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生長性狀選拔16年豬群之產仔性狀遺傳趨勢與遺傳參數估計

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生長性狀選拔16年豬群之產仔性狀遺傳趨勢與遺傳參數估計

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應用行政院農業委員會畜產試驗所育種場1981至1997年間出生之1977頭純種母豬(藍瑞斯891頭、約克夏500頭與杜洛克種586頭)於1982至1998年間分娩的6593胎產仔性能(包括分娩總仔數LS、分娩活仔數LSA與三週齡窩仔數LS3)，進行遺傳趨勢與遺傳參數估計。採用多性狀線性混合模式配合限制最大似然法(REML)估算各項變方與共變方成份，模式包括品種、分娩產次、母豬出生與分娩季節(涼與熱季)等固定效應，而母豬之累加性遺傳效應、同窩出生共同效應與殘差等為隨機效應。LS、LSA與LS3遺傳變異率估值為0.091、0.099與0.095，同窩出生之共同環境效應估值為0.047、0.033與0.024。性狀間遺傳相關估值均在0.85以上(0.863 ~ 0.938)。LS、LSA與LS3具顯著的品種與分娩產次效應($P < 0.001$)，且母豬的出生與分娩季節對其產仔性能LSA與LS3均有顯著的影響；出生或分娩於涼季的母豬顯著地有較大的出生活仔數與三週齡窩仔數($P < 0.05$ 與 $P < 0.001$)。表型與遺傳趨勢均呈現下降的趨勢(-0.083 ~ -0.031與-0.132 ~ -0.049頭/窩/年)，表型方面以約克夏種(-0.132頭/窩/年)之年下降幅度為最大；遺傳趨勢部份，除LS3外，亦以約克夏種(-0.083頭/窩年)之年下滑幅度為最大。同時，各性狀遺傳趨勢佔其表型趨勢之百分率，在藍瑞斯、約克夏與杜洛克種分別為59.6 ~ 75.5%、46.4 ~ 62.9%與59.7 ~ 85.7%。

關鍵語：種豬、遺傳趨勢、遺傳參數、產仔性能。

EVALUATION OF GENETIC TRENDS AND PARAMETERS FOR LITTERING PERFORMANCES IN GROWTH SELECTION-BASED HERD AFTER 16 YEARS

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Record of littering performance data on 891 Landrace, 500 Yorkshire and 586 Duroc pigs in Taiwan Livestock Research Institute between 1982 and 1998 were used. A total of 6593 litters from 1977 sows born between 1981 and 1997 were analyzed. Traits were litter size at birth (LS) and born alive (LSA) as well as litter size at 3 weeks of age (LS3). Mixed linear model via REML for multiple trait analysis was employed for estimation of variance-covariance components. Model for individual genetic evaluations included breed, parity, birth and farrowing seasons of sows as fixed effects, and additive genetic effects, common litter effects and error as random effects. Estimates of heritability from additive genetic variances for LS, LSA and LS3 were 0.091, 0.099 and 0.095. The corresponding estimates for common litter effect were 0.047, 0.033 and 0.024,

respectively. Genetic correlation estimates were larger than 0.85 among traits considered (0.863 ~ 0.938). LS, LSA and LS3 differed among breeds and parities ($P < 0.001$). Significant seasonal effects were also found in LSA and LS3. Sows born or farrowing in cool season produced larger LSA and LS3 than those in hot season ($P < 0.05$ and $P < 0.001$, respectively). However, both estimates of phenotypic and genetic trends for traits considered were negative (-0.083 ~ -0.031 and -0.132 ~ -0.049 piglets/litter/year). Yorkshire sows showed the largest yearly phenotypic decrease (-0.132 piglets/litter/year). Similar trend was also observed in genetic evaluation among sow breeds except LS3. Furthermore, genetic trends accounted for 59.6 ~ 75.5%, 46.4 ~ 62.9% and 59.7 ~ 85.7% of phenotypic trends in Landrace, Yorkshire and Duroc breeds, respectively.

Key Words: Swine breeding stock, Genetic trend, Genetic parameter, Littering performance.

