(2006)

2007/12/3 15:50:14

34.

(1)　　　　(1)　　　(1)　　　(1)　　　(2)
(1)　　　　　　　　　(2)

1 2 4 7 28　　　　　　　　　　MRS　　　　　631　　　　　　　　　　(curdling reaction)　　　(Gramstain)　酶　(catalast test)
177　　　　　16S rDNA　　　　　　　　　　　　　46　　　　Uncultured bacterium Enterococcus faecalis Lactobacillus johnsonii Lactobacillus reuteri Lactobacillus salivarius　　　　6　　　(Lactobacillus)
0.3%　　　　　　Lactobacillus salivarius 28DM68
Lactobacillus johnsonii 4DM45
10% 53%

ISOLATION OF POTENT LACTOBACILLUS STRAINS AS PROBIOTICS FOR THE BROILERS

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The feces from 1, 2, 4, 7 and 28 days old chickens are sampled and cultured on the MRS agar. Screening of the 631 single colonies by curdling reaction, Gramstain test and catalast test, we get 177 strains of lactic acid bacteria (LAB). These LABs are Uncultured bacteria, Enterococcus faecalis, Lactobacillus johnsonii, Lactobacillus reuteri and Lactobacillus salivarius as identified by the 16S rDNA sequencing. The six identified Lactobacillus strains are further studied for their acid productivities, growth rates and tolerance for acid and bile salts. Among them, the Lactobacillus salivarius 28DM68 has the best acid productivity and Lactobacillus johnsonii 4DM45 shows good performance on the tolerance for acid and bile salts. The viability of the freeze-dried culture for Lactobacillus salivarius 28DM68 and Lactobacillus johnsonii 4DM45 are 10% and 53%, respectively.

Key Words: Lactobacillus, Probiotics, Broiler, Isolation

酶

44. 酶

(1) (3)　绣　(1)　　(1)　　(2)　　(2)　　(1)　　(3)

(1)　　　　　　　　　　(2)　　　　　　　　　　　　　　(3)

DNA　　　　　　　　　　　　　　15-17 Kb　　　　　2
ribosomal RNA, rRNA　22　　　　　　　　transfer RNA, tRNA　13　　　　　　protein
coding genes　　　D　　control region, D-loop　　　　　　　　酶
(cytochrome c oxidase subunit 1, CO1)
CO1　苷　　　　　　1545 bp　blast
CO1　　　　　　　　　　　　99　　　　　　　　　　81
82　　81　　81　　77　　　　　CO1

酶　　　　　　　DNA

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

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

Mitochondrial DNA is a circular structure of double strain nucleotide, about 15-17 Kb in mammals. There are 2 ribosomal RNA, 22 transfer RNA, 13 protein coding gene and 1 D-loop region in mitochondrion. Mitochondrial cytochrome c oxidase subunit I (CO1) has become an important marker region for species barcode. Two pair of primers, a total length of 1545 bp, were designed in this trial to sequence CO1 nucleotide in Lanyu pig. Comparing with the sequence of other species by blast software, the similarity of CO1 between Lanyu and other pig breeds reached a high level of 99 %, while the divergence among Lanyu and other species were 81 % in cow, 82 % in goat, 81 % in Sika deer, 81 % in horse and 77 % in chicken. The results implicated that mitochondrial CO1 was applicable for barcode editing and species identity in farm animals.

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

b

45.　　　　　　　　b

(1) (3)　绣　(1)　　(1)　　(2)　　(2)　　(1)　　(3)

(1)   (2)   (3)

                                                                      DNA
                                                                       37
           DNA D-loop   b (Cytochrome
b, Cyt b)
   NADH6 (NADH dehydrogenase subunit 6) tRNA-Glu Cyt b   1737 bp   MEGA3.1
           Cyt b
                                   100   96

               b   DNA

IDENTIFICATION AND PHYLOGENETIC ANALYSIS OF MITOCHONDRIAL CYTOCHROME b OF PIG

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

Key Words Cytochrome b, Mitochondrial DNA, Lanyu pig

54.

