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台灣種豬動情素接受器多產基因頻率

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台灣種豬動情素接受器多產基因頻率

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豬隻動情素接受器(Estrogen Receptor, ESR)基因座位於第一對染色體短臂上,具有兩個對偶基因A和B。文獻報告指出,ESR基因型為BB之母豬較AA型者,每胎分別可多分娩1.5與1.0頭以上仔豬與活仔豬,故亦將ESR基因座之B對偶基因稱為多產基因。本試驗應用單點核³²P-末端標記聚合連鎖反應(MS-PCR)技術,針對台灣地區八家民間種豬場與五個試驗研究單位之種豬,進行ESR基因型鑒機檢測。計完成7657頭種豬檢測,包括藍瑞斯、約克夏、杜洛克(D)、梅山豬(M)、桃園豬、盤克夏、蘭嶼豬、花色豬、迷彩豬與畜試黑豬一號,以及M與D之雜交豬。結果發現:除M與D之雜交豬外,前述各品種ESR基因型為BB型之頻率分別為0.3%、26.6%、0%、100%、80.0%、1.0%、16.7%、10.8%、31.0%與1.9%;B對偶基因頻率則分別為0.05、0.51、0.00、1.00、0.81、0.01、0.42、0.46、0.50與0.16。

關鍵詞:動情素接受器、基因頻率、豬隻。

THE PROLIFIC GENE FREQUENCY OF ESTROGEN
RECEPTOR LOCUS FOR BREEDING PIGS IN TAIWAN

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The estrogen receptor (ESR) locus in swine was mapped at p-arm of chromosome one with two alleles, A and B. Literature indicated that BB homozygotic sows produced 1.0 and 1.5 more piglets at birth and born alive, respectively than did AA homozygotes. And thus, B allele of ESR locus is generally recognized as prolific gene. Mutagenically separated polymerase chain reaction (MS-PCR) technique was applied in the study for ESR genotyping. A total of 7657 breeding pigs from eight private breeding farms and five research stations were blood sampled for genotyping. The genotypic frequencies of BB homozygotes were 0.3%, 26.6%, 0%, 100%, 80.0%, 1.0%, 16.7%, 10.8%, 31.0% and 1.9% for Landrace, Yorkshire, Duroc, Meishan, Taoyuan, Berkshire, Lanyu, Spotty Lanyu, Mitsae and TLRI-Black, respectively. The corresponding gene frequencies for prolific gene B allele were 0.05, 0.51, 0.00, 1.00, 0.81, 0.01, 0.42, 0.46, 0.50 and 0.16, respectively.

Key Words: Estrogen receptor, Gene frequency, Swine.

豬隻肋骨數之遺傳區域

豬隻肋骨數之遺傳區域

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應用豬隻微衛星型標記包括在第一號染色體上的SW552、S0316、SW2130及SW780與第七號染色體上的SW1122、SW147、SW252、S0115及SW764共計九種，檢測自肉豬群中取得之14對和17對肋骨數的肌肉樣本。結果經卡方分析顯示：肋骨數與第一號染色體短臂上的S0316和第七號染色體長臂上的SW1122、SW252及S0115有顯著的相關。由此可知豬第七號染色體長臂的2.4-2.5區域可能含有控制肋骨數的基因。而由雜交豬F1和F2屠體性狀的調查發現，具14對和17對肋骨數的豬隻頻率最低（<5%），具16對者則佔最多數（55.22%），此外，亦可發現肋骨數左右側不等的情形，其發生比率為5.22%（7/134）。綜合初步試驗結果與本研究發現與肋骨數相關的基因可能位於第一號和第七號染色體上。

關鍵語：豬、肋骨、微衛星型標記。

THE GENETIC REGIONS FOR PORCINE RIB NUMBERS

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A total of nine porcine microsatellite markers including SW552, S0316, SW2130 and SW780 on chromosome 1 and SW1122, SW147, SW252, S0115 and SW764 on chromosome 7 were used to genotype 14 and 17 rib-pair samples, which were from hog market. The result of chi-squared test between makers and number of rib pairs indicated that number of rib pairs and markers S0316 on chromosome 1 and SW1122, SW252 and S0115 on chromosome 7 were significantly related. By this, there was probably a gene for number of rib pairs on porcine chromosome 7q 2.4-2.5. In the investigation of carcass traits of hybrids F1 and F2, the frequencies of the pigs with 14 and 17 rib pairs were the least (<5%), but those with 16 rib pairs were the majority (55.22%). Besides, the asymmetry of left and right rib pairs was found in the study, and the frequency was 5.22% (7/134). In conclusion, the genes for number of rib pairs probably located on porcine chromosome 1 and 7 from preliminary result and this study.

