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An integrated RH map of porcine chromosome 10

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Abstract

Background: Whole genome radiation hybrid (WG-RH) maps serve as "scaffolds" to significantly improve the orientation of small bacterial artificial chromosome (BAC) contigs, order genes within the contigs and assist assembly of a sequence-ready map for virtually any species. Here, we report the construction of a porcine: human comparative map for pig (*Sus scrofa*) chromosome 10 (SSC10) using the IMNpRH_{12,000-rad} porcine WG-RH panel, integrated with the IMpRH_{7,000-rad} WG-RH, genetic and BAC fingerprinted contig (FPC) maps.

Results: Map vectors from the IMNpRH_{12,000-rad} and IMpRH_{7,000-rad} panels were merged to construct parallel framework (FW) maps, within which FW markers common to both panels have an identical order. This strategy reduced map discrepancies between the two panels and significantly improved map accuracy. A total of 216 markers, including 50 microsatellites (MSs), 97 genes and ESTs, and 69 BAC end sequences (BESs), were ordered within two linkage groups at two point (2 pt) LOD score of 8. One linkage group covers SSC10p with accumulated map distances of 738.2 cR_{7,000} and 1814.5 cR_{12,000}, respectively. The second group covers SSC10q at map distances of 1336.9 cR_{7,000} and 3353.6 cR_{12,000}, yielding an overall average map resolution of 16.4 kb/cR_{12,000} or 393.5 kb per marker on SSC10. This represents a ~2.5-fold increase in map resolution over the IMpRH_{7,000-rad} panel. Based on 127 porcine markers that have homologous sequences in the human genome, a detailed comparative map between SSC10 and human (*Homo sapiens*) chromosome (HSA) 1, 9 and 10 was built.

Conclusion: This initial comparative RH map of SSC10 refines the syntenic regions between SSC10 and HSA 1, 9 and 10. It integrates the IMNpRH_{12,000-rad} and IMpRH_{7,000-rad}, genetic and BAC FPC maps and provides a scaffold to close potential gaps between contigs prior to genome sequencing and assembly. This map is also useful in fine mapping of QTLs on SSC10.

Background

Radiation hybrid (RH) mapping is an important tool in the construction of high-resolution physical maps, which are key to efficient sequencing and successful genome sequence assembly [1-5] and the construction of comparative maps between species [6-8]. A major advantage of RH mapping is that polymorphic and nonpolymorphic markers, including sequence tagged-sites (STSs), microsatellites (MSs), genes, expressed sequence tags (ESTs), bacterial artificial chromosome (BAC) end sequences (BESs) and single nucleotide polymorphisms (SNPs) can be ordered at high resolution. Although several RH panels are currently available for swine [1,9-14], to date, the IMNpRH2_{12,000-rad} panel [1] offers the highest mapping resolution and has been successfully used to order a variety of markers on swine chromosome (SSC) 2p, 9p, 12 [15,16], and over several chromosome regions, SSC6q1.2 [17], SSC7q11-14 [18], and SSC15q25 [1]. Current RH maps of SSC10 are built on the IMpRH_{7,000-rad} panel [8,19-22] where map resolution and marker density are unfortunately not optimal for either fine-mapping QTLs or genome sequence assembly. Map discrepancies between various RH maps or between RH and the corresponding genetic map(s) also exist [7,22-24]. Therefore, an integrated, high-resolution RH and comparative map for SSC10 should help in resolving discrepancies.

SSC10 is a small metacentric chromosome, comprising ~3.1% (85/2700 Mb) of the pig haploid genome. Sequencing of SSC10 by the International Swine Genome Sequencing Consortium (SGSC) and Pig Genome Sequence Project http://www.sanger.ac.uk/Projects/S_scrofa/ is based on the BAC fingerprinted contig (FPC) map http://www.sanger.ac.uk/Projects/S_scrofa/WebFPC/WebChrom/wcporcine10.shtml and the BES RH map [25,26], which was built on the IMpRH_{7,000-rad} panel. An initial draft assembly of SSC10 sequence has recently been released in Pre-Ensembl http://pre.ensembl.org/Sus_scrofa/index.html, but only contains ~30 Mb, roughly one-third of the entire chromosome. Here we report the generation of an initial high-resolution RH map of SSC10 that integrates the IMpRH_{7,000-rad}/IMNpRH2_{12,000-rad} RH, porcine genetic and BAC FPC maps, and allowed us to construct a comparative map of SSC10 and HSA1, 9 and 10.

Results and Discussion

SSC10 RH_{12,000} and RH_{7,000} maps

Two sets of mapping vectors from the IMNpRH2_{12,000-rad} and the IMpRH_{7,000-rad} panels were used to construct the RH FW map of SSC10. The vectors were merged into one data-set and analyzed using a maximum multipoint likelihood linkage strategy with CarthaGene [27] at a 2 pt LOD score of 8. Two linkage groups were initially identified for SSC10 (Table 1, 2). One linkage group was

