

第三十二卷(2003)

豬隻第六號染色體微衛星型遺傳標記與經產母豬產仔性能相關性研究

日期2006/9/29 16:09:56

豬隻第六號染色體微衛星型遺傳標記與經產母豬產仔性能相關性研究

廖仁寶 賴永裕 吳明哲 黃鈺嘉 張秀鑾

行政院農業委員會畜產試驗所

在豬隻第六號染色體上平均選擇十個微衛星型遺傳標記，此十種標記在第六號染色體連鎖圖譜約佔166分摩根（cM），用以篩檢242頭種母豬DNA基因型。三種產仔性狀包括總產仔數、活仔數及仔豬存活率被分析。基因型檢測結果顯示每個遺傳標記之交替基因分布，皆有品種間差異。以一般線性模式和最小平方方法分析母豬個別遺傳標記交替基因與其產仔性能之結果顯示：一些標記交替基因與三個品種母豬的產仔性能極顯著相關並具有正效應。例如S0099-B7與SW1881-B15對藍瑞斯母豬具有正效應，同時，SW1129-B1對約克夏母豬和SW2406-B1、SW1881-B6及 S0099-B5對杜洛克母豬具有正效應。同樣地，不同品種母豬具有某些交替基因，其產仔性能則會比未具有該交替基因者差。

關鍵語：微衛星型標記、交替基因、產仔性能。

ASSOCIATION STUDY BETWEEN MICROSATELLITE MARKERS ON SWINE
CHROMOSOME 6 AND THE LITTER PERFORMANCE OF PAROUS SOWS

R. B. Liaw, Y. Y. Lai, M. C. Wu, Y. C. Huang and H. L. Chang

Livestock Research Institute, Council of Agriculture, Executive Yuan

A total of ten microsatellite markers averagely spread on swine chromosome 6 (SSC6) were used to genotype 242 parous sows, including Landrace, Yorkshire, Duroc and Berkshire breeds. These markers spanned about 166 cM on the linkage map of SSC6. Three traits including litter size at birth and born alive as well as the corresponding survivability of piglets were considered in the study. Result indicated that there was significant breed effects existed in the distribution of allele frequency for all markers analyzed. The general linear model via least-squared method was further applied to study the relationship between litter performances described above and the presence of individual allele for parous sows in Landrace, Yorkshire and Duroc breeds. Both positive and negative effects of alleles on sows' litter performances were observed. For example, the marker-allele groups (S0099-B7 and SW1881-B15), (SW1129-B1), and (W2406-B1, SW1881-B6 and S0099-B5) were beneficial for Landrace, Yorkshire and Duroc sows, respectively. However, alleles with inferior effects on sows' litter performances were also found in this study.

Key Words: Microsatellite marker, Allele, Litter performance.

多產豬種之培育： . 梅山豬與杜洛克豬雜交後裔之體型性能

多產豬種之培育： . 梅山豬與杜洛克豬雜交後裔之體型性能

張伸彰(1) 黃憲榮(1) 許晉賓(1) 李世昌(2) 涂海南(1) 吳明哲(3) 張秀鑾(2)

(1)行政院農業委員會畜產試驗所高雄種畜繁殖場 (2)行政院農業委員會畜產試驗所遺傳育種組
(3)行政院農業委員會畜產試驗所新竹分所

本研究旨為研究梅山豬與杜洛克豬雜交選育後裔體型性狀之變化，供未來育成新品系豬種之參考。試驗豬群包括用於進行正反雜交一代之種原豬群（梅山豬，M，公與女豬59與60頭、杜洛克，D，公與女豬26與22頭）、M母豬與配D公豬之F1代後裔（MD，公與女豬134與171頭）、D母豬與配M公豬之F1代後裔（DM，公與女豬95與157頭）、MD母豬與配MD公豬之F2代後裔（md，公與女豬104與152頭）、MD母豬與配DM公豬之F2代後裔（dm，公與女豬108與157頭）、md母豬與配md公豬之F3代後裔（mdmd，公與女豬49與67頭）、dm母豬與配md公豬之F3代後裔（dmmd，公與女豬46與69頭）、md母豬與配dm公豬之F3代後裔（mddm，公與女豬47與49頭）、dm母豬與配dm公豬之F3代後裔（dmdm，公與女豬45與70頭），計有公與女豬713與920頭。參試豬隻於210日齡測定體型性狀，包括體高、十字高、體長、胸圍、管圍、尾徑、後幅、胸幅、前幅和胸深等十項。結果顯示：F1代正反雜交之體型性狀，除尾徑外，具顯著的品種效應，MD與DM顯著地較M有較大的體型性狀（P