           (1)   (1)   (1)   (2)   (1)   (1)   (1)
(1)   (2)

2004

L7 L9 L11 L12   998

465   16   95.7 %   17

10   40   26

L7 L9 L11 L12   G1 G2 G3

16   ±   1485 ± 24   1384 ± 17   1406 ± 22   1552 ± 24

1484 ± 19   L9 1491 ± 21   1530 ± 17   1552 ± 24   1507 ± 24

1461 ± 20   1438 ± 20   1512 ± 19   P

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

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

57.

(Coturnix coturnix)

(Phasianus colchicus) 5 5   DNA   SPIN12 SPIN13   鍵
(PCR)

DNA   PCR   Z W
(Spindlin)   intron   W
(internal control)   鍵
(RFLP)

ANALYSIS OF SPINDLIN GENE IN POULTRY

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

Key Words: Poultry, Spindlin gene, Sex identification

59.

(1)   (1)   (1)   (1)   (1)   (1)   (2)
(1)   (2)

85-95%

pH   6.8

PCR   TA   DNA
52   521

Fibrobacter succinogenes (96%)
bacteroidetes(32/52), Fibrobacteres (1/52), Firmicutes (18/52)   unclassified
Bacteria(1/52)   75   74   Neocallimastix sp.
Trichosporon jirovecii
酶

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

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

Key Words: Rumen, Microorganism, Diversity

(G6S)

61. (G6S)

(G6S) 酶
苷
1 12 8
17 G6S 6 (TG) 7 (CG) 4
(G6S) 2 75%(3/4)

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

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

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

63.

(   ) 133

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

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

Key Words: Graphs, additive relationship, Kinship

73.

agrkb.angrin.tlri.gov.tw   XOOPS (eXtended
Object-Oriented Portal System)   PHP

www.angrin.tlri.gov.tw

7   18   9   20   8   13   6
27

KNOWLEDGE DATABASE FOR ANIMAL BREEDING IN TAIWAN

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

Key words: Database, World web, Breeding

DNA

75.　　　　　　DNA

　　(1)　　　(1)　　　(1)　　　(1)　　　(1)　　　(2)　　　(1)
(1)　　　　　　　　　　　　　　(2)

　　　　　　　DNA　　　　　　16　　　(　　12　　　4　　　)
　　　DNA　　(16,785-16,788 bp)　DNA　　　　　56　　　　　30
　　　　11　　　　　　　12　　　　18　　　　　6
　　　RNA(tRNA)　1　　　　　12S　　　(rRNA)　14　　
D-loop　　　2　　　3　　　　　　　16S rRNA　　　DNA

　　　DNA

　　　　　DNA

Complete Sequences of Mitochondrial DNA of Taiwan Native chicken

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

Key Words: Native chicken, Mitochondrial DNA, Sequence variation

77.

　　(1)　　　(1)　　　(1)　　　(1)　　　(1)　　　(1)　　　(2)

(1)   (2)

                                                                    (305-2X-ME)
              10,000   10   10   Ten Tons
                                    (Ten Tons Cow)

         2001   32 (28,381   0.1%)   2002   103
    2003   146   2004   254   2005   312 (37,820   0.8%)
                  9 (312/32)   2001 2005   52 57 50 56
    55   +1113 +988 +1051 +960 +949 kg   +41 +32
    +40 +34 +35 kg 2006   33,064   1,135 (3.4%)   +894
kg   +33 kg   150 (293   51.2%)   10   40
    (293   13.7%)   797   70.22%   2006   12
    44   44   12 (   )   8

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

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

Key Words: Dairy cattle, Selection, Milk yield

88.

(1)　　　　(1)　　　(1)　　　　(1)　　　　(2)　　　　(1)
(1)　　　　　　　　(2)

(L9)　　　(P)
P9(　　P　×L9　)　9P(L9　×　　P　)
9P

16　　　　　　　　　　　　P9　(P

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

97.

(1)　　　　(1)　　　(1)　　　(1)　　　(1)　　　　(2)　　　　(1)　　　　(1)
(1)　　　　　　　　(2)

92-2

L727-11　　　　1.48
2.7　　　　　　　　　　　　　2.26~3.22
3.6　　　　　　　　　　　CC　　　　　　　　　　B
LL2　HL3　HL4　　　　　　50

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

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

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

Key Words: Feed efficiency, Genetic marker, Swine