assigned to the short arm (p), the other group to the long arm (q) (Fig. 1c-d) based on known MSs and ESTs/genes from previous genetic and RH maps [6,7,14,21,25,28]. A FW map for each linkage group was built simultaneously on both RH panels at a likelihood ratio of 1000:1. The orientation of each linkage group was based on markers previously assigned to the porcine cytogenetic (Fig. 1a) and genetic maps (Fig. 1b). A total of 107 FW markers common to the IMpRH_{7,000-rad} (Fig. 1c) and IMNpRH2_{12,000-rad} (Fig. 1d) FW maps were ordered on SSC10 (Table 1, 2). The accumulated map distance of SSC10 was 2075.1 cR_{7,000} on the IMpRH_{7,000-rad} and 5168.1 cR_{12,000} on the IMNpRH2_{12,000-rad} FW maps. This represents a 2.5 fold increase in map resolution over the IMpRH_{7,000-rad} panel (Table 1), which is consistent with our previous observations on SSC2p, 9p and 12, [15,16], and within the 2.2-3.0 fold range reported on SSC6q1.2 [17], SSC7q11-14 [18], and SSC15q25 [1]. If we assume the DNA content of SSC10 is ~85 Mb [25], then the kb/cR ratio is ~16.4 for the IMNpRH2_{12,000-rad} FW map, and 41 kb/cR in the IMpRH_{7,000-rad} FW map, close to the genome average of 15 kb/cR_{12,000} reported for the IMNpRH2 panel [1,15], and slightly better than the 47.5 kb/cR_{7,000} genome average reported for the IMpRH_{7,000-rad} panel [7]. In the second generation pig EST RH_{7,000-rad} map [7], SSC10 had the lowest resolution (highest kb/cR ratio) of the entire genome with a ratio of 71.4 kb/cR_{7,000}, based on an earlier estimate of ~103 Mb for SSC10 [7,28]. As chromosome size estimates (103 vs. 85 Mb; ~17% reduction) alone cannot account for the reported lower resolution in these initial reports, a lower marker density and difficulty in mapping within the nucleolus organizer region (NOR) must be considered (see discussion below).

We used the CarthaGene software [27] to integrate 88 additional, non-FW markers (Table 1, 2) into the IMNpRH2_{12,000-rad} FW map. They are listed to the right of the FW map in Fig. 1d (Table 1). If counting the FW and non-FW markers together, we achieved an average density of 393.5 kb per marker (85 Mb/216 STS) on SSC10, a significant increase in marker density over the ~1.1 Mb/marker reported for the most current SSC10 RH_{7,000-rad} EST and BES maps [7,25].

When marker density on SSC10p and SSC10q was analyzed separately, there was a significant difference in map resolution between the two arms. The standard porcine karyotype, places the SSC10 arm ratio (q/p) at 1.2 [30] with the DNA content of SSC10p estimated at 38.7 Mb (85 × 45.5%), and SSC10q at 46.3 Mb. The kb/cR ratio of SSC10p and SSC10q would be 21.3 and 13.8 in the IMNpRH2_{12,000-rad} and 52.4 and 34.6 in the IMpRH_{7,000-rad} panels, respectively. This suggests that map resolution on SSC10p was lower than that of the genome averages in both panels, whereas SSC10q was higher than the genome