關鍵語：梅山豬、杜洛克豬、體型性狀。

DEVELOPMENT OF PROLIFIC LINE IN SWINE: V. BODY
CONFORMATION IN F23 OF MEISHAN AND DUROC CROSSES

S. C. Chang(1), H. J. Huang(1), C. B. Hsu(1), S. C. Lee(2), H. N. Twu(1), M. C. Wu(3) and
H. L. Chang(2)

(1) Kaohsiung Animal Propagation Station, (2) Breeding and Genetics Division
(3) Hsinchu Branch, Livestock Research Institute, Council of Agriculture, Executive Yuan

The purpose of this study was to evaluate the body conformation of Meishan(M) crossing with Duroc(D) for the reference of potential new strain exploration in Taiwan. Tested herd included F1 pigs of M (59 boars and 60 gilts), D (26 boars and 22 gilts), MD defined as the progeny of M sows sired by D boars (134 boars and 171 gilts), and DM defined as the progeny of D sows sired by M boars (95 boars and 157 gilts), F2 pigs of md defined as the progeny of MD sows sired by MD boars (104 boars and 152 gilts), and dm defined as the progeny of MD sows sired by DM boars (108 boars and 157 gilts), F3 pigs of mdmd defined as the progeny of md sows sired by md boars (49 boars and 67 gilts), mddm defined as the progeny of md sows sired by dm boars (46 boars and 69 gilts), dmmd defined as the progeny of dm sows sired by md boars (47 boars and 49 gilts) and dmdm defined as the progeny of dm sows sired by dm boars (45 boars and 70 gilts). A total of 713 boars and 920 gilts were evaluated at 210 days of age. Ten traits evaluated were body height, body length, cruciate height, chest girth, girth of limb, girth of tail, rump width, chest width, shoulder width and chest depth. Results showed that the effects of breeds were

significant for body conformation considered in F1 except for girth of tail and both MD and DM had larger body conformation when compared with those of corresponding traits in M as expected (P

Key Words: Meishan pig, Duroc pig, Body conformation.

多產豬種之培育： . 梅山豬與杜洛克豬雜交二代產仔性能

多產豬種之培育： . 梅山豬與杜洛克豬雜交二代產仔性能

張秀鑾(1) 黃憲榮(2) 張伸彰(2) 許晉賓(2) 李世昌(1) 涂海南(2) 吳明哲(3)

(1)行政院農業委員會畜產試驗所遺傳育種組 (2)行政院農業委員會畜產試驗所高雄種畜繁殖場
(3)行政院農業委員會畜產試驗所新竹分所

本研究旨在評估梅山豬(M)與杜洛克(D)豬雜交二代產仔性能, 供作未來新品種(系)豬隻培育之參考。試驗豬群源自MD母豬(M母豬與配D公豬)與配MD或DM(D母豬與配M公豬)公豬產生之雜交二代(包括MDMD與MDDM兩種遺傳組合), 經正反雜交產生四種雜交三代遺傳組合。分析資料來自37頭種公豬與119頭種母豬所分娩202胎之產仔性能, 評估性狀包括分娩總仔數、活仔數、三週齡與離乳窩仔數、分娩活仔豬窩重、出生個體重、三週齡與離乳個體重、仔豬出生存活率與三週齡育成率。經矯正母豬分娩季節與分娩產次後, 比較仔豬離乳前之各項窩仔性能發現, 除仔豬出生重(P0.05)。但前述產仔性狀卻顯著地受到分娩季節與母豬分娩產次的影響(P

關鍵語: 豬、品種、產仔性能。

DEVELOPMENT OF PROLIFIC LINE IN SWINE: VI. LITTERING PERFORMANCES IN
F2 OF MEISHAN AND DUROC CROSSES

H. L. Chang(1), H. J. Huang(2), S. C. Chang(2), C. B. Hsu(2), S. C. Lee(1), H. N. Twu(2),
M. C. Wu(3)

(1)Breeding and Genetics Division (2) Kaohsiung Animal Propagation Station
(3) Hsinchu Branch, Livestock Research Institute, Council of Agriculture, Executive Yuan

