(2016)

2017/12/5 10:06:57

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

G8   1
280   A   B   C   68   50   168   266
1   150   210   1   185± 13
280   22   125   280
70. 2± 18. 0   73. 6± 15. 4%   1   280
P

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

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To understand the egg production performance of red feather chickens in Feng Hui breeding farm. Totally, 266 hens from 3 lines of current selection breeding flock including 68 hens of A line, 168 hens of C line and 50 hens of E line were carried out the age at first egg (AFE) and egg number up to 280 days of age (EN280) test. The AFE of hens was ranged from 150 to 210 days, and the average AFE of hens was 185± 13 days. The EN280 of hens was ranged from 22 to 125 eggs, and the average EN280 and egg production rate of hens were 70. 2± 18. 0 eggs and 73. 6± 15. 4%, respectively. There were significant differences in the age at first egg(AFE) and egg number up to 40 weeks of age (EN40) were detected among the three lines (P
Key Words: Red feather native chicken, Egg production performance, Test

LTMR)

LTMR)

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

TDC) www.tlrihc.gov.tw)

LTMR)

http://tmrsite.com.sala1.arvixe.com/)

5

NRC 72

226 3 1)

25

2)

Revised simplex method

3)

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

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It was beneficial to precision management of the total mixed ration for dairy cattle, if the dairy farmer using network system to calculate the feed formulation of dairy cow, it was also an important tool in management of the dairy cows. In order to promote the production technology in dairy industry and develop high quality information service system for animal products in the Hsin-Chu Branch, Livestock Research Institute. A system of the 'Online linear programming of total mixed ration (LTMR) for dairy cattle' was developed in the dairy cloud information service in Taiwan (TDC) (
http://tmrsite.com.sala1.arvixe.com/) of the Hsin-Chu Branch, Livestock Research Institute website. There were five module included 'Easy version','Teaching', 'Dairy cow', 'Row Material' and 'Formula' in the FTMR system. The process of apply was basic on the production performance of dairy cow to adapt grouping on the 'Dairy cow' functional options, then a front file was formed prior to calculate feed formula, then we could establish a raw material file by system increased or creation voluntarily manner. The raw material relation file was designed that basic on 'Nutrient Requirement Council' suggestion, there were 72 ingredient field included and 226 raw species available choice. The methods of the feed formulation calculator were available in this system (1) 'Common formula' – there were 25 species usually used feed formula for farmer in Taiwan, it could be as reference at feed modulation. (2) 'Floor coast feed formulation calculator' – The 'Revised simplex method' in the Linear program was used to plan solving, both nutrition demand of dairy cow and smallest coast benefit were balance considerable, that was suitable for precision management of cows for dairy farmer. (3) 'Raw nutrition calculator' – The nutrition demand was main considered in principle, we could set up variable raw apply quantity, then the nutrition demand ratio was calculated by computer.

Key Words: Calculator system, Dairy cow, Feed formula

Arduino Mega 2560　　　) PT580
Handheld Reader　　　　) Load Cell　　　) RTC Real time clock,　　　)
LCD　　)
SD　　Secure Digital Memory Card　　　)　　　　　SD

BOSCHE　　101-001　)
100　300 kg　　　30 cm
SD
BOSCHE　10　　1/3　Handheld Reader　　　134.2 KHz
7000　　　　　9　22 cm

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

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

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

Key Words: Breeding pigs, Litter test, Weighting traits

37° C   55° C

                                                                9

                37° C   5   55° C   4
    9   DNA   16S rRNA   9   5
   Bacillus licheniformis 2   Bacillus pumilus 1   Bacillus subtilis   1
Bacillus mojavenis   B. mojavenis

Isolation of lipolytic enzyme producing bacteria from activated sludge

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

Key Words: Activated sludge, Lipolytic activity, Selective medium

3   2   R6

7~9   240.00 ±

66.55 182.50 ± 38.41   177.58 ± 61.71   3.93 ± 9.2 3.24 ± 8.89

3.43 ± 1.45 /   897 ± 164 571 ± 133 608 ± 216   89.67

± 4.30 85.52 ± 10.08 75.51 ± 22.00 %   76.85 ± 6.14 69.86 ±

14.37 60.64 ± 20.82 %   17.33 ± 2.79 21.81 ± 19.68   19.29 ±

13.86 %   93.48 ± 2.05 96.23 ± 1.58 87.28 ± 27.37 %

Sperm quality of LRI Duroc boar in summer season

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An early prediction of semen quality by regular microscopic examination would help predicting donor sperm fertility ability thereby elevating the pregnancy rate of sows. It is not enough to accurately predict fertility ability of boar via the traditional semen assessment includes sperm concentration, vitality and morphology, and etc. Three R6 LRI Duroc boars at age of 2 years old (on average) were used in this study for assessment of semen quality in summer season (July, August, and September). All boars were not raised in wet pad and forced ventilation house. The results showed that respectively, in July, August and September, the semen volume was 240.00 ± 66.55, 182.50 ± 38.41 and 177.58 ± 61.71 mL; average semen density was 3.93 ± 9.2, 3.24 ± 8.89, 3.43 ± 1.45× 108/mL; average sperm count was 897 ± 164, 571 ± 133 and 608 ± 216 × 108; percentage of live sperm was 89.67 ± 4.30, 85.52 ± 10.08 and 75.51 ± 22.00 %; percentage of live sperm with acrosome intact was 76.85 ± 6.14, 69.86 ± 14.37 and 60.64 ± 20.82 %; percentage of mitochondrial status was 17.33 ± 2.79, 21.81 ± 19.68 and 19.29 ± 13.86 %; and percentage of live sperm with normal structural chromosome was 93.48 ± 2.05, 96.23 ± 1.58 and 87.28 ± 27.37 %. These finding demonstrated that sperm quality of LRI Duroc boar not only did not influenced by summer heat stress, but even at high quality.