Key Words: Swine, Rib, Microsatellite marker.

牛先天性下痢致死基因與單譜症基因同時檢測的方法

牛先天性下痢致死基因與單譜症基因同時檢測的方法

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建立多種基因同時檢測的方法不僅可節省檢測時間與人力，亦可降低檢測成本。本試驗嘗試利用Multiplex PCR針對牛淋巴球黏力缺失症(Bovine Leukocyte Adhesion Deficiency, 曾譯為牛遺傳性白血症, BLAD)與牛單譜症(Deficiency of Uridine Monophosphate Synthase, 直譯為尿核 單磷酸鹽合成 缺失症, 國際上簡稱為 DUMPS)兩個重要的遺傳疾病開發同時檢測的方法。以已知檢測牛淋巴球黏力缺失症引子與牛單譜症的引子同時進行PCR增幅不同特定DNA片段, 再同時以限制 TaqI與AvaI依序以37 3小時與65 4 小時進行分切, 分切後產物以4% Agarose電泳分析。由於所得的DNA片段長度有明顯的差異, 所以易於判讀不同的遺傳型, 顯示本方法確實可同時檢測此兩種遺傳疾病。

關鍵語：多樣的聚合 連鎖反應、牛淋巴球黏力缺失症、單譜症。

SIMULTANEOUS ANALYSIS OF BOVINE BLAD AND DUMPS ALLELES BY MULTIPLEX PCR FOLLOWED BY DIGESTION WITH TWO RESTRICTION ENZYMES

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An improved and simplified method allowing simultaneous genetic typing of Bovine Leukocyte Adhesion Deficiency(BLAD) and Deficiency of Uridine Monophosphate Synthase(DUMPS) loci has been developed. The method is based on simultaneously amplified the fragments of two genetic disease alleles by multiplex PCR, and concurrently digested the products by two restriction enzymes(TaqI and AvaI mixed together; 37 3hr and then 65 4hr) in the same buffer. All combinations of the known normal and mutant alleles could be detected by electrophoretic separation performed on the same agarous gel owing to the obvious differences in the length of the restriction fragments. The expected benefits of increased speed and decreased labour and cost seem to be worthwhile to use this improved method.

Key Words: Multiplex PCR, BLAD, DUMPS.

系譜矩陣與數值模擬協助乳用公牛遺傳資源保存

系譜矩陣與數值模擬協助乳用公牛遺傳資源保存

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遺傳物質。以現有保存的68頭源自多國的公牛冷凍精液，就2001年美國貢獻最大的20頭公牛遺傳資源保存進行模擬分析，發現標示顏色的系譜矩陣與保存特定遺傳資源的估算，可作為保種研究的協助工具。

關鍵語：矩陣式系譜圖、模擬、遺傳資源。

A MATRIX PEDIGREE ALONG WITH CHROMOSOME SEGREGATION SIMULATION FOR GENETIC RESOURCE CONSERVATION OF DAIRY CATTLE Y. C. Huang, S. C. Lee, D. Y. Lin, R. B. Liaw, C. H. Cheng and H. L. Chang Taiwan Livestock Research Institute, Council of Agriculture A color edited pedigree matrix ($k \times 15$, k offsprings with semen tanked and his 15 ancestors, including animal self) displays three generation genetic information for evaluation the desired genetic resources conserved. Mean and standard deviation of percentage of gene deposited from a particular sire was asymptotic estimated by sex-constrained chromosome segregation simulations through a serial of Bernoulli trails. Collection of semen from two and eight different sons can gather $74.1 \pm 4.5\%$ and $98.0 \pm 0.8\%$ chromosomes of the desired bull respectively. But, collection of semen from grandsons of the same son do not improve the conservation efficiency, four grandsons from the same son can only accumulate $47.0 \pm 2.2\%$ chromosomes of the interested male ancestor. Semen from grandsons of different sons will be helpful to increase the percentage of the desired genomic material reserved when sons' is not available. Analysis pedigrees of 68 bulls of a semen bank, the 20 most popular ancestors of USA top bulls in 2001 were estimated as ideal genomic source individually. Results from pedigree matrices and simulations offer feasible directions in targeting favorite genetic resource. Key words: Matrix pedigree, Simulation, Genetic resources

