料，並設定母豬的出生年是在1994年以前者方納入本研究範圍。首先估算母豬產下女兒豬的年齡，並依該母豬分娩女兒豬時的年齡區分其所產女兒豬為'大女兒豬'或'小女兒豬'；意即該母豬在一歲齡以前產下的女兒豬為'大女兒豬'，而在四歲齡以後產下的女兒豬則為'小女兒豬'。隨後追蹤'大女兒豬'和'小女兒豬'產下第一頭孫女豬的年齡，依前述早熟母豬之定義，在一歲齡以前產下'大孫女豬'之女兒豬即視為早熟母豬。本研究計有12,160頭登錄為種母豬之孫女豬，其初產日齡最早者在藍瑞斯、約克夏和杜洛克品種分別為266、296和283天。分析結果發現三個品種中，早熟母豬的'大女兒豬'也是早熟母豬的機率，在藍瑞斯、約克夏和杜洛克種分別為7.38、4.41和9.19％；而'小女兒豬'是早熟母豬的機率則顯著地較低，分別為2.57、1.91和1.84％。不分品種比較時，'大女兒豬'和'小女兒豬'為早熟母豬的機率則分別為7.45和2.29％，顯示早熟母豬所產下的'大女兒豬'也是早熟母豬的機率為同母'小女兒豬'的三倍以上。因此，建議選留初產的女兒豬為種畜，應可縮短世代間距，加速選拔。

關鍵語：世代間距、品種、母性效應。

PROBABILITY OF EARLY MATURE DAUGHTER FROM EARLY MATURE DAM IN PIGS

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Sows with 1st daughter by one year of age were defined as early mature sows in this study. Data of registered sows born by 1994 was used for analysis. Ages of sow at daughters born were calculated and used to identify the groups of daughters. Gilt was classified in 'eldest daughter' group if age of corresponding dam was by one year of old when gilt was born. Again, gilt was classified in 'younger daughter' group if age of corresponding dam was above 4 years of old when gilt was born. The same definition was applied in identification of granddaughter groups. In total, there were 12,160 registered granddaughter sows with minimum ages at first littering being 266, 296 and 283 days of old in Landrace (L), Yorkshire (Y) and Duroc (D) breeds, respectively included in the study. Results showed that probabilities of 'eldest daughter' from early mature dam being early mature sow were 7.38, 4.41 and 9.19％in L, Y and D breeds, respectively. Nevertheless, the corresponding probabilities of 'younger daughter' from early mature sow were 2.57, 191 and 1.84％in L, Y and D breeds, respectively which were significantly lower than those observed in 'eldest daughter'. Furthermore, probabilities of the 'eldest' and 'younger' daughters from early mature sows being early mature ones were 7.45和2.29％, respectively which indicated that the probability of the 'eldest daughter' being early mature one was three times that observed in the corresponding maternal 'younger ' female sibs when comparison was made in pooled data with breed effects

negligence. In conclusion, it is suggested to select gilts from primiparous sows for replacement in order to shorten generation interval and thus to accelerate the genetic improvement in pig selection program.

Key Words: Generation interval, Breed, Maternal effect.

迷彩豬種採全同胞配種後之產仔數

迷彩豬種採全同胞配種後之產仔數

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迷彩豬種的仔豬身體兩側有白色橫條紋與紅棕色橫條紋交複排列型態之棕白條紋體色。本研究選用1998年出生的12公24母仔豬，育成後予以全同胞配種。母豬初產日齡介於280~456天，平均335±48天。初產之產仔總頭數為3至9頭(5.0±1.6頭)，活頭數為1至9頭(4.7±1.8頭)，以及三週齡離乳時活頭數平均為3.9±1.9頭，育成率為83.0%。初產母豬哺乳三週後的離乳體重為80.3±15.7kg。第二產與初產的胎距為155±12天，第二產產仔總頭數為5.3±1.8頭。仔豬出生重公的為1.04±0.22kg(N=53)，母的為1.05±0.25kg(N=54)。公母仔豬三週齡離乳體重分別為3.63±0.94kg(N=44)和3.36±0.91 kg(N=45)，五月齡體重亦分別為27.8±6.1kg(N=19)和24.1±6.1kg(N=22)。本研究顯示迷彩豬種雖經全同胞配種，其產仔數仍維持在5頭以上，且其仔豬生長正常，並未有近親衰退的現象。