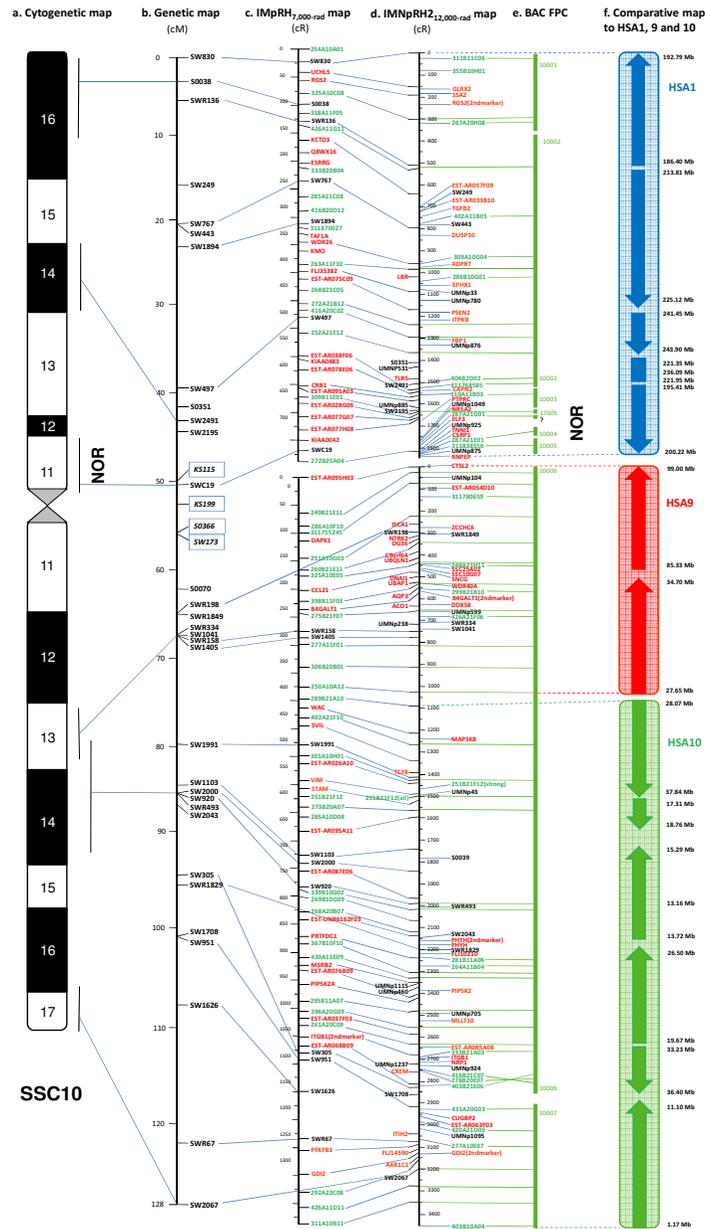


Figure 1

High-resolution RH comprehensive and comparative maps of SSC10. (a) Cytogenetic map of porcine chromosome (SSC) 10. The nucleolus organizer region is indicated as NOR; (b) Genetic map of SSC10. Those MS markers that are mapped in the current 7,000- and 12,000-rad FW maps and non-FW maps are listed in the genetic map. The four singletons that were not in FW maps are marked in italics in a box; (c) The 7000-rad IMpRH framework (FW) map; (d) The 12,000-rad IMNpRH2 FW map. MSs highlighted in black, genes/ESTs in red, and BESs in magenta. Markers listed between the 7,000- and 12,000-rad FW maps are framework markers; those on the right of the IMNpRH2 FW map are non-framework markers; (e) BAC fingerprinted contig (FPC). Contig number, e.g. 10001, corresponds to the FPC maps at http://www.sanger.ac.uk/Projects/S_scrofa/WebFPC/porcine/; Question mark (?) indicates that the BES 287A21G01 is lack of information in the FPC maps; (f) Comparative to human chromosome (HSA) 1, 9 and 10. Synteny blocks between pig and human, as well as the orientation of the human sequences in reference to the SSC10 RH map, are indicated by arrows, with HSA1 in blue, HSA9 in red and HSA10 in green. Sequence position of each synteny block in the human genome sequences (Build 36.3) is listed (in Mb) on the right side of the chromosomes.

average [1,14-16]. There are two possible explanations for this finding. One is marker density, which is lower in SSC10p (Table 1). RH FW map length for a given region is influenced by marker density; the higher the marker density, the longer the map length (cR); thus, the higher the map resolution. A second is the localization of the NORs, or the ribosomal RNA genes (RNR, or rDNA) on SSC10p near the centromere [31-34]. SSC10 is one of two chromosomes (the other one is SSC8) in the porcine genome that harbors ribosomal RNA genes (RNR, or rDNA) in NORs located in the proximal region of SSC10p near the centromere. Silver-staining (Ag-NOR) indicates that the porcine RNR genes on SSC10 are constitutively active in all pig breeds, while their activity on SSC8 varies among different pig breeds [31]. The ratio of FW vs. non-FW markers was 1:4 (3 FW/12 non-FW) in the NOR region (Fig. 1d), significantly biased from the average 1:0.85 on SSC10 suggesting that building an accurate map for this region will be difficult. The swine BAC FPC map is also not contiguous over the same region http://www.sanger.ac.uk/Projects/S_scrofa/WebFPC/WebChrom/wcporcine10.shtml. In the human genome, there are between 150 and 300 copies of ribosomal RNA gene per haploid genome, that map to the short arms of acrocentric chromosomes 13, 14, 15, 21, and 22 [35]. Unfortunately, the copy number of the porcine RNR gene on SSC10 is currently unknown, which limits our ability to specifically define the extent of the NOR.

It is also worth noting that a pair of markers for five genes (RGS2, B4GALT1, PHYH, ITGB1, and GDI2) was typed separately on the IMNpRH2_{12,000-rad} panel. As shown in Fig. 1c and 1d, all five-paired markers mapped next to each other within a small interval. Since the paired markers were designed from different laboratories (in Japan and USA) and typed anonymously, they provide an additional indication of the resolution and accuracy of the IMNpRH2_{12,000-rad} SSC10 map [15].

Integration of SSC10 RH and genetic maps

Thirty-six of 54 (67%) MSs ordered on the IMNpRH2 panel were mapped on the latest SSC10 genetic map <http://www.marc.usda.gov/genome/swine/swine.html> (Fig. 1b), of which 23 are FW markers, 9 are non-FW markers,

and the remaining 4 are singletons (a linkage group with only one marker) (Fig. 1b-d). The order of all FW and non-FW MS, except for SWR1829 on the SSC10 RH map, is in agreement with the order on the genetic map (Fig. 1b-d). In addition, the five bins (≤ 5 cM), each with two to five MSs, on the genetic map (USDA-MARC v. 2.) of SSC10 (Fig. 1b) <http://www.thearkdb.org/arkdb/do/getMappableDetails?accession=ARKCHR00000010> were all ordered on the IMNpRH2_{12,000-rad} map (Fig. 1c and 1d), significantly increasing the resolution on the genetic map.

However, two small regions of SSC10 did not completely align with the genetic map. The first is the NOR-centromere region. The four singleton MSs (KS115, KS199, S0366, and SW173) (Fig. 1b) were all located in this region. The second region is close to SSC10qter between SW2043 and SW1626, where there is a gap between FPC contigs 10006 and 10007. We determined MS SWR1829 and SW305 were flipped when compared to the genetic map (Fig. 1b-d). In previous studies, SWR1829 and SW2043 were reversed [22,24], while the order of SW951 and SW305 was reversed in the IMpRH_{7,000-rad} maps for SSC10 reported by Aldenhoven et al. [24] and Rink et al. [7], indicating the difficulty in assigning marker order within this region.