The objective of this study was to evaluate the littering performances in F2 of Meishan (M) and Duroc (D) crosses for the reference of potential new breed/strain exploration in Taiwan. Parental stocks of tested animals were originated from MD (progeny of M sow sired by D boar) sows mated with MD or DM (progeny of D sow sired by M boar) boars, i.e., MDMD or MDDM genetic combination group in the F2 generation. Thus, all animals evaluated could be classified as one of the four genetic groups, which were from MDMD and MDDM crosses. A total of 37 boars and 119 sows were used to produce 202 litters. Littering traits evaluated were liter size at birth, born alive, at three weeks of age, and at weaned, litter weight and individual weight at birth, at three weeks of age and at weaned, and piglet survivability at birth and at three weeks of age. Results indicated that no significant genetic group effects on traits analyzed in this study except for piglet birth weight after records being pre-adjusted for farrowing season and sow's parity. However, F2 sows produced larger litters in cool season than those in hot season (P

Key words: Pig, Breed, Littering performances.

登錄種豬取得產肉登錄號的世代間距

登錄種豬取得產肉登錄號的世代間距

賴永裕 李世昌 張秀鑾 黃鈺嘉 吳明哲

行政院農業委員會畜產試驗所

種豬檢定站完檢的公豬和母豬會取得產肉登錄號，從1983年1月1日至2003年3月6日出生，計有11,812頭；包括5,643頭杜洛克（D）、4,110頭藍瑞斯（L）2,014頭約克夏（Y）與45頭漢布夏（H）。產肉登錄的完檢豬是2,897頭血統登錄種公豬和6,684頭血統登錄種母豬的後裔豬。血統登錄種豬可取得產肉登錄號的資格為需有參頭後裔豬在檢定站完檢而取得產肉登錄，但這參頭後裔豬要來自不同胎，意即同父異母三胎或同母異父三胎。結果顯示，計有999頭血統登錄種公豬和139頭血統登錄種母豬可藉此而取得產肉登錄號。進一步分析親子代間出生日期之間距，並視為產肉登錄的世代間距。種公豬為親代時，則D、L、Y與H品種之平均世代間距分別為809、815、888與758天；種母豬為親代時，在D、L與Y品種分別為1,332、1,472與1,506天，無H品種母豬取得產肉登錄號。在D、L與Y品種，同父異母的世代間距較同母異父者均縮短1.5年。然同母異父的產肉登錄世代間距最短者也有兩年以內者，在D、L與Y品種分別為669、704與638天；而同父異母時，更有一年內者，在D、L與Y品種分別為346、337與350天。結果顯示產肉選拔可在一年一世代內完成。

關鍵語：登錄、生長、選拔。

GENERATION INTERVAL OF MEAT PRODUCTION IN BREED REGISTRATION OF PIGS

Y. Y. Lai, S. C. Lee, H. L. Chang, Y. C. Huang and M. C. Wu

Livestock Research Institute, Council of Agriculture, Executive Yuan

Registration on meat production of growing pigs must be tested at the Boar Test Station and the pig was granted from the growth performance test. A total of 11,812 head of granted pigs with registration on meat production was analyzed with their birth dates from 1983/1/1 to 2003/3/6 and there were 5,643 head of Duroc (D), 4,110 head of Landrace (L), 2,014 head of Yorkshire (Y) and 45 head of Hampshire (H). They were progeny of 2,897 and 6,684 blood registered boars and sows, respectively. Blood registered boar or sow can be proved as meat registered breeding stock when three of the corresponding progeny receiving meat registration from the Test Station. However, the three progeny must come from three different litters either from paternal half siblings or maternal half siblings. There were 999 boars and 139 sows having the progeny proof on meat production. Generation interval was then calculated from both birth dates between parent and offspring. When paternal siblings used, the mean generation interval were 809, 815, 888 and 758 days in D, L, Y and H boar, respectively. The corresponding intervals were 1,332, 1,472 and 1,506 days in D, L and Y sows, respectively. None of H sows received meat registration. Results concluded that paternal siblings for meat registration in D, L and Y boars were 1.5 years lesser than that of maternal siblings. However, there were still cases of maternal siblings with a generation interval of 2 years or less and were 669, 704 and 638 day in D, L and Y sows, respectively. In paternal siblings, the corresponding interval could be even shorter and less than one year, which were 346, 337 and 350 days of generation interval in D, L and Y breed, respectively. It confirmed that one year one

generation on meat production via mass selection program could be done.