關鍵語：豬、全同胞配種、產仔數。

LITTER SIZE IN MITSAI BREED OF PIGS BY FULL-SIB MATING

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Mitsai piglets exhibit coat color with several longitudinal stripes from head to tail, and the brown stripe appears to the white stripe side by side. There were 12 males and 24 females born in 1998 were used and mated by full-sib mating in the study. Gilts produced first litters during 280 and 456 days of age with average age being 335±48 days. Litter size at birth and born alive in first parity were 5.0±1.6 and 4.7±1.8 piglets with ranges from 3 to 9 and 1 to 9 piglets, respectively. Furthermore, litter size at weaned and survival rate at 3 weeks of age were 3.9±1.9 piglets and 83.0% , respectively, with body weight of weaning sows at first parity being 80.3±15.7kg. The farrowing interval between the first and second parities was 155±12 days. Litter size at birth in second parity was 5.3±1.8 piglets with birth weights being 1.04±0.22kg(N=53) and 1.05±0.25 kg(N=54) for males and females, respectively. Body weights at weaned and at 5 months of age were 3.63±0.94kg(N=44) and 27.8±6.1kg(N=19) for males, and 3.36±0.91kg(N=45) and

24.1±6.1kg(N=22) for females, respectively. Results showed that Mitsai sows produced more than 5 piglets per litter at birth and all piglets grew normally when full-sib mating was applied. Also, inbreeding depression due to full-sib mating did not observed in the study.

Key Words: Pig, Full-sib mating, Litter size.

蘭嶼豬GPI-PGD純合品系全同胞配種後之產仔數

蘭嶼豬GPI-PGD純合品系全同胞配種後之產仔數

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蘭嶼豬種GPI-PGD基因型純合品系於1992年建立，GPI和PGD分別為BB型和AA型。第零代的母豬之初產活仔數為4.22+1.02頭(45胎)，爾後採半同胞配種和兩個世代選拔後，14.1%之高近親係數並未影響到母豬的產仔數(3.78±1.13頭，37胎)。本研究利用這個半同胞配種選育的族群，進一步以全同胞配種方式來建立一個更高度近親的品系。因此，同一胎留一公兩母做為種畜。結果僅有16胎(16公32母)仔豬於五月齡被選留，這16個家族的全同胞豬隻分別併欄進行全同胞配種，直至女豬懷孕為止。除3頭女豬未產下活仔豬外，其餘的29頭女豬之產仔日齡平均為320±59天，範圍在243至479天不等。每胎活仔數之平均為3.34±1.34頭，有1至6頭不等。綜合言之，全同胞配種後的蘭嶼豬GPI-PGD純合品系之產仔數並未顯著地降低。

關鍵語：迷你豬、產仔數、近親選拔。

LITTER SIZE OF THE HOMOZYGOTIC GPI-PGD LINE IN LANYU BREED OF PIGS WITH FULL-SIB MATING

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The homozygotic GPI-PGD line of Lanyu breed of pigs was established in 1992 with genotypes of GPI-BB and PGD-AA. The founder sows had 4.22+1.02 piglets born alive at their first parity (N=45). Then, half-sib mating was applied for two generations. An inbreeding coefficient of 14.1% did not affect the litter size of selected gilts at the first parity (3.78+1.13, N=37). In the study, full-sib mating was applied on the half-sib mated population to establish a higher inbreeding line. Hence, one male and two female littermates were selected as stocks, however, there were only 16 litters being selected to form full-sib families (16 male and 32 female pigs) at five months of age. Each family of littermate pigs was raised together in a mating pen till gilts in pregnant. Three out of 32 gilts were no live piglets born. The most of gilts farrowed at 320+59 (N=29) days

of age with a range of 243 to 479 days. Number of piglet born alive per litter was 3.34+1.34 head with a range of 1 to 6 piglets. In conclusion, the number of piglet born alive per litter was not affected by the full-sib mating in the homozygotic GPI-PGD line of Lanyu pigs.