梅山豬與杜洛克豬雜交後裔之毛色及耳朵顯隱性遺傳

梅山豬與杜洛克豬雜交後裔之毛色及耳朵顯隱性遺傳

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豬毛色及耳朵下垂之遺傳基因，常被認為是顯隱性遺傳，亦曾被認為與豬肉的風味有關。耳下垂的黑色梅山豬(M)與立耳的紅棕色杜洛克豬(D)之雜交後裔於出生時紀錄其毛色，毛色區分為黑色(B)、黑金斑(L)、紅金斑(Q)及紅色(R)等四種。M與D正反雜交之雜交一代(F1)仔豬毛色為L、B、R與Q依序有50.6、47.3、2.15與0.0%。F1交配所產生雜交二代(F2)之仔豬毛色為L、B、R與Q分別為18.7、57.0、11.3及13.0%。F1母豬回交D公豬所產生仔豬毛色為L、B、R與Q分別為30.9、27.4、27.1及14.6%。仔豬於70日齡紀錄其站立時耳朵性狀，依據前傾下垂的耳尖所在位置，而區分為五種耳朵：短立耳(耳尖未蓋眼)、短垂耳(耳尖未超過眼與鼻吻端之中線)、中垂耳(耳尖至眼與鼻吻端之中線)、垂耳(耳尖超過眼與鼻吻端之中線)與長垂耳(耳尖與鼻吻齊或超過)。F1仔豬耳朵為短垂耳、中垂耳與垂耳分別為16.3、64.6及19.1%，F2仔豬耳朵為短垂耳、中垂耳與垂耳分別為30.0、40.0及20.0%。F1仔豬與F2仔豬的毛色頻率符合矯正卡方分布所進行遺傳分離適合度測定，其估值 2估值與理論值相符；但F1母豬回交D公豬所產仔豬，則出現L與B比率遠較正常分離比率高。F2仔豬並未有短立耳和長垂耳，顯示耳朵大小並非單一顯隱性基因所控制。

關鍵語：梅山豬、杜洛克豬、膚色、耳朵大小。

DOMINANCE AND RECESSIVE INHERITANCE ON COAT COLOR AND EAR SIZE OF HYBRID PIGLETS BETWEEN MEISHAN AND DUROC BREEDS

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Generally, lop ear is dominant and prick recessive. Uniform black coat color is dominant and uniform red is recessive. Quite apart from personal preferences and the desire to use color and ear as the meat badge of taste quality. Coat color and ear size traits of hybrid piglets between Meishan (M) and Duroc (D) breeds were recorded at birth. M has black coat color and D has red coat color. M has lop ears and D has prick ears. Coat color was classified into black (B), golden longitudinal stripes of black (L), golden longitudinal stripes of red (Q) and red(R). Frequency of L, B, R and Q coat color in hybrid piglets (F1) between M and D were 50.6, 47.3, 2.15 and 0.0%, respectively. The coat color of F2 piglets with L, B, R and Q patterns were 18.7, 57.0, 11.3 and 13.0%, respectively. In analysis of piglets produced from F1 sows and backcrossing with D boars, L, B, R and Q coat color were 30.9, 27.4, 27.1 and 14.6%, respectively. At 70 days of age, piglets were examined on their ears while standing. The lop-eared pig had a larger ear in size than those of prick-eared pigs. Therefore, according the position of the tip of ear short near to the eye or long enough to the snout, five types were designated: short-prick ear (short near to the eye), short-lop ear (between eye and snout but near to eye), medium-lop ear (between eye and snout but in half way), lop ear (between eye and snout but near to snout), and long-lop ear (over the snout). F1 piglets with short-lop, medium-lop or lop ear were 16.3, 64.6 and 19.1%, respectively. F2 piglets with short-lop, medium-lop or lop ear were 30.0, 40.0 and 20.0%, respectively. The values of adjusted χ^2 test on goodness of fit for Mendelian segregation of F1 and F2 hybrid piglets between M and D. The segregation percentage of coat color in piglets from F1 sow sired by D boars was greater than control did. There were no short-prick or long-lop eared piglets in F2 generation, which indicated that the ear size was not inherited as a single dominant gene.

Key Words: Pig, Coat color, Ear.