生長豬活體超音波掃描與屠體性狀之遺傳與表型相關

生長豬活體超音波掃描與屠體性狀之遺傳與表型相關

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應用超音波即時顯像儀 (Aloka SSD-500 B-模式) 掃描不同月齡 (4.0、4.5與5.0月齡) 生長豬之第十肋骨處腰眼面積與同部位長軸中點1/2處背脂厚度, 進而估計不同掃描日齡性狀間之遺傳參數與相關。同時, 逢機選取150頭達110公斤之完檢豬隻, 進行屠前活體重、第十肋骨處背脂厚度和腰眼面積, 以及屠後體重、屠體長、平均背脂厚度、最後肋骨處背脂厚度、第十肋骨處腰眼面積、屠宰率與瘦肉率間之遺傳與表型相關探討。統計分析係以多性狀線性混合模式配合限制最大似然法 (REML) 估算變方與共變方成份, 統計模式包括品種、性別、出生產次與出生季節等固定效應, 以及累加性遺傳效應、同窩出生共同效應與殘差等逢機效應。結果顯示: 不同月齡活體性狀表型變方估值隨月齡增加而增大; 且除4.5和5.0月齡之活體背脂與5.0月齡體重外, 其餘性狀之同窩出生之共同效應均較累加性遺傳效應大。同時, 在本研究評估之各性狀中, 累加性遺傳效應與同窩出生之全同胞顯性效應均佔表型變異50%以上。此外, 由遺傳相關估值發現, 完檢豬隻屠前活體掃描性狀與對應之屠體性狀均呈顯著的遺傳正相關 ($r_G = 0.233 \sim 0.843$, $P < 0.05$); 而經由Pearson相關分析所得之表型相關估值, 除屠前活體背脂與屠體腰眼面積為負值外 ($r_P = -0.184$), 餘均與遺傳相關具相同的趨勢; 惟各估值均較小 ($r_G = 0.515 \sim 0.843$ vs. $r_P = 0.443 \sim 0.622$)。

關鍵語: 豬、遺傳相關、超音波測定、屠體性狀。

GENETIC AND PHENOTYPIC CORRELATION AMONG ULTRASOUND
AND CARCASS MEASUREMENTS IN GROWING PIGS

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Aloka Model SSD-500 B-mode real-time ultrasound scanner was used to scan growing pigs at 4.0, 4.5 and 5.0 months of age. Ultrasound measurements of loin muscle area at the tenth rib and 1/2 point overlying fat were taken for genetic parameter estimation and correlation analysis. 150 off-tested pigs near 110 kg live weight were also randomly sampled to evaluate the genetic and phenotypic correlation for measurements taken before (live weight, ultrasound measurements of backfat and loin muscle area at the tenth rib) and after (carcass weight, carcass length, average backfat thickness, backfat thickness of the last rib, loin muscle area at the tenth rib, dressing percentage and lean percentage) slaughtered. Mixed linear model via REML for multiple trait analysis was used to estimate variance components. Model used included breed, sex, birth parity and birth season as fixed effects, additive genetic effects, common litter effects and error as random effects. Results showed that estimates of phenotypic variance for ultrasound measurements were increased as age increased. Larger common litter effects than additive genetic ones were observed in most of traits except in ultrasound backfat at 4.5 and 5.0 months of age, and weight at 5.0 months of age. Furthermore, additive genetic and common litter effects accounted for more than 50% of phenotypic variance for traits considered in this study. Positive genetic correlation were found between measurements taken before and after slaughter ($r_G = 0.233 \sim 0.843$, $P < 0.05$) and similar trend was also obtained in Pearson correlation coefficients of phenotype except the one between backfat taken before slaughtered and loin muscle area of carcass ($r_P = -0.184$). However, the estimates of correlation were smaller in phenotype than in genotype ($r_G = 0.515 \sim 0.843$ vs. $r_P = 0.443 \sim 0.622$).

Key Words: Pigs, Genetic correlation, Ultrasound measurement, Carcass trait.

多產豬種之培育I. 梅山豬與杜洛克豬雜交之產仔性狀

多產豬種之培育I. 梅山豬與杜洛克豬雜交之產仔性狀

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母豬生產力為養豬產業經濟效率的一項重要因素，其主要組成性狀為分娩窩仔數和哺育期間仔豬育成率；然因其為遺傳變異率低之性狀，故很難經由選拔達到改進的目的。因此，應用具高繁殖力之中國本土豬種如梅山豬，進行雜交即為另一項選擇。本研究旨在評估多產梅山豬與杜洛克豬正反雜交之產仔性能，期供作選育適合台灣地區環境氣候高繁品系豬種之依據。應用梅山豬(M)公12頭、母53頭與杜洛克豬(D)公24頭、母42頭，於1997至1999年間進行正反雜交試驗，計分娩122窩(初產95胎與二產27胎)；其中M、D、MD(M母豬與配D公豬)與DM(D母豬與配M公豬)分別為18、14、50與40胎。評估性狀包括分娩總仔數(LS)與活仔數(LSA)、三週齡(LS3)與離乳窩仔數(LSW)、分娩活仔豬窩重(LTRWT)、仔豬出生(WT0)、三週齡(WT21)與離乳(WWT)平均體重、仔豬出生存活率($LSA/LS = SURV1$)與三週齡育成率($LSA/LS3 = SURV2$)。結果發現：母豬產仔性能具顯著的品種效應，M母豬顯著地較D母豬有較大的LS、LSA、LS3與LSW(P