Key Words: Miniature pig, Litter size, Inbreeding selection.

總乳體細胞數分級與高體細胞數個體分隔集乳策略模擬

總乳體細胞數分級與高體細胞數個體分隔集乳策略模擬

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本試驗的第一個目的為估計在不同的體細胞數(SCC)分級系統下，不同乳牛(或羊)族群的生乳等級分布。假設場總乳體細胞數平均值變數源自一截去單尾的常態分布，模擬族群平均為 10萬 到 250萬(SCC/毫升)，標準偏差 (SD) 為平均值的 2/3，2/4 ,2/5，2/6至 2/7，來估計總乳的SCC 累積頻率。 如果總平均是 60萬而SD 是20萬，則比 100萬高而受罰的牧場估計為2.3%. 當族群平均為 40萬，而SD是13.3萬時,即使收乳標準降為 80萬，受罰的牧場仍將少於 0.2%。但是，如果牧場規模縮小或其他原因而使場間變異增大時，例如SD增加到總平均的 1/2，在前述情況的收乳標準，將有 8.3% 與2.3%的牧場受罰。 本試驗的第二個目的為探討區隔少數高體細胞母牛乳以符合收乳要求的因應策略。假設個體的體細胞分數為常態分布，模擬分析一萬個牧場，泌乳頭數從 30 到 250 頭，體細胞分數 (SCS)變動於 3.0 到 6.3間，SD為1.5 到 2.5間。一般而言，分隔百分之一到百分之五的高體細胞數個體，能使許多原場平均為 100~150萬的牛場降至100萬以下，以一組不同 場-年-月 的田間乳牛資料來查證這個模擬，當分隔 3.67% 高於500萬的母牛，能使場的月平均由 120萬降到 101萬，為協助酪農策略演練,一個以網為基礎的計算程式編寫於 http://www.angrin.tlri.gov.tw 可供參用。

關鍵語：體細胞數、體細胞分數、分級方法。

SIMULATION OF GRADING MILK BY SOMATIC CELL COUNT AND SEPARATING HIGH SOMATIC CELL COUNT MILK FROM BULK TANK

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The first objective of this experiment is to explore the grade distribution of bulk milk of dairy farmers (cows and goats) under different somatic cell count (SCC) grading systems. Truncated normal distribution with population means from 100,000 to 2,500,000(SCC/ml) and different standard deviations (SD) from 2/3, 2/4, 2/4,2/5,2/6 to 2/7 of means, were used to estimate the cumulated frequency of the SCC of bulk milk. If the population average of SCC is 600,000 and SD is 200,000, there were be 2.3% farms in

penalty for higher than 1,000,000. As the population mean of SCC down to 400,000 and SD is 133,333, the farms in penalty will be less than 0.2% for higher than 800,000. But, as variance increased, such as reducing the herd size in all farms and the SD increased to 1/2 of mean, there will be more than 8.3% and 2.3% in penalty for the same population means and thresholds. The second objective is to understand the influence of few high somatic cows to SCC of bulk milk. Ten thousands farms with 30 to 250 milking cows with different somatic scores (SCS, 3.0 to 6.3) and different SD (1.5 to 2.5) were simulated under normal distribution assumption. In general, separating one to five percent high somatic cell cows can reduce SCC to less than 1,000,000, if herd average is higher than 1,000,000 but less than 1,500,000. A set of herd-year-month cow field data was used to verify this simulation, as 3.67% high SCC cows, higher than 5,000,000, was assembled separately which can reduce SCC from 1,198,128 to 1,006,221. For practicing the strategies, a web-based program for forecasting the possible outcomes of separately milking cows was available on http://www.angrin.tlri.gov.tw.

Key Words: Somatic cell count, Somatic cell score, Grading methods.