臺灣地區黑色豬隻的基因組及粒線體DNA分析

臺灣地區黑色豬隻的基因組及粒線體DNA分析

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為了解臺灣各地區黑色豬隻基因組及粒線體DNA之差異，乃應用隨機增殖DNA多態性指紋、粒線體DNA單股構形多態性及DNA序列分析技術，將來自臺灣嘉義、三峽、淡水、樹林、關廟、峨嵋、彰化及畜產試驗所畜試黑豬一號之樣品進行基因組及粒線體DNA之差異分析，並以臺灣地區現有之洋品種純種豬隻者做比較。以隨機增殖DNA多態性指紋分析結果為：1.比較畜試黑豬一號與各地區黑色豬隻的遺傳相似性，峨嵋與關廟兩地區黑色豬隻與畜試黑豬一號相似性較高(0.894與0.876)。2.若以桃園種、杜洛克、漢布夏及盤克夏四個品種與各地區黑色豬隻進行遺傳相似性分析，嘉義、彰化、三峽及樹林黑色豬隻各分別與桃園種相似性較高，而關廟、淡水及峨嵋黑色豬隻則各分別與杜洛克相似性較高。由粒線體DNA單股構形多態性分析結果得知，可依環帶之形態將之分出四種電泳態樣(定為A, B, C及D態樣)。歐美品種豬隻的粒線體DNA單股構形多態性電泳態樣皆有A 態樣，而亞洲品種豬隻的粒線體DNA單股構形多態性電泳態樣則無A態樣，關廟地區黑色豬隻的粒線體DNA單股構形多態性態樣皆為A態樣，由此結果顯示其雌親物質來自歐美品種。所有參試黑色豬隻的單股構形多態性態樣分佈為107 A (43.7%) , 47 B (19.2%) , 31 C (12.6%)及60 D (24.5%)態樣。粒線體DNA D-loop區域DNA片段序列分析顯示臺灣各地區黑色豬隻遺傳差異介於0.00 4.84 %。

關鍵語：黑色豬隻、基因組DNA、粒線體DNA。

STUDIES ON THE GENOMIC AND MITOCHONDRIAL DNA OF BLACK PIGS IN TAIWAN

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(1)Taiwan Livestock Research Institute, (2)National Cheng Kung University, (3)National Chung Hsing University In order to investigate the characterizations of genomic and mitochondrial DNA among black pigs raised in Taiwan. The randomly amplified polymorphic DNA fingerprinting, single strand conformation polymorphism of the mitochondrial DNA (mtDNA) and DNA sequencing techniques were employed for the studies. The animal DNA samples were collected from the areas in Chiai, Sanshia, Danshuei, Shulin, Guanmiaw, Emei, Changhua and Taiwan Livestock Research Institute (TB). Some foreign pure breeds of pigs were used for the control. The results of RAPD fingerprinting analysis showed that: 1. To compare the between-population genetic similarity between TB and black pigs from the other areas, the black pigs from two areas, Emei and Guanmiaw, were higher than the other areas (0.894 and 0.876). 2. To consider the between-population genetic similarity between black pigs of all areas in Taiwan and four pure breeds, Taoyuan, Duroc, Hampshire and Berkshire, the genetic characteristic of black pigs that came from Chiai, Changhua, Sanshia and Shulin were closely related to Taoyuan, and the genetic characteristic of black pigs that came from Guanmiaw, Danshuei and Emei were closely related to Duroc. Four types of SSCP band patterns (designated as A, B, C and D) were identified. 'A' type of SSCP pattern was in all European-American breeds, but not in Asian breed. SSCP patterns of all black pigs that came from Guanmiaw area belonged to 'A' type, this result indicated that their maternal parents were diverged from European-American breed. SCP analysis of black pigs of Taiwan revealed that the distributions for four SSCP patterns were 107 A (43.7%), 47 B (19.2%), 31 C (12.6%) and 60 D (24.5%). DNA sequence analysis of mtDNA D-loop region showed the genetic diversity among black pigs of all areas ranged from 0.00 to 4.84 %.

Key Words: Black pig, Genomic DNA, Mitochondrial DNA.

台灣畜產種原鳴叫聲資料庫之建立

台灣畜產種原鳴叫聲資料庫之建立

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本研究之目的為收集台灣畜產種原各種不同生活行為聲音檔，建立台灣畜產種原聲音資料庫，並比較物種間鳴叫聲音的崎異度。第一期作業共收錄雞、鴨、牛、羊、馬與豬的不同成長期鳴叫聲音，製成WAV格式純聲音檔，並進行頻譜分析，及提供網際網路線上下載(<http://www.angrin.tlri.gov.tw/>)。頻譜分析結果顯示，畜產種原鳴叫聲音具有豐富的多樣性，家禽的間歇短持續性音波較家畜出現頻繁，幼禽畜主基音音頻(如北京仔鴨3456Hz)較成禽畜(如北京成鴨1257Hz)高，而相近物種間亦存在極大的差異，如水牛常發出短而高的鳴叫聲但乳牛則較常發出低而持續的長音。畜產動物鳴叫音的收錄除了可充實國家多元化自然科學教材外，並可與其它設備結合(如錄音棒、發情偵測器、榨乳機械與仔畜人工哺乳器等)，協助畜群生產管理器械研發與畜產噪音管控研究。