Key words: Registration, Growth, Selection.

台灣DHI牛群遺傳監控 - 泌乳母牛父畜追蹤

台灣DHI牛群遺傳監控 - 泌乳母牛父畜追蹤

黃鈺嘉 李世昌 楊德威 張秀鑾 陳志毅 李素珍 曾青雲 張菊犁 吳明哲

行政院農業委員會畜產試驗所

以近五年(1999 – 2003)牛群改良計劃(DHI)之測乳母牛進行父畜遺傳檢測追蹤，結果發現 1999 年79596 頭次測乳之父畜單譜症之雜合型與正常型(DP/ TD) 比值為 0/603、淋巴球黏力缺失症之雜合型與正常型(BL/ TL) 比值為 72/2502，脊椎畸形複合症之雜合型與正常型(CV/ TV) 比值為 175/210。2003 年(1 – 10月15日) 188430 頭次測乳之父畜DP/ TD 比值為 0/13962、BL/ TL 比值為 673/54625， CV/ TV 比值為 4671/19348。由近五年資料顯示，DHI計劃推動，除測乳頭數增加外，可追蹤遺傳檢測之系譜數比例亦大幅增加(2652/79596 至 58135/188430)。五年內除已無單譜症雜合型父畜外，由 2003年淋巴球黏力缺失症之雜合型與正常型(BL/ TL) 比值為 673/54625(1.23%)，預計母牛群之淋巴球黏力缺失症亦可在未來五年內漸降至1% 以下，但脊椎畸形複合症之雜合型之頻率則偏高(即使假設未檢測公畜均為正常型，亦至少為 4671/188430=2.48%)，進一步系譜追蹤脊椎畸形複合症之雜合型父畜來源，發現一頭高頻度使用的 AI 公牛 PARADISE-R ROEBUCK 為 494 頭母牛之父畜，2003年共有2043 頭次女兒的測乳紀錄，每 100 頭次DHI 測乳中至少有一次為 ROEBUCK 的女兒牛乳樣(2043/188430)，佔約為全部雜合型的一半(2043/4671)。短期內除需嚴格進行精液進口把關外，酪農需注意自留小公牛選拔與庫存精液系譜追蹤。

關鍵語：台灣、荷蘭牛、遺傳缺陷。

GENEIC MONITORING DHI COWS BY PEDIGREE TRACING

Y. C. Huang, S. C. Lee, T. W. Yang, H. L. Chang, J. Y. Chen, S. J. Lee, C. Y. Tseng, C. L. Chang and M. C. Wu

Livestock Research Institute, Council of Agriculture, Executive Yuan

This trail traced genotypes of sires of DHI test records in 1999 – 2003 period. Results found sire's carrier/normal ratios of 79596 test records in 1999 were 0/603(DP/TD) for DUMPS((Deficiency of Uridine Monophosphate Synthase), 72/2502 (BL/TL) for BLAD(Bovine Leukocyte Adhesion Deficiency) and 175/210 for CVM(Complex Vertebral Malformation). Sire's carrier/normal ratios of 188430 test records in 2003(Jan. to 15 Oct.) were 0/13962 (DP/TD) for DUMPS, 673/54625(BL/TL) for BLAD and 4671/19348(CV/TV) for CVM. The progresses of the DHI program were not only increased the enrolled cow numbers but also increased the completed pedigrees with genotypes. The traced pedigrees with genotypes were from 2652 in 79596 milk samples of 1999 to 52652 in 188430 milk samples of 2003. No carrier sires was found for DUMPS. Carrier frequency of BLAD could be expected to reduce to less than 1% in 5 years. However, high frequency of CVM, at least 2.48%(4671/188430)

were found, even if all null-genotype bulls were normal assumed. Further pedigrees tracing found a carrier bull, PARADISE-R ROEBUCK*CV was the main erosion source from. 494 DHI cows were daughters of ROEBUCK. Half carries(2043/4671) were from ROEBUCK daughters' which come to about 1% (2043/188430) DHI samples. In addition to restrict the CV carrier semen import, dairy farmers need traced the pedigree to select young bulls for nature service and look out what semen inventoried carefully.