關鍵語：梅山豬、杜洛克豬、正反雜交、產仔性能。

DEVELOPMENT OF PROLIFIC LINE IN SWINE I. LITTERING TRAITS OF MEISHAN CROSSING WITH DUROC

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Sow productivity is a major component of the production efficiency in pig industry. Litter size at birth and pre-weaning survival rate are the major component traits. However, these traits are difficult to improve through selection due to their low heritabilities. Crossbreeding could be another way to increase sow productivity by taking advantage of high prolificacy in some native Chinese breeds such as Meishan. The purpose of this study was to evaluate the littering performances of Meishan(M), Duroc(D) and reciprocal crosses(MD and DM defined as M sows sired by D boars and D sows sired by M boars, respectively) for the reference of the outstanding reproductive breeds selection in Taiwan. A total of 36 boars(including 12 M and 24 D breeds, respectively) and 95 sows(including 53 M and 42 D breeds, respectively) were used to produce 122 litters(95 and 27 litters produced at first and second parities, respectively) during 1997 and 1999. The data included 18, 14, 50 and 40 litters of M, D, MD and DM, respectively. Traits evaluated were litter size at birth(LS), born alive(LSA), at three weeks of age(LS3) and at weaned (LSW), litter weight born alive(LTRWT), average piglet weight at birth(WT0), at three weeks of age(WT3) and at weaned(WWT), piglet survival at birth(SURV1 = LSA/LS) and at three weeks of age(SURV2 = LSA/LS3). Results showed that sow breed effects was significant for littering traits considered and M sows had larger LS, LSA, LS3 and LSW than D females (P

Key Words: Meishan pigs, Duroc pigs, Reciprocal crosses, Littering performances.

多產豬種之培育II. 梅山豬與杜洛克豬雜交一代之生長性狀

多產豬種之培育II. 梅山豬與杜洛克豬雜交一代之生長性狀

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本研究旨在探討多產梅山豬與高產肉杜洛克豬種正反雜交後裔豬之生長性能，期供作培育具產品區隔新品系豬種之遺傳資源。試驗豬群包括梅山豬（M，公豬60頭，女豬64頭）、杜洛克（D，公豬27頭，女豬25頭）、杜洛克公豬與配梅山母豬之後裔（MD，公豬165頭，女豬197頭）和梅山公豬與配杜洛克母豬之後裔（DM，公豬97頭，女豬112頭），計有公豬349頭與女豬398頭。參試豬隻生長性能檢定期間自70至210日齡，測定性狀包括70（W70）、90（W90）、120（W120）、150（W150）、180（W180）與210日齡（W210）之體重，以及150（BF150）、180（BF180）與210日齡（BF210）之第五肋、最後肋與

最後腰椎離背中線5公分處之背脂厚度平均。公豬因採個檢方式進行，故亦測定檢定期間之飼料效率（FE）；而女豬則以群檢方式進行。分析結果發現：不論公豬或女豬，各階段體重不僅具顯著的品種效應（P0.05）。

關鍵語：梅山豬、杜洛克豬、正反雜交、生長性狀。

DEVELOPMENT OF PROLIFIC LINE IN SWINE II. GROWTH TRAITS OF (MEISHAN X DUROC) PIGS

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The objective of this study was to investigate the growth performances of Meishan (M), Duroc (D) and their reciprocal crosses for the reference of potential new strain exploration in Taiwan. Tested herd included growing pigs of M (60 boars and 64 gilts), D (27 boars and 25 gilts), MD defined as the progeny of M sows sired by D boars (165 boars and 197 gilts), and DM defined as the progeny of D sows sired by M boars (97 boars and 112 gilts). A total of 349 boars and 398 gilts were evaluated during 70 and 210 days of age. Traits analyzed were body weights at 70 (W70), 90 (W90), 120 (W120), 150 (W150), 180 (W180) and 210 (W210) days of age, and averaged backfat thickness at 150 (BF150), 180 (BF180) and 210 (BF210) days of age which were measured at 5 cm from dorsal line of the fifth and last ribs as well as the last lumbar. Boars were tested individually and thus the corresponding feed efficiency during testing period was also evaluated. However, tested gilt were group housed without feed consumed information. Result indicated that breed effects was significant for body weights considered in this study (P0.05).

Key Words: Meishan pigs, Duroc pigs, Reciprocal crosses, Growth performances.

