PORCINE LINKAGE MAPS FROM AUSTRALIAN LARGE WHITE AND LANDRACE: A COMPARISON WITH MAPS FROM DIVERGENT CROSSES

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SUMMARY

A linkage map has been developed from two-generation resource families of Australian Large White and Landrace pigs. The lengths of chromosomes analysed so far are comparable with other reported maps (Nordic map, PiGMaP map and USDA-MARC map). An excess male recombination was found on chromosome 1 in the region CGA-S0313 that suggests there might be a hotspot of recombination in that region.

Keywords: pig, genome, linkage mapping, recombination

INTRODUCTION

Genetic maps of the porcine genome have been developed very rapidly during the past five years (Archibald *et al.* 1995; Ellegren *et al.* 1994; Rohrer *et al.* 1996). There are now more than 1,800 markers on the porcine map, including more than 1,200 microsatellite markers. These make it possible to search for QTL with genome scans with evenly spaced markers less than 20 cM apart. These maps also contribute to our understanding of porcine genome evolution and function. All published genetic maps, including the PiGMaP map, Nordic map and USDA-MARC map, were developed using divergent crosses, involving a European breed parent crossed with either a Chinese breed or with Wild Boar. Although most of the marker orders are consistent between these studies, some difference have been revealed in map distance between markers and recombination rate between sexes. The object of this paper is to present a linkage map constructed using Australian Large White and Landrace breeds, and compare it with maps developed using divergent crosses.

MATERIAL AND METHOD

Animal resource. A two-generation pedigreed population consisting of 556 animals (8 boars and 65 sows in the parental generation) was bred at Bunge Meat Industries Ltd in 1995. All animals are from commercial lines used at Bunge and can be broadly classified as Landrace or Large White. DNA was extracted from blood (sows), semen (boars) or spleen (offspring). All the offspring were recorded for growth, carcase and meat quality traits.

Panel of markers. The population has been genotyped for a total of 65 markers. The number of genotyped markers on each chromosome is shown in Table 1. For each marker, one of the primers was labelled with fluorescent dye (Fam, Hex or Tet). Markers were multiplexed in sets of 3 or 4 amplified using 100 ng of genomic template DNA, 2.0mM dNTPs, 2.0mM MgCl2 100nM of each primer and 0.2 U AmpliTaq DNA polymerase in a 10 µl reaction volume. PCR products were multi-

loaded in sets of 8-14 loci with internal standard (Genescan-350 Tamara) in an automatic sequencer (ABI 373). Genotypes were called and data were managed with GEMMA database software (Iannuccelli.*et al* . 1996).

Table 1. Number of markers per chromosome

Chromosome	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
No of Marker	5	9	6	4	2	7	5	3	4	4	1	2	2	2	3	2	2	2

Linkage analysis. Linkage analysis was performed using CRIMAP version 2.4 software (Green *et al.* 1990). The BUILD option was used to determine the most likely order. Multipoint recombination intervals and odds for the probability of inverse orders among markers were calculated by the FIXED and FLIPS functions, respectively. CHROMPIC was used to detect possible genotyping errors. The animals with tripple recombinants were removed if after reexamination, there were no obvious genotyping errors. Markers with segregation distortion were removed from the data sets.

RESULT AND DISCUSSION

Four chromosomes only, namely 1, 2, 3 and 6 currently have enough markers on them for a meaningful comparison with previously published maps and the results are shown in Table 2. As an example, Figure 1 shows our linkage maps of chromosome 2 for female, male and sex average compared with USDA map. The marker orders from our within-European breed map are generally consistent with published maps using divergent crosses. However order CGA-S0313-S0155of chromosome 1 in the PRDC map and USDA map differs from CGA-S0155-S0313 in the PiGMaP and Nordic maps (Figure 2). Further, the map distances between identical markers on our PRDC map are generally equivalent to those in the Nordic map, PiGMaP and USDA-MARC map. Similar results were reported by Zhang, *et al* (1995) for comparative alignment of six markers on chromosome 2 between the PiGMaP and the USDA-MARC maps.

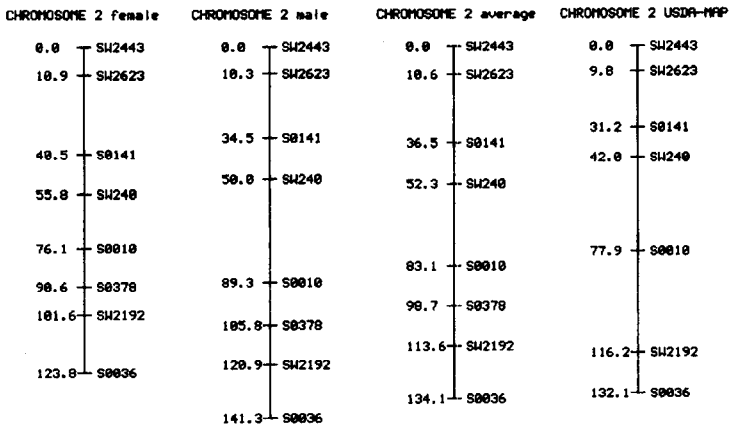

Figure 1. Linkage map for chromosome 2

Table 2 Chromosome length in PRDC-map and published linkage maps on chromosome 1, 2, 3 and 6