Key Words: Taiwan, Holstein, Genetic defects.

個別種禽產蛋評估系統

個別種禽產蛋評估系統

李世昌 張秀鑾 黃鈺嘉 鍾秀枝 吳明哲

行政院農業委員會畜產試驗所

本系統已進入實測階段，並應用於行政院農委會畜產試驗所土雞育種計畫，完成4830隻土雞集蛋記錄。籠飼種禽產蛋記錄資料需配合現場作業方式採用籠飼位置記錄個別種禽產蛋數與性狀。傳統上，應用電腦系統進行產蛋記錄資料管理時，需先建立籠號位置與種禽羽號對照表，隨後再依現場產蛋記錄表設計產蛋記錄輸入畫面，俾利資料正確輸入與個別種禽產蛋評估，並進一步提供育種專家統計分析。此種作業模式，常因籠號位置與種禽羽號對照表業已事前固定，故無法在產蛋資料蒐集期間隨意更改，且必須俟所有資料蒐集完畢後再由育種專家統計分析決定更新種禽後再進行選留，同時通知現場選優汰劣與準備下一世代更新用種蛋收集，最後才將籠飼家禽移開並騰出位置供下一批使用。如此繁複之作業將導致在有限設備與人力下，無法增加檢定批次與縮短檢定期間。因此，如何應用資料庫系統管理籠飼家禽產蛋記錄資料，有效運用有限設備與人力，達到增加檢定批次與縮短檢定期間為本研究之目的。本研究應用Microsoft SQL Server關聯式資料庫管理系統進行資料記錄，分別建立家禽基本資料、籠號位置、產蛋記錄等所需相關資料表與關聯圖。為使終端使用者不受時空限制且更方便操作，採用3Tier架構，程式開發以JScript、VBScript等程式語言工具開發動態伺服器網頁ASP(Active Server Pages)，使用者可用網際網路透過瀏覽器方式建立與管理資料，育種者則可依其愛好應用統計分析軟體，如SAS，透過ODBC介面連結資料庫系統進行分析與評估。

關鍵語：產蛋記錄、資料庫、網際網路。

EVALUATION SYSTEM FOR LAYING PERFORMANCE OF
INDIVIDUAL HEN IN POULTRY BREEDING

S. C. Lee, H. L. Chang, Y. C. Huang, H. C. Chung and M. C. Wu

Livestock Research Institute, Council of Agriculture, Executive Yuan

The system has been practiced in breeding project of native chicken in Institute in which had laying records from 4,830 hens. Breeding hen in cage was recorded by its cage location with laying records plus egg traits. Traditionally, application of computer system on data management must have cage identification and individual tag of breeding hen to make data recording as the recording sheet from the farm. Such data management

system created the bird fixed in cage and made the substitution impossible status during the tested period. Therefore, all selected hens must be removed to empty the cages before establish another batch. Thus, both the number of test and test period were fixed and the latter could not be shortened. The objective of the study is to provide a flexible recording system without empty all cages from batch to batch. Microsoft SQL Server link module on data management system was used and the evaluation system for laying performance of individual hen in poultry breeding included basic records on each bird, cage location, date of egg laid, and other items. Application of 3Tier structure along with Jscript and VBScript program language to make ASP (Active Server Pages) homepage via World Wide Web for the System, the user is able to link the system at any time in any place. The animal breeder could also use ODBC connection to obtain data set and analyze.

Key words: Laying records, Databank, World Wide Web.

畜試土雞台畜肉十三號生長性能與雞冠大小之關係

畜試土雞台畜肉十三號生長性能與雞冠大小之關係

鍾秀枝 黃祥吉 林德育 張秀鑾

行政院農業委員會畜產試驗所

本試驗目的在探討畜試土雞台畜肉十三號生長性能與雞冠大小之關係，期增加其體型外觀之一致性，俾便提高產品價值。應用438隻畜試土雞台畜肉十三號，進行2、4、6、8、12、14與16週齡體重及12、14與16週齡之雞冠面積相關分析。結果顯示：12、14與16週齡公和母雞平均體重(平均值±標準機差)分別為1232±9和960±9公克、1467±10和1135±11公克及1692±12和1288±13公克；而12、14與16週齡公和母雞平均雞冠面積(平均值±標準機差)分別為19.5±0.4和2.8±0.4cm²、27.7±0.6公分和5.1±0.6cm²、36.5±0.7和8.9±0.8cm²。體重與雞冠面積在各週齡皆具顯著性別差異(P