Integration of SSC10 RH and BAC FPC maps

When the SSC10 RH map was integrated with the corresponding BAC FPC maps based on common BES (Fig. 1c-e), a total of 7 BAC contigs (10001-10007) were identified. Contigs 10001-10005 cover SSC10p, while contigs 10006-10007 cover the entire SSC10q (Fig. 1e) with the order of BESs in the current RH map identical to the FPC map for the entire chromosome http://www.sanger.ac.uk/Projects/S_scrofa/WebFPC/WebChrom/wcporcine10.shtml except for the two small regions also encountered in the genetic map. We estimate the 4 singleton MSs (KS115, KS199, S0366, and SW173) in the genetic map, the NOR and centromere region of SSC10 cover ~ 5.5 cM (from 50 cM to 55.5 cM) (Fig. 1b) with the NOR between 1550 cR_{12,000-rad} and 1850 cR_{12,000-rad} (Fig. 1c) where several small BAC FPCs including contig 10003, 10004 and 10005 are assigned. There were two "free" BES markers found between contigs 10003 and 10004 in the

Table 1: Comparison between the 12,000- and 7,000-rad RH framework (FW) maps

Linkage group	No. of marker*	12,000-rad FW map			7,000-rad FW map		Fold change** (cR _{12,000} /cR _{7,000})
		FW marker	Non-FW marker	Map distance (cR)	FW marker	Map distance (cR)	
SSC10p	87	31	39	1814.5	41	738.2	2.5
SSC10q	129	76	49	3353.6	59	1336.9	2.5
Total	216	107	88	5168.1	100	2075.1	2.5

* Number of marker was the sum of FW and non-FW markers in both RH_{12,000} and RH_{7,000} maps (Fig. 1c & 1d).

** Fold change was calculated by dividing the map distance in the 12,000-rad FW map by the map distance in the 7,000-rad FW map.

Table 2: A list of markers mapped on SSC10 RH map

Marker type	RH panel	Linkage group	MS	BES	Gene/EST	Total*
FW	1,2000-rad	SSC10p	8	8	15	31
		SSC10q	16	26	34	76
	7,000-rad	SSC10p	7	15	19	41
		SSC10q	10	28	21	59
Non-FW		SSC10p	8	12	19	39
		SSC10q	13	15	21	49

*Some of the markers in each linkage group are not common markers to both RH panels, leading to the total number of markers in this table being greater than 216.

RH map (Fig. 1e). One was 309B11E01, which mapped to the middle of the large FPC contig 17005 http://www.sanger.ac.uk/Projects/S_scrofa/WebFPC/porcine/. The other was 287A21G01, for which no information is available in the BAC FPC database. It is worth noting that since neither RH mapping nor BAC fingerprinting were able to accurately map the NOR region, more attention should be paid to marker assignment and sequencing in this "problematic" region.

The order of three non-FW BESs (416B21C07, 278B20E07, 403B21E06) at the end of BAC contig 10006 was also inverted (Fig. 1e). Four FW MSs, SW305, SW1708, SW951 and SW1626 are located in this region where discrepancies between the genetic and RH maps were previously reported [7,23,24]. CarthaGene identified two likely FW map orders for this region, with only a slight statistical difference in Log₁₀-likelihood (-409 vs. -410). One order was CREM-ESTAR068B09-SW305-SW1708-SW951-SW1626. The alternative order was SW951-SW1708-SW305-ESTAR068B09-CREM-SW1626. The final RH map (Fig. 1c and 1d) was built according to the first order based on the assumption that marker order in the genetic map (Fig. 1b) was correct. However, adoption of the alternative order would not invert the three non-FW BESs in contig 10006. At present, we are unable to resolve whether the genetic or the FPC map is correct without additional markers.

Comparative map between SSC10 and HSA 1, and 9 and 10

All gene, EST, and BES sequences were BLAT <http://genome.ucsc.edu/> and BLAST <http://www.ncbi.nlm.nih.gov/BLAST/> searched against the human genome sequence (Build 36.3) to identify regions of synteny between the human and porcine genomes (see Additional file 1). The coordinates of 127 markers based on their positions in the current SSC10 RH map and their sequence locations in HSA1, 9 and 10 are shown in Fig. 2. The pig-human comparative map (Fig. 1) built in this work, not only supports the previous findings by bidirectional fluorescence *in situ* hybridization (Zoo-FISH) that SSC10 is in synteny with regions of HSA1, 9 and 10