雞肌肉蛋白-旋光抑制素 (TnI) 多態性研究

雞肌肉蛋白-旋光抑制素 (TnI) 多態性研究

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旋光抑制素 (TnI) 為肌肉纖維內重要的肌絲蛋白，可調節肌肉收縮活性與穩定肌纖維結構之功能。本研究之主要目的在探討不同品系間雞肉內肌絲蛋白分子多態性表現之差異性。試驗組雞隻為畜產試驗所選育之8週齡近親品系土雞 (L7、L9、L11、L12)、二元雜交雞 (PS) 及公土雞與配絲羽 (CW) 或黑羽 (CB) 烏骨母雞之雜交品系，而對照組雞隻則採用坊間一般有色雞隻。動物犧牲後取下大胸肌，隨後去除細胞膜的結構製備成去膜肌纖維，以降低水解蛋白分解肌絲蛋白分子的酵素活性。同時應用聚

丙醯凝膠蛋白電泳 (SDS-PAGE) 分離不同分子大小之肌肉蛋白，並且利用分子專一性肌絲蛋白抗體辨識肌肉中特定的蛋白分子。試驗雞隻大胸肌纖維內雖均表現兩種不同分子大小的旋光抑制素 (分子量分別為23.2與22.6 kD)，但不同品系間肌肉纖維內之分子同分異構物分佈比例，則有顯著的差異 (P
關鍵語：旋光抑制素 (TnI)、多態性表現、台灣土雞。

POLYMORPHIC EXPRESSION OF MYOFILAMENT PROTEIN TROPONIN I IN THE PECTORALIS MAJOR MUSCLE OF DOMESTIC CHICKENS

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Troponin I (TnI) is a regulatory protein of myofilament protein. TnI regulates the contractile activities of muscle and stabilizes the structure of myofilaments. The aim of this study was to investigate if strain-dependent differences of muscle protein expression exist in skeletal muscle of various domestic chickens. Taiwan country chicken inbred lines (L12, L7, L11 and L9), and their hybrid (PS) as well as Silkie-Country hybrids (CW and CB) provided from Taiwan livestock Research Institute (TLRI) were used along with several commercial strains of colored chickens. The Pectoralis Major muscle taken from experimental animals were prepared for chemically skinned muscle fibers in which membranous structures of muscle fibers were removed. This treatment of skinning would decrease the proteinase activity and prevent proteolysis of muscle proteins. SDS polyacrylamide gel electrophoresis in combination with immuno-blotting method was used to identify specific myofilament proteins in muscle fibers. Results obtained showed that two different molecular size (MW: Heavy/23.2 kD and Light/22.6 kD) of Troponin I (TnI) expressed in the Pectoralis Major of all chickens from TLRI. However, the expressed ratios of these two TnI isozymes are different in muscle fibers of different strains. The expression of the heavy TnI isozyme in muscle fibers is greater for the strains L12 (71.7%), L7 (60.3%), L11 (81.1%) and L9 (68.7%) than for strains PS (26.6%), CW (40%) and CB (57.1%). Interestingly, only one band of high molecular weight of TnI (23.2 kD) was found in other originated chickens. Thus, polymorphic expression of myofilament proteins in chicken muscles could be strain-specific, and that might provide a means for further characterizing muscle differences between a variety of domestic chickens.

Key Words: Troponin I (TnI), Polymorphic expression, Taiwan country chicken.

累加性親屬係數距離分組法與加總法選留"代表性"種畜群

累加性親屬係數距離分組法與加總法選留"代表性"種畜群

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為保有畜群的遺傳變異，本試驗提出兩種選擇種畜的方法，方法一為利用距離分組的方法將(1-累加性親屬係數)視為距離，再利用彼此間最短距離進行分群(如single linkage 法)，最後再由各子群抽出代表，將此抽出的集合視為"代表性"種畜群。方法二為利用組合的方法，取出 $C(N, n)$ 組種畜群， N 為全部畜群數， n 為擬選留的"代表"個數，再加總兩兩間共 $0.5n(n-1)$ 個累加性親屬係數(A 為上三角與對角線為0的矩陣， $a_{..}$ 為其所其有元素 a_{ij} 加總)，即選出最小的 $a_{..}$ ，此組內的成員即視為選留的"代表"。方法一主要的困擾為子群內個體的選擇，方法二則需面臨一個以上的可代表群的選擇($a_{..}$ 相同，最小值不唯一)。雖然利用分生的遺傳多態性分組，如血型或是DNA指紋等，也可作為個體間分組選留"代表性"畜群的方法。然而採血、分生分析等工作需要相當的人力與物力。從機率的關點，分生的分組方法只是在一個子集合下(能被度量的性狀)的分組法之一，且亦需面臨所提方法一中所面臨的問題。本試驗『累加性親屬係數距離分組法與加總法選留"代表性"種畜群』提供了較經濟的選留方法，可用於有限資源下，種畜群留種的參考。