關鍵語：畜試土雞、生長、雞冠。

THE RELATIONSHIP BETWEEN GROWTH TRAIT AND COMB
SIZE IN TLRI NO. 13 NATIVE CHICKEN

H. C. Chung, H. C. Huang, D. Y. Lin and H. L. Chang

Livestock Research Institute, Council of Agriculture, Executive Yuan

The objective of this study was to estimate the correlation between growth trait and comb size in TLRI No. 13 native chicken and thus to increase the carcass uniformity and thus promote the value of products. A total of 438 birds were used in the study. Traits included body weights at 2, 4, 6, 8, 10, 12, 14 and 16 weeks of age and comb sizes at 12, 14 and 16 weeks of age. Body weights (mean±SE) at 12, 14 and 16 weeks of age in cocks and hens were 1232±9 and 960±9 gm; 1467±10 and 1135±11 gm; 1692±12 and 1288±13 gm, respectively. The comb size at 12, 14 and 16 weeks of age in cock and hen were 19.5±0.4 and 2.8±0.4 cm²; 27.7±0.6 and 5.1±0.6 cm²; 36.5±0.7 and 8.9±0.8 cm², respectively. Significant differences were observed in both body weight and comb size (P

Key Words: TLRI native chicken, Growth trait, Comb size.

黑天鵝性別鑑定的RAPD標記

黑天鵝性別鑑定的RAPD標記

林德育 劉瑞珍 陳若菁 吳國欽 葉力子 張秀鑾

行政院農業委員會畜產試驗所

為尋求黑天鵝性別遺傳標記，本研究應用隨機複製多態性 DNA (RAPD)分析方法，以行政院農業委員會畜產試驗所彰化種畜繁殖場所選育的黑天鵝個體全血 DNA，進行性別遺傳標記探討。第一階段以6公6母黑天鵝個體 DNA作為模版，共使用220組寡核酸 RAPD 引子，進行RAPD分析，尋找區分性別的後選遺傳標記。分析結果顯示 220 組寡核酸引子中，引子 AE03(5' - CATAgAgCgg -3') 所產出的 PCR 產物之 690 bp DNA 片段為雌黑天鵝特有的片段，可作為區分性別的標記。第二階段，再以引子 AE03 分析該場2001年全場58隻黑天鵝DNA樣本，檢測結果顯示DNA判讀之性別均與實際性別吻合，準確率為 100% (58/58)；意即所有檢測雌黑天鵝PCR 產物 DNA 片段中均具有690 bp DNA 片段，而在所有受檢雄黑天鵝則無，證實 RAPD 引子 AE03 可作為區分性別之遺傳標記。

關鍵語：黑天鵝、性別鑑定、隨機複製多態性 DNA。

RAPD MARKER FOR SEX IDENTIFICATION OF BLACK SWAN

D. Y. Lin, J. J. L. Tai, J. C. Chen, G. C. Wu, L. T. Yeh and H. L. Chang

Livestock Research Institute, Council of Agriculture, Executive Yuan

To search for Black Swan sex identification candidate markers, whole blood DNA of individual Black Swan from Changhua Animal Propagation Station of Livestock Research Institute, Council of Agriculture (LRI, COA) were analyzed by random amplified polymorphic DNA (RAPD). In phase I, 220 different 10-mer primers of arbitrary sequence were used to screen twelve Black Swan (6 males and 6 females) in 1996. A RAPD marker (AE03, 5' - CATAgAgCgg -3') demonstrated high sensitivity and accuracy in gender diagnosis. The PCR polymorphism results indicated a specific DNA fragment (690 bp) amplified with primer AE03 could distinguish females from males. The proof stage, phase II, AE03 was used to test other 58 birds (28 males and 30 females) from the Station in Sep. 2001. Results showed 100% (58/58) accurate. The specific DNA fragment (690 bp) amplified with primer AE03 could be a sex identification marker of Black Swan.

Key words: Black Swan, Sexing, Random amplified polymorphic DNA (RAPD).