關鍵語：聲音資料庫、家畜禽、音譜分析

CONSTRUCTION AN INTEGRATED SOUND DATABASE FOR LIVESTOCKS IN TAIWAN

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The objective of this study is to collect sound resources of farm animals to construct a sound database of Taiwan livestock and to compare their diversities. In phase I, "normal" sounds in different growth stages were collected for chickens, ducks, cows, goats, horses and pigs, which are recorded in digital format WAV files. A web page (<http://www.angrin.tlri.gov.tw/>) was designed for download or real-time playing the sound files. From sound spectrum analysis, high diversity existed in livestock of Taiwan. Poultry play short time sound with blank period inserted more often than other stocks. Major base tone of livestock is higher in early growth stage than mature stage (e.g., 3456Hz vs. 1257Hz sampled for duckling and fully developed Peking ducks). Significant difference between sound spectrum patterns was found among animals with phenotypes alike, e.g., buffalo often plays a short and high sound, but dairy cow play a long and low sound instead. The collected livestock sounds in database can be provided as one of good resources for natural science education of Taiwan. The other potential of applications are on improving machines and facilities for livestock management and noise control in livestock production.

Key Words: Sound database, Livestock, Spectrum analysis.

高乳量牛群乳質性狀選拔

高乳量牛群乳質性狀選拔

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乳量與乳質是泌乳牛群改良的重要經濟性狀。乳質性狀有脂肪率、蛋白質率、乳糖率和體細胞數。乳品工廠逐漸注重生乳體細胞數，並要求酪農生產高品質的生乳，因此，乳質性狀選拔是牛群育種的重要項目。在2001年1月至10月期間，參加個別牛隻乳樣品質檢測戶有290戶，生乳乳樣計有148251頭次。在不矯正個別乳量時，每日乳量平均21.4kg，脂肪率平均3.82%，蛋白質率平均3.27%，蛋白質脂肪比平均0.90，乳糖率平均4.66%，總固形物(%)平均12.45%，體細胞數平均41.5萬/毫升。體細胞數的場平均在30萬/毫升以內者，有93戶，進一步比較總固形物含量的場平均，在12.45%以上者，有42戶。當以夏季7月份乳量為基準，把超出族群平均者，視為乳量高的牛群，並就個別牛予以計算乳質選拔指數，篩選後的母牛群可登錄為耐熱品系。在2001年7月參加乳質檢測的泌乳牛有16384頭，其305-2X-ME乳量之平均為6336kg，場平均超過6336kg者有48戶，最高者有7751kg，這些場分佈於苗栗、彰化、雲林、嘉義、台南、高雄和屏東地區，佔當月DHI參測牛群22%。脂肪率、蛋白質率、乳糖率和體細胞數等乳質性狀選拔牛群是以總固形物含量、蛋白質脂肪比和體細胞數所組成的選拔指數，母牛依選拔指數配與進口的冷凍精液，改進目標每日乳量平均28.8kg，總固形物(%)平均13.44%，體細胞數平均26.6萬/毫升。

關鍵語：乳牛、乳質、選拔。

SELECTION ON MILK QUALITY IN HIGH YIELDING DAIRY COWS

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Milk yield and quality are major economic traits of dairy herd improvement. Milk quality traits are fat%, protein%, lactose%, and somatic cell counts (SCC). In order to meet the requirements of modern dairy factory with an upper limit of 300,000 cells/ml on SCC, selection on milk quality is a major concern in dairy herd improvement program at present. In analysis of 148251 milk samples from January to October of 2001 on 290 farms, means for daily yield of milk was 21.4 Kg with 3.82% of fat, 3.27% of protein, 4.66% of lactose, 12.45% of total solid content, and 415,000 cells/ml of SCC. There were 93 farms with their SCC values were less than 300, 00cells/ml, furthermore, 42 farms with the total solid content greater than 12.45%. Therefore, selection index will be formed with total solid content, protein to fat ratio and SCC after mid-term lactation. In July of 2001, the population mean of 305-2X-ME milk yield was 6336 Kg from 16384 milking cows. High yielding dairy herd was defined as herd with milking yield mean greater than population mean, 6336kg. A total of 48 herds were classified as high yielding herds with mean of top one herd being 7751Kg. Farms of 48 high yielding herds were scattered along western region of Taiwan, which accounted for 22% of total testing herds concurrently. Quota of frozen semen with high breeding value will be distributed by selection index.

The selection goals of the high yielding population are 28.8 Kg daily yield, total solid content 13.44% and SCC 266,000 cells/ml.

Key words: Cow, Milk quality, Selection.