[36,37], but also refines the conserved synteny blocks between the two species. Five synteny blocks are conserved between SSC10p and the distal region of HSA1q (1q31-43) from 186.4 to 243.9 Mb (Fig. 1a, f, Fig. 2). However, SSC10q shares regions of synteny with two other human chromosomes, HSA9 and HSA10. Two blocks of conserved synteny were identified between the proximal region of SSC10q (q11-12) and HSA9p13.1-21.2 (27.7 to 34.7 Mb) and HSA9q21.32-22.32 (85.3 to 97.89 Mb), while six blocks were identified between the distal region of SSC10q (q13-17.2) and the entire HSA10p (10p11-15) (1.0 to 37.8 Mb) (Fig. 1f, Fig. 2), reflecting the macro-rearrangements that occurred during the evolution of the two species. In addition, several micro-rearrangements such as those observed on SSC12, SSC2p and 9p [15,16] were also identified. For example, the FBP1 (fructose-1,6-bisphosphatase 1) gene located on HSA10q (see Additional file 1) did not map to the conserved region between SSC10 and HSA10, but to the region where SSC10 and HSA1 are conserved at 1310.0 cR/96.57 Mb (Fig. 2). It is reasonable to assume that the map position of FBP1 in SSC10 is an indication (or a relic) of an inversion in the region (1310–1860 cR_{12,000}) between FBP1 and CTSL2 (cathepsin L2) (see Fig. 1d) during the evolution of SSC10 which may include the entire centromere. Two BESs, 309A10G04 at 960.0 cR/239.74 Mb and 404B2D02 at 1505.0 cR/236.09 Mb, were also not aligned with their synteny blocks. Further characterization of regions of conserved synteny as well as micro-rearrangements between pig and human should improve our understanding of mammalian genome evolution and assist in swine genome sequencing and assembly.

Gene density across a genome of any mammalian species is not uniform with some human and swine chromosomes described as "gene-rich", and others as "gene-poor" [1,2]. The first- and second-generation porcine EST RH maps [6,7] suggested that SSC10 had less than the expected number of genes based on DNA content [29]. However, none of the corresponding human chromosomes/regions (HSA1, 9, and 10) are listed as "gene-poor" in the human genome [38]. This inconsistency in gene density within homologous regions of the pig and human

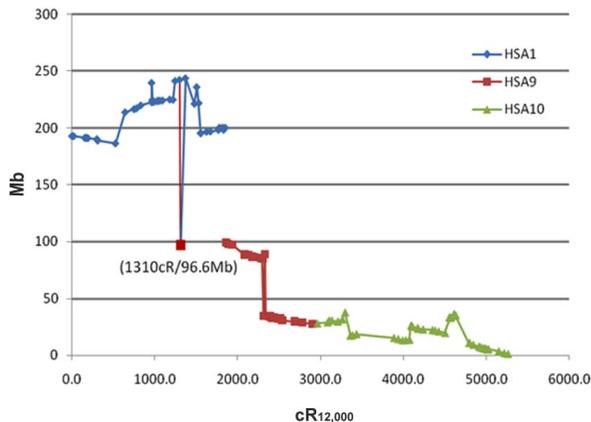


Figure 2
Comparison of gene order between SSC10 and HSA1, 9, and 10. A total of 127 genes/ESTs and BESs were compared based on their positions on SSC10 and HSA1, 9 and 10. The sequence positions (Mb) of genes on human chromosomes (Build 36.3) are compared with corresponding genes on the SSC10 RH_{12,000-rad} map (Fig. 1). Map distances (cR) for SSC10 are the accumulated sum of the linkage groups from Fig. 1. Each diamond represents the Cartesian coordinates for a sequence on HSA1, squares for HSA9, and triangles HSA10. Any significant change in coordinates between adjacent genes indicates a rearrangement. The map position of FBPI at coordinate 1310.0 CR/96.6 Mb is indicated and discussed in the text.

genome may be explained by two factors. The size of SSC10 may have been over-estimated as the initial report of 103 Mb for SSC10 [29] used in subsequent reports [6,7] has been revised to ~85 Mb [26]. Alternatively, the NOR region contains a large number of tandem repetitive DNA sequences and harbors multiple copies of the RNR genes that is likely to confound the estimate of gene density.

Conclusion

We merged mapping vectors from the IMNpRH2_{12,000-rad} and the IMpRH_{7,000-rad} panels to construct the highest resolution FW RH and comparative map for SSC10, to date, containing a total of 216 markers. Average map resolution was 16.4 kb/cR_{12,000} or 393.5 kb per marker on SSC10. Although the proximal region of SSC10p (NOR-centromere region) remains a difficult target for physical as well as linkage mapping, the current map provides a platform to integrate additional STS from the wealth of data submitted to the IMNpRH2_{12,000-rad} and IMpRH_{7,000-rad} genetic and BAC FPC maps. This should improve our ability to identify breakpoints and micro-rearrangements and close potential gaps between BAC contigs prior to sequencing and assembly, as well as provide a useful starting point for higher resolution mapping of QTLs includ-

ing those for meat quality, growth, feed intake and reproductive traits [8,39-41] on this chromosome.

Methods

Genes/ESTs, MSs and BAC end markers

Primer pair sequences were acquired from normalized, essentially full-length cDNA libraries [42] or from the literature. EST markers were derived from a panel of normalized porcine cDNA libraries as described earlier [7]. BAC end primers were used essentially as reported [25]. MS primer sequences were obtained from the literature and public databases [14,28,43]. All primers were optimized by determining the highest annealing temperature at which successful amplification of porcine genomic DNA took place. Primers were then tested with both porcine and Chinese hamster genomic DNA at species-specific temperatures [15].