關鍵語：累加性親屬係數、分群、距離。

SELECT POPULATION REPRESENTATIVES BY MINIMIZING THE SUMMATION
OR CLUSTERING THE ADDITIVE RELATIONSHIP COEFFICIENTS

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In order to keep the population genetic variation, two methods are proposed to select representative breeding stocks in this study. Method I, distance matrix $D=(1-A)$, where element $d_{ij}=(1-a_{ij})$, a function of additive relationship coefficient, a_{ij} , is used as distance between two individuals. With linkage methods can cluster animals into n groups, where n is the upper limit of number of selected animals. Each cluster chooses an animal to form the representative set. Method II is to minimize the summation of the additive relationship coefficients of the selected animals. $C(N, n)$ combination sets need be computed for the minimization, and N is the number of candidates. In each set, there is $0.5n(n-1)$ elements from the lower triangular of matrix A for summation. Individuals in the set with minimum $a_{..}$, summation all lower triangular elements, will be the selected representatives. In method I, the main puzzle is how to choose representative for each cluster, and dilemma of the method II is the minimization might not be unique. Although biotechnology such as blood typing or DNA finger prints data can be used to select representatives, the puzzle of method I existed also and need cost for sampling and lab works. Comparing with the molecular methods, the methods proposed in this study are less expensive.

Key Words: Additive relationship coefficient, Cluster, Distance.

台灣牛群之瓜胺酸症頻率檢測

台灣牛群之瓜胺酸症頻率檢測

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瓜胺酸症是一種是一種“尿循環”的遺傳缺陷疾病，雙隱性純合型的罹患仔牛在出生後一週內就會死亡。這種“尿循環”的遺傳缺陷無法正常的排氨，剛出生的得病的小牛外觀正常，然而小牛出生後卻因為自己無法自行排毒，因此神經問題會逐步的嚴重，通常仔畜在一週內就會死亡。為了解瓜胺酸症在台灣牛隻之分布情形，本試驗共檢測六個牧場(南部及北部各三場)與來自北部與東部地區參與 DHI 計畫的自留小公牛，全部共 1690頭荷蘭乳牛。採集血樣後，進行瓜胺酸症 DNA基因型鑑定。在全部 1690頭荷蘭乳牛中僅檢測出一頭雜合型牛(0.06%)，顯示此一曾廣汎發生澳洲的荷蘭牛族群遺傳疾病，對本省乳牛影響不大。

關鍵語：台灣、荷蘭牛、瓜胺酸症。

LOW INCIDENCE OF DEFICIENCY OF CITRULLINEMIA
CARRIERS AMONG DAIRY CATTLE OF TAIWAN

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Bovine citrullinemia is an autosomal recessive disorder in Holstein cattle that results in calf mortality. Affected calves are unable to get rid of ammonia and display neurological symptoms that become progressively worse, leading to death within one week of birth. For understanding the defect gene frequency of Taiwan Dairy cattle, a total of 1690 samples, Holstein cows and young bulls from different herds, were sampled and tested for genotypes of citrullinemia. With a mutation-specific assay of leukocyte DNA, one heterozygote cow was detected among all samples tested, corresponding to an incidence of 0.06%. With evidence of less than .1% (1/1690=0.06%) carrier, citrullinemia, a serious genetic defect of Holsteins in Australia, is not a significant genetic disease in Taiwan.

Key Words: Taiwan, Holstein, Citrullinemia.

台灣種公牛系譜與遺傳檢測資料庫網際網路化之研究

台灣種公牛系譜與遺傳檢測資料庫網際網路化之研究

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使用畜產試驗所新竹分所自民國64年起記錄的進口冷凍精液資訊為基礎，結合美國、荷蘭、加拿大等國荷蘭牛協會提供的進口冷凍精液遺傳檢測資訊，與新竹分所AI公牛遺傳檢測的資訊，逐步建立台灣公牛系譜與遺傳檢測資料庫，應用程式以HTML配合Active Server Pages (ASP)方式開發，以IE 5.0為操作環境，配合微軟公司的Microsoft SQL Server 7.0資料庫軟體，以VB Script為主要開發語言，系統則建置於PC SERVER上，作業系統使用Microsoft NT 4.0版本，網際網路服務環境採用Microsoft Internet Information Server (IIS) 4.0版本，已建置的進口冷凍精液系譜與遺傳檢測查詢系統(<http://www.angrin.tlri.gov.tw/>)，提供酪農戶能自網際網路由單一視窗以登錄號、NAAB碼、精液碼與短名等進行查詢公牛系譜與遺傳檢測資訊。