Chromosome	1	2	3	6
PRDC map (cM)	106.5	134.1	113	154
Nordic map (cM)	167	65.2	143.2	171
PiGMaP map (cM)	140	72	147	169
USDA-MARC map (cM)	144	132.1	129.3	165.7

The PRDC map confirms an excess of male recombination on chromosome 1 as found in previous studies. The distance between CGA and S0313 is 8.8 cM in females and 53.6 cM in males (Figure 2). Generally the heterogametic sex displays a lower rate of genetic recombination than the homogametic sex (Haldane, 1926). For the human genome, Morton (1991) has reported a mean female-to-male ratio of map length of 1.7:1. In pigs, the equivalent figure has been estimated as 1.4:1 (Ellegren *et al.* 1994b). Despite the overall higher rate of recombination in female mammals, regions with excess male recombination have been observed both in mouse (Davisson *et al.* 1989) and human (Donis-Keller *et al.* 1987).The excess of male recombination on pig chromosome 1 has been observed in the Nordic map, where the distance between CGA and S0082 is 10 cM in females and 41 cM in males, and in the PiGMaP, where the distance between CGA and S0082 is 13 cM in females and 63 cM in males. The PiGMaP map is derived from crosses between Chinese Meishan pigs and Large White pigs, Wild Boar and Large White and Pietrain and Wild Boar, while the Nordic map was developed using Wild Boar and Large White. Thus the excess of male recombination in this region of chromosome 1 is quite consistent across these different resource populations

Future work: The major objective in constructing the current PRDC map is to perform a genome scan for QTL in an Australian commercial pig population. Further genotyping will be carried out to achieve a 20 cM marker interval for this genome scan which will also permit a more complete comparison of the within European breed and divergent cross maps.

ACKNOWLEDGMENT

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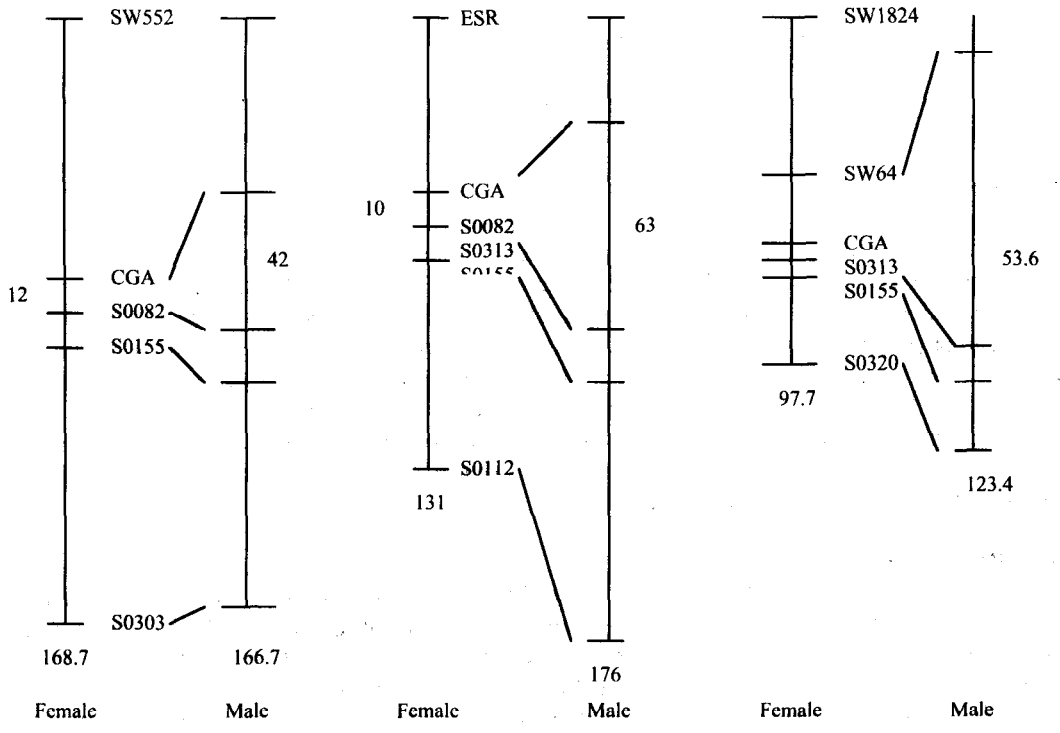

Figure 2. Female and male linkage map of pig chromosome 1 in the PRDC map (from left: Nordic map, PiGMaP, PRDC map).

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