As discussed by Liu et al. [15], we avoided designing redundant primer pairs for a given gene. However, we identified five genes with two pairs of primers because mapping primers were designed from either the gene cDNA sequence (synthesized in Japan), or from the corresponding EST (synthesized in the USA), that were annotated only recently. The two pairs of primers were treated as two individual markers and typed separately on the IMNpRH2_{12,000-rad} panel, where they served as internal controls to evaluate mapping accuracy and resolution. Additional file 1 provides detailed information regarding all markers mapped in this work.

RH typing, data merging, and map construction

Two sets of mapping vectors from the IMNpRH2_{12,000-rad} and the IMpRH_{7,000-rad} panels were used to construct the RH FW map of SSC10 RH as previously described [15,16]. The first set was generated in this work on the IMNpRH2_{12,000-rad} panel (Tables 1 and 2, Additional file 3). The second set was previously typed on the IMpRH_{7,000-rad} panel (see Additional file 2) [7,25]. The two data sets were merged using Carthage software <http://www.inra.fr/mia/T/Carthage/> [27] and merged data analyzed using a maximum multipoint likelihood linkage strategy. Each marker was assigned into linkage groups on the IMNpRH2_{12,000-rad} SSC10 map at a 2 pt LOD score of 8 and a threshold distance ≤ 100 cR between markers. Common markers refer to the 13 MSs, 61 ESTs/genes and 43 BESs assigned on both panels. A framework (FW) map was constructed for each linkage group with a likelihood difference threshold of 1000:1. Additional (non-FW) markers were then mapped on the IMNpRH2_{12,000-rad} panel with CarthaGene [27]. Final maps were drawn using MapCreator <http://www.wesbar.com/mapcreator/>.

Comparative mapping

All sequences of the porcine ESTs and BESs were BLAT <http://genome.ucsc.edu/cgi-bin/hgBlat> or BLAST <http://www.ncbi.nlm.nih.gov/BLAST/> searched against human genome sequence (Build 36.3). Once a sequence match (95% and greater similarity of length 40 bp or more) [15] was identified, the start position of the sequence in the human genome was collected (see Additional file 1). Chromosome locations and start positions of their orthologs in the human genome were also established for all genes analyzed (Fig. 1 and 2) using the NCBI human Map Viewer (Build 36.3) <http://www.ncbi.nlm.nih.gov/mapview/>. Cartesian coordinates of 127 genes/ESTs and BESs based on their map position in HSA 1, 9, and 10 in SSC10 were also developed (Fig. 2). Map distance (cR) for SSC10 in Fig. 2 were the accumulated sum of the linkage groups from Fig. 1c and 1d.

Authors' contributions

JGM participated in data analysis, developed the SSC10 7000-rad and 12,000-rad RH maps, and the pig-human comparative map; the main author for drafting and revising the manuscript. HY participated in porcine gene isolation, primers design, RH typing on the 7000-rad panel, and data analysis. KE carried out RH typing on both 12,000-rad and 7000-rad panels and the consensus mapping (vector); participated in porcine EST sequencing, EST primers design, and data collection and analysis. HH participated in porcine gene isolation, primers design, RH typing on the 7000-rad panel, and data analysis. TS participated in porcine gene isolation, primers design, data collection and analysis. SNM participated in porcine BAC end sequencing, BES primers design, RH typing on the 7000-rad panel, and data analysis. JEB participated in porcine BAC end sequencing, BES primers design, RH typing on the 7000-rad panel, and data analysis. LBS participated in porcine BAC end sequencing, BES primers design, RH typing on the 7000-rad panel, and data analysis. CWB participated in the research design, coordination, porcine EST sequencing, EST primers design and mapping, and helped to revise this manuscript. WSL, principal author, coordinated the research project, carried out consensus mapping (vector), CarthaGene analysis, and map construction; involved in drafting the manuscript and revising it critically for important intellectual content; and edited the final version for publication.

Additional material

Additional file 1

SSC10 marker information. This file provides detailed information regarding all markers mapped in this work.

Click here for file

[<http://www.biomedcentral.com/content/supplementary/1471-2164-10-211-S1.doc>]

Additional file 2

IMpRH7,000-rad mapping vectors for the markers on SSC10. This file provides mapping vector and retention frequency of all SSC10 markers in the IMpRH panel.

Click here for file

[<http://www.biomedcentral.com/content/supplementary/1471-2164-10-211-S2.doc>]

Additional file 3

IMNpRH2-12,000-rad mapping vectors for the markers on SSC10. This file provides mapping vector and retention frequency of all SSC10 markers in the IMNpRH2 panel.