關鍵語：資料庫、公牛、全球資訊網。

DEVELOPMENT OF INTERNET-BASED GENETIC DATABASE FOR
TAIWAN BULLS AND IMPORTED FROZEN SEMEN

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Based on imported semen database updated by TLRI, Hsinchu Branch Institute, since 1975, an internet bull genetic database was established. Genetic test data from TLRI AI bull station, and pedigree with genetic test data from Holstein associations of different countries were merged and cumulated. Microsoft IE5.0 was the default browser for developing the Active Server Pages (ASP), and PC based Microsoft SQL Server 7.0 was used for data table creation. With Microsoft NT 4.0 and VB Script under Microsoft Internet Information Server V4.0 environment, remote dairy farmers can choose registration number, NAAB code, semen code or short name to search pedigree and genetic test data.

Key words: Database, Bull, World Wide Web.

母豬造骨蛋白交替基因對產仔性能之影響

母豬造骨蛋白交替基因對產仔性能之影響

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以造骨蛋白基因 (OPN) 微衛星型遺傳標記檢測180頭經產種母豬啟動子區域之[TG]序列重複數交替基因，其交替基因類型依所具[TG]雙核 酸重複數區分，計發現九種交替基因，28種基因型。在不同品種的分布分別為：於51頭藍瑞斯種母豬中，有[TG]13、[TG]14、[TG]19和 [TG]21等四種交替基因，共組成九種基因型；於54頭約克夏種母豬中，計有[TG]8、[TG]14、[TG]21、[TG]23、[TG]24和[TG]26等

六種交替基因，共組成20種基因型；於25頭杜洛克豬種母豬中，計有[TG]14、[TG]21、[TG]23和[TG]24等四種交替基因，共組成六種基因型；而於50盤克夏種母豬中，所發現的五種交替基因分別為[TG]8、[TG]13、[TG]23、[TG]24和[TG]25，共組成八種基因型。進一步分析種母豬具不同OPN交替基因對產仔性能之影響，結果顯示：具[TG]14交替基因之約克夏種母豬所分娩活仔數顯著地較未具該交替基因者為佳（ 8.41 ± 0.74 vs. 7.25 ± 0.36 頭， $P < 0.0257$ ）；具[TG]21或[TG]24交替基因之杜洛克種母豬所分娩仔豬之存活率亦顯著地較未具該交替基因者為佳（ 85.8 ± 4.6 vs. $74.3 \pm 4.2\%$ ， $P < 0.0196$ ； 87.9 ± 4.9 vs. $72.1 \pm 4.0\%$ ， $P < 0.0019$ ）；然而具[TG]13交替基因之盤克夏種母豬，其所分娩活仔數顯著地較未具該交替基因者為差（ 6.10 ± 1.00 vs. 7.20 ± 0.80 頭， $P < 0.0495$ ）。

關鍵語：造骨蛋白、交替基因、產仔性能。

INFLUENCE OF SOWS' OSTEOPOINTIN ALLELES TO THEIR LITTER PERFORMANCE

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A total of 180 parous sows were genotyped with osteopontin (OPN) microsatellite marker by PCR. The OPN allele was defined as consisting of different number of [TG] dinucleotide repeats in the promoter region of OPN gene. In this study, nine alleles were found and making up 28 genotypes. There were different alleles distributed among four swine breeds. In 51 Landrace pigs, four alleles including [TG]13, [TG]14, [TG]19 and [TG]21 were found and making up nine genotypes. In 54 Yorkshire pigs, six alleles including [TG]8, [TG]14, [TG]21, [TG]23, [TG]24 and [TG]26 were found and making up 20 genotypes. In 25 Duroc pigs, four alleles including [TG]14, [TG]21, [TG]23 and [TG]24 were found and making up six genotypes. In 50 Berkshire pigs, five alleles including [TG]8, [TG]13, [TG]23, [TG]24 and [TG]25 were found and making up eight genotypes. When we further analyzed the litter performance of sows with different OPN alleles, the results indicated that the number of alive piglets born from Yorkshire sows with [TG]14 allele were significantly more than those without such an allele (8.41 ± 0.74 vs. 7.25 ± 0.36 , $P < 0.0257$). For Duroc sows, the survival rate of piglet born from sows with [TG]21 or [TG]24 allele was significantly higher than those without [TG]21 or [TG]24 allele (85.8 ± 4.6 vs. $74.3 \pm 4.2\%$, $P < 0.0196$; 87.9 ± 4.9 vs. $72.1 \pm 4.0\%$, $P < 0.0019$). But for Berkshire sows, the number of alive piglets born from sows with [TG]13 allele were significantly less than those without [TG]13 allele (6.10 ± 1.00 vs. 7.20 ± 0.80 , $P < 0.0495$).