應用總乳檢測牛隻淋巴球黏力缺失症之基因型

應用總乳檢測牛隻淋巴球黏力缺失症之基因型

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傳統乳牛遺傳疾病的遺傳型鑑定是由牛隻個體血樣、精液或乳樣萃取 DNA後，利用已知特異性引子藉由PCR增幅特定DNA片段，再以限制腖處理後，由電泳所呈現的結果來判定。然而，對於一些頻率較低的遺傳疾病的篩檢，若以個體一一檢測，則將費時費力又耗費經費，如果能藉由總乳或混合精液來進行全場牛隻突變基因的檢測將可快速而經濟地對特定遺傳疾病進行篩檢。本試驗針對先天性下痢致死基因(CD18)，將已萃取的總乳或混合樣本 DNA，先以限制腖於特定位置將正常型 DNA截斷，以提高於後續特異性引子PCR增幅步驟中，雜合型 DNA的競爭能力。於PCR增幅後，再以限制腖作第二次處理，截切殘留的正常型特定DNA片段，而後經電泳所呈現的結果來判定樣本中是否含有雜合型或有病型的個體。以現階段台灣乳牛頭數約十萬頭，酪農戶約一千戶計算，平均每戶僅約有50~60頭牛供榨乳。因此，本試驗以牛淋巴球黏力缺失症雜合型與正常型牛隻之牛血與牛乳依不同比例(1:9、1:24、1:49與1:99)混合後萃取DNA隻進行檢測。結果顯示，無論是牛血樣或乳樣，既使在1:99混合樣品亦能測出在均能測出牛淋巴球黏力缺失症突變基因特異性片段。此種混合樣本的檢測方法，可應用於監控族群中突變或稀有的重要基因，藉總乳或混合血樣全面篩檢後，再進一步檢測可疑的家族或個體，以節省成本與時間。

關鍵語：混合樣本、總乳、牛淋巴球黏力缺失症。

DETECTION OF GENOTYPES OF BOVINE LEUKOCYTE ADHESION DEFICIENCY SYNDROME USING MIXED MILK SAMPLE

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Conventional genetic disease test was based on individual blood, semen or milk samples. Starting with DNA extraction from the raw sample, specificity primers were used to amplify DNA fragments by PCR. Finally, the PCR product was digested by restriction enzyme and diagnosed the genotype using the electrophoresis prints. Because defect gene was rare in general, individual genetic test will consume intolerable money and time for population screen. If carriers in bulk tank milk or other mixed samples can be detected, genetic screen will reduce total cost tremendously. Bovine Leukocyte Adhesion Deficiency(BLAD) is a serious genetic defect of Taiwan dairy cattle. In this study, milk or blood from identified genotypes(BL, TL and BLAD) were mixed by proposed ratio. DNA was digested by restriction enzyme before PCR procedure. The purpose is to cut the normal DNA into fragment to decline the primer competition with the rare mutant DNA. Then, following conventional procedures, PCR and 2nd restriction enzyme treatment(for cutting residual normal DNA into short fragments), carriers in sample will be discovered by electrophoresis prints. Milk samples and whole blood of both genotypes (carrier BL and normal TL), were mixed from 1:9, 1:24, 1:49 to 1:99 and then extracted the DNA and followed with genotyping procedures. Because there were only about 100,000 dairy cows and 1000 dairy farmers in Taiwan, bulk tank milk of each farm was mixed from 50 to 60 cows in average. Results showed the method can detect the exist of the carriers(BL) in all mixed samples, up to 1:99. This modified method can be used for rare gene detection and genetic disease control program. Tests may concentrate on suspected family and individuals only, farms with carriers, and total cost will be decreased notably.

Key Words: DNA mixes, Bulk tank milk, Bovine leukocyte adhesion deficiency syndrome.