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References

- Yerle M, Pinton P, Delcros C, Arnal N, Milan D, Robic A: **Generation and characterization of a 12,000-rad radiation hybrid panel for fine mapping in pig.** *Cytogenet Genome Res* 2002, **97(3-4)**:219-228.
- Womack JE: **Mapping animal genomes.** *Advances in veterinary medicine* 1997, **40**:157-189.
- Williams JL, Eggen A, Ferretti L, Farr CJ, Gautier M, Amati G, Ball G, Caramorr T, Critcher R, Costa S, et al.: **A bovine whole-genome radiation hybrid panel and outline map.** *Mamm Genome* 2002, **13(8)**:469-474.
- Murphy WJ, Sun S, Chen Z, Yuhki N, Hirschmann D, Menotti-Raymond M, O'Brien SJ: **A radiation hybrid map of the cat genome: implications for comparative mapping.** *Genome research* 2000, **10(5)**:691-702.
- Cox DR, Burmeister M, Price ER, Kim S, Myers RM: **Radiation hybrid mapping: a somatic cell genetic method for constructing high-resolution maps of mammalian chromosomes.** *Science (New York, NY)* 1990, **250(4978)**:245-250.
- Rink A, Santschi EM, Eyer KM, Roelofs B, Hess M, Godfrey M, Karajusuf EK, Yerle M, Milan D, Beattie CW: **A first-generation EST RH comparative map of the porcine and human genome.** *Mamm Genome* 2002, **13(10)**:578-587.
- Rink A, Eyer K, Roelofs B, Priest KJ, Sharkey-Brockmeier KJ, Lekhong S, Karajusuf EK, Bang J, Yerle M, Milan D, et al.: **Radiation hybrid map of the porcine genome comprising 2035 EST loci.** *Mamm Genome* 2006, **17(8)**:878-885.
- Nonneman D, Rohrer GA: **Comparative mapping of human chromosome 10 to pig chromosomes 10 and 14.** *Animal genetics* 2004, **35(4)**:338-343.
- Rattink AP, Faivre M, Jungerius BJ, Groenen MA, Harlizius B: **A high-resolution comparative RH map of porcine chromosome (SSC) 2.** *Mamm Genome* 2001, **12(5)**:366-370.
- Cao H, Robinson JA, Jiang Z, Melville JS, Golovan SP, Jones MW, Verrinder Gibbins AM: **A high-resolution radiation hybrid map of porcine chromosome 6.** *Animal genetics* 2004, **35(5)**:367-378.
- McCoard SA, Fahrenkrug SC, Alexander LJ, Freking BA, Rohrer GA, Wise TH, Ford JJ: **An integrated comparative map of the porcine X chromosome.** *Animal genetics* 2002, **33(3)**:178-185.
- Hamasima N, Suzuki H, Mikawa A, Morozumi T, Plastow G, Mitsuhashi T: **Construction of a new porcine whole-genome framework map using a radiation hybrid panel.** *Animal genetics* 2003, **34(3)**:216-220.