Key Words: Osteopontin, Allele, Litter performance.

豬粒腺體DNA D-loop區域之序列分析

豬粒腺體DNA D-loop區域之序列分析

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藍瑞斯及梅山豬的豬粒腺體DNA D-loop區域序列已經被提出，並發現藍瑞斯、梅山豬及大白豬之間特殊DNA D-loop區域有差異，此結果顯示豬粒腺體DNA D-loop區域的歧異性具有潛力供豬隻細胞質遺傳的分析用。本試驗設計了一組可以豬之基因組DNA為模板，經由聚合連鎖反應，增殖出D-loop區域392 bp片段的引子，利用此組引子增殖出不同品種豬隻之D-loop區域392 bp片段，進行序列分析。結果發現此片段序列共有16個核 酸位置發生變異，而在這16個變異中有13個變異為同類置換。進一步計算不同品種豬隻間之序列分歧度，發現歐美與亞洲品種內豬隻的序列分歧度分別為 $0.63 \pm 0.59\%$ 與 $0.51 \pm 0.27\%$ ，而歐美與亞洲品種豬隻之間的序列分歧度較為 $1.31 \pm 0.59\%$ 。此結果可供豬隻細胞質遺傳演化之參考。

關鍵語：豬、粒腺體DNA、序列分析。

SEQUENCE ANALYSIS OF D-LOOP REGION IN THE
MITOCHONDRIAL DNA OF PIGS

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The entire mitochondrial DNA (mtDNA) displacement loops (D-loops) of Landrace and Meishan have been sequenced, and the divergences of specific D-loop region among Landrace, Large White, and Meishan have been compared. The results hinted that D-loop polymorphism and/or sequence diversity is potential for molecular analysis of cytoplasmic genetic in pigs. A pair of primer was designed for the amplification by PCR to generate a 392 bp fragment of the D-loop region from the template DNA of pure pig breeds. These 392 bp PCR products were verified by their sequences. The results showed that there were 16 site substitutions in the 392 bp fragment of D-loop region. Thirteen nucleotide variations were transition. The average sequence diversities of D-loop region of the European-American and Asian breed pigs were $0.63 \pm 0.59\%$ and $0.51 \pm 0.27\%$, respectively. The average sequence diversity of D-loop region between the European-American breed and Asian breed pigs was $1.31 \pm 0.59\%$. It showed that the sequence diversity of D-loop region is useful for evolution analysis of cytoplasmic genetic in pigs.

Key Words : Pig, mtDNA, Sequencing.

畜試土雞近親品系與烏骨雞雜交一代生長性狀

畜試土雞近親品系與烏骨雞雜交一代生長性狀

鍾秀枝 張秀鑾 吳明哲 黃祥吉

台灣土雞為一著名的地方雞種，而烏骨雞則為中國著名的地方雞種之一，其以藥用與觀賞用聞名。本試驗之目的為探討源自台灣土雞之畜試土雞近親品系與烏骨雞雜交一代之生長性狀。利用畜產試驗所育成之畜試土雞近親品系(C)公雞5隻，大陸引進之黑羽(B)與及絲羽(W)烏骨母雞各11與10隻為試驗動物。應用人工授精方式進行雜交試驗，調查雜交後裔F1之生長性狀與腳脛長度。計收集近親品系土雞與黑羽烏骨雞雜交組(CB)種蛋126個，受精率89.7%，孵化率87.6%；近親品系土雞與絲羽烏骨雞(CW)雜交組種蛋101個，受精率80.2%，孵化率82.7%。雜交後裔F1生長性狀結果顯示：CB雞隻達18週齡之公與母雞平均體重分別為 1574.7 ± 33.4 (N=43)與 1158.5 ± 34.0 (N=42)公克；腳脛長度分別為 11.66 ± 0.08 與 9.68 ± 0.08 公分。CW組之相對應性狀則分別為公與母雞平均體重 1458.9 ± 49.0 (N=20) 與 1113.0 ± 39.2 (N=31)公克；腳脛長度 11.20 ± 0.11 與 9.60 ± 0.09 公分。此外，CB組雞隻之18週齡體重與腳脛長度均顯著地較CW者為大(1366.6 ± 23.8 vs. 1285.9 ± 31.4 公克； 10.67 ± 0.06 vs. 10.40 ± 0.07 公分)。