絲羽烏骨雞外表特徵之遺傳模式：I．羽色、爪型與腳脛毛

絲羽烏骨雞外表特徵之遺傳模式：I．羽色、爪型與腳脛毛

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絲羽烏骨雞為東方國家的地方雞種，有核桃冠、縷頭、藍耳、鬍鬚、白色絲羽、五爪、腳脛毛、烏皮、烏肉與烏骨等十大特徵。本試驗為探討絲羽烏骨雞外表特徵之遺傳模式，應用10隻絲羽烏骨母雞為母本，畜試土雞近親品系公雞3隻為父本，於夏季採人工授精方式生產雜交後裔。計收集101個種蛋，孵育7天的受精率為80.2% (81/101)；隨後計孵出67隻雜交雞，孵化率為82.7%(67/81)。雛雞於四週齡時，已可分辨羽色、爪型、有無腳脛毛與烏皮等外表特徵。雜交雞的羽毛顏色均為父本土雞之黃褐色，腳脛顏色與皮膚顏色皆為黑色，結果顯示絲羽烏骨雞之白色絲羽為隱性，近親土雞之黃褐色羽毛為顯性，絲羽烏骨雞之黑色皮膚為顯性。雜交雞的左右腳爪型有4/4、4/5、5/4、5/5和6/6者，分別佔31.3、9.0、9.0、49.2%和1.5%。本試驗採用的10隻絲羽烏骨母雞，有4隻沒有腳脛毛，其雜交後裔均不具腳脛毛；而有6隻是具有腳脛毛，但其雜交後裔中僅有44.1% (15/34)具腳脛毛。當左右腳脛

毛(F)和爪型一起評估時，發現有17.6%為4F/4F、29.4%為4－/4－、17.6%為5F/5F、17.6%為5－/5－、5.9%為5F/4－、3.0%為4F/5F、以及5.9%為4－/5－和3.0%為6－/6－。結果顯示：雜交雞左右腳的爪數並不一定相同，腳脛毛與爪數係獨立分離表現。

關鍵語：雞、雜交、外表特徵。

INHERITANCE MODE OF CHARACTERIC FEATURES IN WHITE SILKIER CHICKEN: I. FEATHER COLOR, NUMBER OF TOES AND FEATHERS ON SHANKS

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White Silkier is one of the oriental local chicken with 10 characteristic features, such as the walnut comb, the presence of crest, the blue ears, the bearded, the white silky feather, the presence of five toes on each foot, the feathered shanks, the black skin and the black muscle as well as the black bone. The objective of the experiment was to study the inheritance mode of characteristic features in white silkier chicken. Birds used in the study included 10 white silkier hens and 3 TLRI inbred cocks as dams and sires, respectively. Artificial insemination technique was used to produce cross progeny in summer. There were 101 fertilized eggs collected and hatched with 80.2% (81/101) of hatchability at day 7, and resulted 67 chick crosses produced with 82.7%(67/81) of hatchability during days 7 and 21. Feather color, pattern in number of toes, feathers on shanks and black skin of chicks can be identified at 4 weeks of age. All crossed chicks showed black shanks and skin with yellowish brown feather as sires', which indicated white silkier feather being recessive to yellowish brown feather of inbred chicken but black skin of White Silkier being dominant to yellow skin of native chicken. The patterns of number of toes in left and right shanks were 4/4, 4/5, 5/4, 5/5 and 6/6 which accounted for 31.3, 9.0, 9.0, 49.2% and 1.5%, respectively, in F1 cross. In addition, 4 of 10 hens used in the study had no feathers on shanks and thus none of the corresponding F1 chicks was observed with feathered shanks. However, 44.1% (15/34) of progeny from 6 hens with feathered shanks had feathers on shanks. When feathers on shanks (F/－) and number of toes (4, 5 or 6) were jointly evaluated, there were 17.6, 29.4, 17.6, 17.6, 5.9, 3.0, 5.9 and 3.0% of F1 progeny with 4F/4F, 4－/4－, 5F/5F, 5－/5－, 5F/4－, 4F/5F, 4－/5－ and 6－/6－, respectively. Results indicated that number of toes in left and right sides might not be symmetric for F1 progeny. Also, the inheritance of feathers on shanks and pattern in number of toes were segregated independently.

Key Words: Chicken, Crosses, Characteristic features.