13. Yerle M, Pinton P, Robic A, Alfonso A, Palvadeau Y, Delcros C, Hawken R, Alexander L, Beattie C, Schook L, et al.: **Construction of a whole-genome radiation hybrid panel for high-resolution gene mapping in pigs.** *Cytogenetics and cell genetics* 1998, **82(3-4)**:182-188.
14. Hawken RJ, Murtaugh J, Flickinger GH, Yerle M, Robic A, Milan D, Gellin J, Beattie CW, Schook LB, Alexander LJ: **A first-generation porcine whole-genome radiation hybrid map.** *Mamm Genome* 1999, **10(8)**:824-830.
15. Liu WS, Eyer K, Yasue H, Roelofs B, Hiraiwa H, Shimogiri T, Landrito E, Ekstrand J, Treat M, Rink A, et al.: **A 12,000-rad porcine radiation hybrid (IMNpRH2) panel refines the conserved synteny between SSC12 and HSA17.** *Genomics* 2005, **86(6)**:731-738.
16. Liu WS, Yasue H, Eyer K, Hiraiwa H, Shimogiri T, Roelofs B, Landrito E, Ekstrand J, Treat M, Paes N, et al.: **High-resolution comprehensive radiation hybrid maps of the porcine chromosomes 2p and 9p compared with the human chromosome 11.** *Cytogenetic and genome research* 2008, **120(1-2)**:157-163.
17. Martins-Vess F, Milan D, Drogemuller C, Vobeta-Nemitz R, Brenig B, Robic A, Yerle M, Leeb T: **A high resolution physical and RH map of pig chromosome 6q1.2 and comparative analysis with human chromosome 19q13.1.** *BMC genomics* 2003, **4(1)**:20.
18. Demeure O, Renard C, Yerle M, Faraut T, Riquet J, Robic A, Schiex T, Rink A, Milan D: **Rearranged gene order between pig and human in a QTL region on SSC 7.** *Mamm Genome* 2003, **14(1)**:71-80.
19. Karnuah AB, Uenishi H, Kiuchi S, Kojima M, Onishi A, Yasue H, Mitsuhashi T: **Assignment of 64 genes expressed in 28-day-old pig embryo to radiation hybrid map.** *Mamm Genome* 2001, **12(7)**:518-523.
20. Garrido JJ, Jimenez-Marin AM, Yerle M, de Andres-Cara DF, Morera L, Llanes D, Barbancho MJ: **Assignment of the ITGB1 (integrin beta1 subunit) gene to pig chromosome band 10q17 with somatic cell hybrids.** *Cytogenetics and cell genetics* 2001, **94(1-2)**:84-85.
21. Yasue H, Kiuchi S, Hiraiwa H, Ozawa A, Hayashi T: **Assignment of 101 genes localized in HSA10 to a swine RH (IMpRH) map to generate a dense human-swine comparative map.** *Cytogenetic and genome research* 2006, **112(1-2)**:121-12.
22. Aldenhoven J, Chen Y, Backofen B, Moran C: **Improving the comparative map of porcine chromosome 10 with respect to human chromosomes 1, 9 and 10.** *Cytogenet Genome Res* 2003, **102(1-4)**:121-7.
23. Hamasima N, Mikawa A, Suzuki H, Suzuki K, Uenishi H, Awata T: **A new 4016-marker radiation hybrid map for porcine-human genome analysis.** *Mamm Genome* 2008, **19(1)**:51-60.
24. Aldenhoven J, Spotter A, Distl O: **Radiation hybrid mapping of 10 genes to porcine chromosomes.** *Animal genetics* 2005, **36(6)**:540-542.
25. Meyers SN, Rogatcheva MB, Larkin DM, Yerle M, Milan D, Hawken RJ, Schook LB, Beever JE: **Piggy-BACing the human genome II. A high-resolution, physically anchored, comparative map of the porcine autosomes.** *Genomics* 2005, **86(6)**:739-752.
26. Humphray SJ, Scott CE, Clark R, Marron B, Bender C, Camm N, Davis J, Jenks A, Noon A, Patel M, et al.: **A high utility integrated map of the pig genome.** *Genome biology* 2007, **8(7)**:R139.
27. Schiex T, Gaspin C: **CARTHAGENE: constructing and joining maximum likelihood genetic maps.** *Proceedings/International Conference on Intelligent Systems for Molecular Biology; ISMB* 1997, **5**:258-267.
28. Fahrenkrug S, Wagner M, Morrison L, Alexander LJ: **Map assignments of 373 previously unreported porcine microsatellites.** *Animal genetics* 2005, **36(1)**:76-86.
29. Schmitz A, Chaput B, Fouchet P, Guilly MN, Frelat G, Vaiman M: **Swine chromosomal DNA quantification by bivariate flow karyotyping and karyotype interpretation.** *Cytometry* 1992, **13(7)**:703-710.
30. Gustavsson I: **Standard karyotype of the domestic pig. Committee for the Standardized Karyotype of the Domestic Pig.** *Hereditas* 1988, **109(2)**:151-157.
31. Liu WS, Lu XZ, Qiu H: **Number and distribution of silver-stained nucleolar organizer regions and evolutionary relationships in domestic pigs.** *Animal genetics* 1995, **26(5)**:293-298.
32. Lin CC, Biederman BM, Jamro HK, Hawthorne AB, Church RB: **Porcine (*Sus scrofa domestica*) chromosome identification and suggested nomenclature.** *Canadian journal of genetics and cytology* 1980, **22(1)**:103-116.
33. Toga-Piquet C, Henderson AS, Grillo JM, Vagner-Capodano AM, Stahl A: **[Localization of ribosomal genes and nucleolar activity in lymphocytes of swine (*Sus scrofa domestica*) stimulated by phytohemagglutinins].** *Comptes rendus de l'Academie des sciences* 1984, **298(14)**:383-386.
34. Miyake Y, O'Brien SJ, Kaneda Y: **Regional localization of rDNA gene on pig chromosome 10 by in situ hybridization.** *Nippon juigaku zasshi* 1988, **50(2)**:341-345.
35. Huschenbett J, Gasch A, Katzer A, Affeldt M, Speer A: **Mapping of a human rRNA gene in the YAC contig surrounding the SMA candidate gene.** *Human genetics* 1995, **96(3)**:335-338.
36. Fronicke L, Chowdhary BP, Scherthan H, Gustavsson I: **A comparative map of the porcine and human genomes demonstrates ZOO-FISH and gene mapping-based chromosomal homologies.** *Mamm Genome* 1996, **7(4)**:285-290.
37. Goureau A, Yerle M, Schmitz A, Riquet J, Milan D, Pinton P, Frelat G, Gellin J: **Human and porcine correspondence of chromosome segments using bidirectional chromosome painting.** *Genomics* 1996, **36(2)**:252-262.
38. Venter JC, Adams MD, Myers EW, Li PW, Mural RJ, Sutton GG, Smith HO, Yandell M, Evans CA, Holt RA, et al.: **The sequence of the human genome.** *Science* 2001, **291(5507)**:1304-1351.
39. Duthie C, Simm G, Doeschl-Wilson A, Kalm E, Knap PW, Roehe R: **Quantitative trait loci for chemical body composition traits in pigs and their positional associations with body tissues, growth and feed intake.** *Animal genetics* 2008, **39(2)**:130-140.
40. Nonneman DJ, Rohrer GA: **Comparative mapping of a region on chromosome 10 containing QTL for reproduction in swine.** *Animal genetics* 2003, **34(1)**:42-46.
41. Nonneman DJ, Wise TH, Ford JJ, Kuehn LA, Rohrer GA: **Characterization of the aldo-keto reductase 1C gene cluster on pig chromosome 10: possible associations with reproductive traits.** *BMC veterinary research* 2006, **2**:28.
42. Fujisaki S, Sugiyama A, Eguchi T, Watanabe Y, Hiraiwa H, Honma D, Saito T, Yasue H: **Analysis of a full-length cDNA library constructed from swine olfactory bulb for elucidation of expressed genes and their transcription initiation sites.** *The Journal of veterinary medical science/the Japanese Society of Veterinary Science* 2004, **66(1)**:15-23.
43. Krause E, Morrison L, Reed KM, Alexander LJ: **Radiation hybrid mapping of 273 previously unreported porcine microsatellites.** *Animal genetics* 2002, **33(6)**:477-485.

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