關鍵語：台灣土雞、烏骨雞、生長性狀、腳脛長度。

GROWTH TRAITS OF (TAIWAN NATIVE CHICKEN INBRED LINES X SILKIER CHICKEN)

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Taiwan native chicken and Silkier chicken are famous local chicken in Taiwan and Mainland China, respectively. The latter is also famous for its medical usage and known as one of the fancy breeds. The objective of this study was to assess the growth traits of F1, Taiwan native chicken TLRI inbred lines X Silkier chicken. Samples of 5 cocks of Taiwan native chicken TLRI inbred line (C), 11 and 10 hens of black (B) and white (W) Silkier chicken, respectively, were used as sire and dam to produce F1 hybrid progeny via artificial insemination. A total of 126 fertilized eggs from B hens sired by C cocks (CB) were collected and hatched with fertilization rate and hatchability being 89.7% and 87.6%, respectively. The corresponding fertilization rate and hatchability were 80.2% and 82.7% for 101 fertilized eggs from W hens sired by C cocks (CW) contemporaneously. Body weights at 18 weeks of age for male and female in CB hybrid were 1574.7 ± 33.4 (N=43) and 1158.5 ± 34.0 (N=42) gm with 11.66 ± 0.08 and 9.68 ± 0.08 cm in shank length, respectively. There were (1458.9 ± 49.0 gm and 11.20 ± 0.11 cm, N=20) and (1113.0 ± 39.2 gm and 9.60 ± 0.09 cm, N=31) for the male and female birds of CW in corresponding traits. Furthermore, Both weight and shank length at 18 weeks of age in CB hybrids were significantly larger than those in CW hybrids (1366.6 ± 23.8 vs. 1285.9 ± 31.4 gm, P

Key Words: Taiwan native chicken, Silkier chicken, Growth traits, Shank length.

台灣藍瑞斯、約克夏與杜洛克登錄豬活仔數之育種價預測

台灣藍瑞斯、約克夏與杜洛克登錄豬活仔數之育種價預測

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應用種豬登錄資料庫之種母豬分娩資料(自1989年4月至2000年1月間分娩者),計包括33,931頭登錄母豬之112,000胎分娩記錄;其中藍瑞斯、約克夏與杜洛克頭數分別為17,127、6,287與10,517頭,相對應之分娩胎數為56,687、20,947與34,366胎。繁殖性狀之遺傳評估模式係針對登錄豬之活仔數產仔能力為觀測值,而以品種、出生年別與季節、分娩該胎之年別與季節、以及分娩該胎之產次為固定效應,母豬分娩該胎之日齡與日齡平方為共變數,母豬之累加性遺傳效應與殘差等為隨機效應;其中季節分為熱(每年5至10月)與涼(每年11至隔年4月)季,產次則分為初產與經產。應用前述動物混合模式所得之累加性遺傳效應與殘差之限制極大似然估值(REML)換算之遺傳變異率估值為0.237,隨後應用於前述遺傳評估模式進行固定效應之最佳線性無偏估計(BLUE)檢定與登錄種豬產活仔數之遺傳值最佳線性無偏預測(BLUP)。分娩時,經產母豬顯著地較初產者多 0.79 ± 0.02 頭活仔數(P <http://www.angrin.tlri.gov.tw/>)中,供業者選種用。

關鍵語: 育種價、最佳線性無偏預測、登錄豬。

PREDICTION OF BREEDING VALUES FOR REGISTERED STOCKS IN TAIWAN LANDRACE, YORKSHIRE AND DUROC PIGS

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There were 112,000 litters produced during April 1989 and January 2000 from 33,931 registered sows in Taiwan Swine Herdbook used in the study, including 56,687, 20,947 and 34,366 litters from 17,127 Landrace, 6,287 Yorkshire and 10,517 Duroc sows, respectively. Litter size born alive was the reproductive trait considered. Genetic evaluation model included breed, season and year of sow at birth, season and year as well as parity of sow at farrowing as fixed effects, age in days at farrowing and its quadratic as covariates, additive genetic effects and error as random effects. There were two classes in sows' birth and farrowing seasons, hot and cool seasons. The former was defined as from April to October and the latter was for the rest months of the year. Parity of sows at farrowing was also classified as two levels, first parity and parous sows. Estimates of heritability from additive genetic variances via REML for the trait evaluated was 0.237, which was then implemented in the animal mixed linear model to estimate and test the corresponding fixed effects (BLUE) and to predict the random additive genetic values of animals (BLUP). Parous sows produced 0.79 ± 0.02 piglets more than those of first parity sows (<http://www.angrin.tlri.gov.tw/>) available for selection purpose.

Key Words: Breeding value, BLUP, Registered pigs.