畜試土雞父系與母系生長性能和腳脛長度之關係

畜試土雞父系與母系生長性能和腳脛長度之關係

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本試驗之目的在探討畜試土雞台畜公十一號(父系)與母十二號(母系)生長性能與腳脛長度之關係，期增加其體型之一致性，俾便生產畜試土雞台畜肉十三號，提供家禽產業之大規模飼養管理。試驗雞隻源自畜產試驗所1997年經過命名的畜試土雞台畜公十一號與母十二號雞隻共585隻，進行8、12、14、與16週齡之生長性能及腳脛長度之測定，並探討兩者之關係。結果發現：台畜公十一號8、12、14與16週齡平均體重(平均值±標準機差)分別為650±6公克、1158±9公克、1376±10公克與1611±11公克；達16週齡之平均腳脛長度±標準機差為11.2±0.03公分，且體重與腳脛長度之皮爾森相關係數估值為0.49。台畜母十二號8、12、14與16週齡平均體重(平均值±標準機差)分別為581±5公克、932±8公克、1079±10公克與1193±11公克；達16週齡之平均腳脛長度±標準機差分別為9.3±0.03公分，且體重與腳脛長度皮爾森相關係數估值為0.39。此外，體重與腳脛長度具顯著的品系間差異 (P
關鍵語：畜試土雞、生長性能、腳脛長度。

THE CORRELATION BETWEEN GROWTH PERFORMANCE AND SHANK LENGTH IN SIRE AND DAM LINES OF TLRI NATIVE CHICKEN

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The objective of this investigation was to estimate the correlation between growth performance and shank length in sire (Taishu No.11) and dam lines (Taishu No.12) of TLRI native chicken and thus to increase the carcass uniformity for large-scale meat production purpose. There were 585 birds of Taishu No. 11 and No. 12 lines used in the study, which were officially nominated by provincial government in 1997. Body weights and shank lengths at 8, 12, 14 and 16 weeks of age were measured and the relationship between traits was also evaluated. Body weights (mean±SE) at 8, 12,.14 and 16 weeks of age in sire line were 650±6 gm, 1158±9 gm, 1376±10 gm and 1611±11 gm, respectively. Shank length (mean±SE) at 16 weeks of age in sire line was11.2±0.04 cm with the corresponding estimate of Pearson correlation coefficient between body weight and shank length being 0.49. Also, body weights at 8, 12,.14 and 16 weeks of age in dam line were 581±5 gm, 932 ±8 gm, 1079±10 gm and 1193±11 gm, respectively. Again, shank length (mean±SE) at 16 weeks of age in dam line was 9.3±0.03 cm with the corresponding estimate of Pearson correlation coefficient between body weight and shank length being 0.39. In addition, significant differences between lines were observed in both traits considered in the study.

Key Words: TLRI native chicken, Growth performance, Shank length.

白羅曼鵝逢機複製多態性DNA片段指印之分析

白羅曼鵝逢機複製多態性DNA片段指印之分析

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由種鵝族群中依公鵝性成熟體重及母鵝產蛋數分成高體重 (HBW)、低體重 (LBW)、高產蛋 (HEP)及低產蛋 (LEP) 4 組, 共48 隻, 利用逢機複製多態性 DNA(RAPD)方法分析白羅曼鵝 DNA 多態性。由蹼靜脈採集 3 ml 血液, 以 DNA 萃取套組萃取全血之基因組 DNA, 測定並調整適當濃度後。將所得之DNA作為模板, 再以合成之 10 鹽基對 (10bp) 寡核 酸作為引子, 進行聚合 連鎖反應 (polymerase chain reaction, PCR)。PCR 複製後之產物以 1.5％瓊脂糖膠體進行電泳分析。利用 328 種不同寡核 酸序列之逢機引子分析各組鵝隻混合 DNA 及個體 DNA, 並以 Gelcompare 影像掃描分析軟體分析其 DNA 片段型, 尋求可能與鵝隻性成熟體重及產蛋數相關之遺傳標記。結果顯示檢測所有供試鵝隻DNA所使用之 328 種引子中, 有 85% 引子可得到 PCR 產物, 41%引子可檢測出具變異性的片段。在引子AC09(890bp)、AE03(690bp) 、AE06(920bp) 、AG10(1350bp,1370bp) 、AL13(1288bp) 可得具性別特異性的片段；而引子AD06(720bp)、AD14(700bp)、AH13(2400bp) 及 AJ15(510bp) 四種引子所產生之特異性DNA片段在高低產蛋數組間之頻率具較大差異。