Key Words: LRI Duroc Pig, Sperm, Summer

DNA   2

    DNA   ORF   2   2

LipoR1 LipoR2)   LipoR1   1, 155 bp   384-aa   LipoR2   960 bp

    319-aa   2

            39%   86%   Arpigny & Jaeger

    LipoR1   LipoR2

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

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

Key Words: Lipolytic gene, Metagenomics, Rumen

                28   DNA

    5   BS   4

        BS   10. 71%

Genotyping of genetic defects for young bull candidates

R. B. Liaw, J. C. Chen, K. H. Lee, J. Y. Chen, Y. S. Jea and M. C. Wu
Livestock Research Institute, Council of Agriculture, Executive Yuan

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

Key Words: Genetic defect, Genotype, Young bull candidate

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

DH

DH   99060201
        www.tlri.gov.tw)   10
    4   6   305-2X-ME   305MY)   8362 ± 194 kg
SCS)   5.67 ± 0.94
        SCS   20%   305MY   50%   15,439
                                    RA)
        NAAB)   007H008778
            PTAM   352.9 kg SCS   2.7   RA   - 1.7%
                305MY   352.9 kg SCS   2.7
            1.7%

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

selection of candidate dairy bulls

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It was important breeding strategy for dairy farmer by mating simulation system to choose adapted breeding bull and improve dairy production, these genetic information of the candidate dairy bulls from data editing would link the imported frozen semen database, then we could know more imported data. Took the DH cow NO. of ' 99060201' for instance, which was the fourth lactation and the latest six tested milk data, the mean of the 305-2X-ME milk yield (305MY) was 8362 ± 194 kg and the somatic cell count score was 5.67 ± 0.94, and the data source from 'Dairy cloud information service in Taiwan' web site (www.tlri.gov.tw). This dairy cow was likely some problem with high production milk yield with subclinical mastitis. If we used mating simulation system to choose 20% bull select intensity grade for the SCS and 50% for the MY, after the computer calculation, there were 15,439 bull were choose and we further assessed the cow with slope rump angle (RA), the ' 007HO08778' bull of the NAAB code was considerable. We could find the 'Predicted Transmitting Abilities' for Milk yield (PTAM), the 'Predicted Transmitting Abilities' for SCS and the 'Standard Transmitting Abilities' for RA were 352.9 kg, 2.7 and -1.7% for this bull, respectively. That means we could predict the genetic improved volume were increase 352.9 kg, reduced 2.7 score for the SCS and then corrected 1.7% of the RA mean of same period for the offspring dairy cows, respectively. It was favorable for us to take corresponded breeding method for the different performance of dairy cattle by using the mating simulation system.

Key Words: Mating simulation, Frozen semen, Bull

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

                                          2010   1
   40   4   B
   D   2012   2013   2014
                  E   C   31
           9   SAS   2010
2016   13,690   A   C   E   4,453   5,782
3,454   A   C   G2 G3 G4 G5 G6 G7 G8 G9
              0.1367 ± 0.0106   0.1391± 0.0396   0.2229± 0.0367   0.2213± 0.0927
   0.3096± 0.0118   0.3121± 0.0220   0.3471± 0.0474   0.3857± 0.0154   0.4175± 0.0123
0.4517± 0.0515   0.4801± 0.0106   0.5142± 0.2482   0.5370± 0.0113   0.1974± 0.2482

0.5842± 0.0171   0.2735± 0.0243 E   G2 G3   G4
        0.1250± 0.0178   0.1250± 0   0.2496± 0.0235   2,331
    0.3755± 0.1536   C   G7   A
    G8   0.5

Inbreeding coefficients of red feather native chicken selction flork in Feng Hui breeding farm

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

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

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

                                                              G8   3   152   7
                        54   A   57   C   41   E
    1   5   3
                        16-17   10   3

8   18   21   100

99   A C   E   92.8%   956/1,036)

86.6% 828/956)   91.0% 1,238/1,360)   79.1% 979/ 1,238)   90.2% 753/835)   76.4%

575/753)   3   91.2%

2,947/3,231)   80.8% 2,382/2,947)

P > 0.05)   P = 0.088)

P

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

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

Key Words: Fertility, Hatchability, Red feather native chicken

?   DNA

?   DNA

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

(1)   (2)

                                        pituitary specific transcription

factor, POU1f1)   ?   Calpastatin, CAST)DNA
             DNA   POU1f1   GenBank
   DQ826413   91   10-446
        8   18-19   CT   TC   45-370
   3   48   102   365   ?   T   G   T/G   G   T   G/T   C
   T   C/T   437-439   6   CAST   DQ414516
             (1) 174   CAST   1-254   18
6   CAST   157   G-A   (2)   60   5'-GT
2 bp   0-6   (3)   63   T   G   T/G
POU1f1   CAST   DNA

                    ?

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

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

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

                    XY

                    XY

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

(D)   (L)   (Y)   110Kg(100Kg)
160+7   201101   201604   42   4,713   D
2,482   D   201   L   1,154   L   313   Y   466   Y   97
SY11(   ) X   73cM   (bp)
161~177bp   9   (   )
     D   175+0   171+0   D   171+4   175+0   L   171+0   167+0   L   167+4
171+0   Y   171+0   169+0   Y   171+0   169+2   D
175   171   167bp   L   171   167bp   Y   171   169bp
                                                     204
          D L Y   175+0 171+0 171+0

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

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

Key Words: Breeding pig, Genetic marker, Conformation contest