關鍵語：白羅曼鵝、逢機複製多態性 DNA、多態性。

STUDY POLYMORPHISM OF RANDOM AMPLIFIED POLYMORPHIC DNA IN WHITE ROMAN GOOSE

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The purpose of this study was to explore the association between production performance and RAPD (random amplified polymorphic DNA) polymorphism of White Roman Goose. Blood samples of 48 geese were collected based on mature body weight(male) and egg production performance(female). Twelve best or worst geese were assorted into each low body weight(LW), high body weight(HW), low egg production(LE) and high egg production(HE) groups. Individual genomic DNA was extracted from blood sample and detected concentration for DNA template. There were 328 kinds of a single, short (10 bp) oligonucleotide for RAPD tests. After electrophoresis in 1.5% agarose gels and stained with ethidium bromide, prints of the PCR amplified products were scanned and analyzed by Gelcompar software. The results showed 85% of these primers got PCR products, and 41% got polymorphic PCR products. The primers, AC09(890bp), AE03(690bp), AE06(920bp), AG10(1350bp, 1370bp) and AL13(1288bp), produced distinct PCR products for different genders and polymorphic patterns of AD06(720bp), AD14(700bp), AH13(2400bp) and AJ15(510bp) were not independent between high and low egg production groups.

Key Words: White Roman Goose, Random amplified polymorphic DNA (RAPD), Polymorphism.

梅山豬粒腺體DNA D-loop區域的單股構形多態性與繁殖性狀之相關性

梅山豬粒腺體DNA D-loop區域的單股構形多態性與繁殖性狀之相關性

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本試驗的目的是探討依據母系血緣推定之梅山母豬粒腺體DNA D-loop區域SSCP態樣與其繁殖性狀之相關性。於1994年7月兩公三母梅山豬由日本引進台灣，至1999年5月已繁殖141胎。引進之三頭母梅山豬來自兩個母系血緣，Meda和Nehime。利用設計之引子增殖40頭梅山豬之D-loop區域392 bp片段，進行單股構形多態性(Single strand conformation polymorphism, SSCP)分析，分析結果梅山豬粒腺體DNA D-loop區域之SSCP態樣可分出兩種環帶態樣，B和C態樣。Meda和Nehime 的SSCP環帶態樣分別為B和C態樣。所有測試之梅山豬粒腺體DNA D-loop區域單股構形多態性皆符合母系遺傳，故依據系譜推定所有參試梅山母豬之SSCP環帶態樣，將此推定之SSCP環帶態樣與141胎繁殖性狀進行分析，分析結果發現來自SSCP B態樣母豬之仔豬其21日齡體重顯著地比C態樣母豬之仔豬重(p
關鍵語: 梅山豬、單股構形多態性、繁殖性狀。

ASSOCIATION OF SSCP POLYMORPHISM OF MITOCHONDRIAL DNA
D-LOOP REGION WITH REPRODUCTIVE TRAITS IN MEISHAN PIGS

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The purpose of this study was to investigate the relationship between SSCP band patterns in the D-loop region of mitochondrial DNA (mtDNA) and reproductive traits of Meishan (M) sows. Two male and three female M pigs were imported from Japan to Taiwan on July of 1994, and one hundred and forty one litters were propagated from these foundation female M pigs until May of 1999. The foundation female M pigs originated from two maternal lineages, Meda and Nehime. Using the designed primers, the most polymorphic 392 bp fragment in the D-loop region of pigs mtDNA were amplified from 40 M pigs and applied to single-strand conformation polymorphism analysis. Two types of electrophoresis band patterns, B and C, were identified from SSCP analysis. The SSCP band patterns for Meda and Nehime were B and C types, respectively. Because the SSCP genotypes from 40 sampled M pigs followed maternal inheritance, genotypes of the rested animals in this trail were predicted by pedigree information. From analysis of the reproductive traits of M dams with predicted SSCP band patterns, the average body weight at 21 days of piglets from dams of B type was significant heavier than from C type (p
Keywords: Meishan pig, SSCP, Reproductive traits.