

Molecular Strategies in the Analysis of the Porcine Genome

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To my family

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1 LIST OF PUBLICATIONS

This thesis is based on the following papers:

--- Peer-Reviewed Journals

1. Chen KF, Beck J, Huang LS, Knorr C, Brenig B (2004) Assignment of the phosphoglycerate kinase 2 (*PGK2*) gene to porcine chromosome 7q14-q15 by fluorescence *in situ* hybridization and by analysis of somatic cell and radiation hybrid panels. *Anim Genet*, 35: 71-72.
2. Chen KF, Beck J, Huang LS, Knorr C, Brenig B (2004) Assignment of the phosphoglycerate kinase 1 (*PGK1*) gene to porcine chromosome Xq12-q13 by fluorescence *in situ* hybridization and confirmation by hybrid panel analyses. *Anim Genet*, doi: 10.1111/j.1365-2052.2004.01092.x.
3. Chen KF, Knorr C, Bornemann-Kolatzki K, Huang LS, Brenig B (2004) Isolation and characterization of the highly polymorphic porcine STS-marker *S0719* adjacent to the 5' region of the phosphoglycerate kinase 2 (*PGK2*) gene. *Revised version in preparation*.
4. Chen KF, Knorr C, Moser G, Gatphayak K, Brenig B (2004) Molecular characterization of the porcine testis-specific phosphoglycerate kinase 2 (*PGK2*) gene and its association with male fertility. *Revised version in preparation*.
5. Chen KF, Knorr C, Bornemann-Kolatzki K, Huang LS, Brenig B (2004) Targeted isolation of microsatellites and their application in phylogenetic analyses of European and Chinese pig breeds. *Revised version in preparation*.
6. Gatphayak K, Knorr C, Chen KF, Brenig B (2004) Structural and functional analysis of the porcine *FUS2* gene. *Gene*, accepted for publication.

--- Congress Contribution

1. Chen KF, Knorr C, Bornemann-Kolatzki K, Brenig B (2003) Microsatellite isolation and phylogenetic analyses of European and Chinese pig breeds. *Proceedings of the DGfZ/GfT convention*, September 17/18 2003, Goettingen, Germany, B10.

2 ABSTRACT

The main goal of genome research in livestock is to map and characterize trait loci controlling various phenotypic characters like disease resistance, reproduction and other production traits of economic importance (e.g. meat quality). Although identification and mapping of functional genes and quantitative trait locus (QTL) regions associated with traits of interest increased significantly in pigs, the number of genes mapped is still small compared with human and mouse. Comparative analysis and bioinformatic tools combined with genomic and post-genomic techniques enable to achieve greater progress in the analysis of the porcine genome. The present thesis focuses on structural and functional analysis of genes of the porcine phosphoglycerate kinase (*PGK*) family which have previously been identified as candidate genes for inherited male fertility along with other inherited disorders in human and mouse. The second part of the thesis describes the isolation of microsatellite markers either from specific chromosomal region of interest, or from large-insert library clones harboring targeted trait genes, and the application of these informative markers in phylogenetic studies.

The porcine functional *PGK* genes, i.e. the ubiquitously expressed X-linked *PGK1* gene and the autosomally determined testis-specific *PGK2* gene, were identified and mapped on *SSCXq12-q13* and *SSC7q14-q15*, respectively. The 1665 bp of full-length *PGK2* cDNA were compiled using the modified rapid amplification 5'-RACE and 3'-RACE information. The results of genomic and cDNA sequences of the porcine *PGK2* gene demonstrated that it is a single-exon intronless gene with a complete open reading frame of 1251 bp encoding a PGK protein of 417 amino acids. Real time PCR results showed that *PGK2* mRNA was solely expressed in the testis. There was a lower amount of *PGK2* expression in the testis from a herniated boar and a very small amount of *PGK2* expression in the testis of an 8-week-old piglet compared to an adult boar. Two SNPs of *PGK2* gene (SNP-A: T427C; SNP-B: C914A) resulting in amino acid substitutions (SNP-A: Ser¹⁰²-Pro¹⁰²; SNP-B: Thr²⁶⁴-Lys²⁶⁴) were detected and genotyped among six pig breeds. The SNP-A mutation of proline could lead to the loss of a casein kinase II (CK2) phosphorylation site in the PGK2 peptide. Association analyses between the *PGK2* gene and some traits of sperm quantity and quality were performed. The results showed that SNP-B has a significant effect on semen volume in the Pietrian breed ($p = 0.08$).

Fifteen (GT)_n porcine microsatellites (*S0701* – *S0715*) were isolated from nine PAC clones by an improved efficient and rapid flanking sequence-based approach. Eight of the newly developed microsatellites were gene-associated, and the other seven microsatellites within the poorly covered chromosome region *SSC16q* were isolated to refine this region. The microsatellite markers were genotyped for a panel of 245 unrelated animals representing 15 European and Chinese indigenous pig breeds. A set of eleven microsatellite loci with a total of 136 alleles was used to analyze the phylogenetic relationships between the pig populations. Breed differentiation was significant as shown by the high average fixation index ($F_{ST} = 0.271$). Neighbor-joining (NJ) tree and unweighted pair group method with arithmetic mean (UPGMA) dendrogram were constructed. The results revealed that European and Chinese indigenous pig breeds had diverged into two distinct groups, apart from the German Göttingen Minipig and the European wild boar, which clustered into the branches of Chinese pig populations.

3 INTRODUCTION

The pig was one of the first animals domesticated over 7,000 years ago (Rothschild and Ruvinsky, 1998). The adaptation to different environmental conditions and phenotypic selection by human beings has created a wide diversity of pig breeds. As the genetic diversity rapidly erodes, the necessity to maintain diversity and to develop alternative stocks to meet a wide variety of production/market conditions is recognized, as well as the ensuing need to establish sound conservation programs (Ollivier *et al.*, 2001). Nowadays, the pork is the major red meat consumed (43%) worldwide and the pig can also be considered as an important model system for human health. The pig industry has made remarkable progress in the last 40 years: each sow produces 50% more progeny per year, which eat one third less feed in order to produce 33% more lean meat (Plastow, 2003). Genetics and breeding has played an increasingly significant role in the pig industry, which is accomplished by using combined approaches of molecular genetics and quantitative genetics enabling the pig industry to reduce the incidence of diseases, and to respond more rapidly to the changing demands of consumers.

In the early 1990s, several international gene mapping projects in livestock were launched including the PiGMaP gene mapping project initiated in Europe (Archibald *et al.*, 1995), two efforts (USDA-ARS; USDA-CSREES) initiated by the USDA in the USA, and the AGP animal genome research program by the NIAS-STAFF in Japan to unravel the pig genome. The main goal of genome research in livestock is to map and characterize trait loci that control various phenotypic characters (Andersson, 2001). To date, great progress has been achieved as more functional genes and QTL regions associated with traits of interest continue to be identified and mapped in pigs, however, the number of genes mapped is still small compared with the situation in humans and mice.

3.1 Tools for genome analysis

3.1.1 Molecular marker systems

To evaluate qualitative and quantitative information on diversity molecular genetic markers are essential aspects of both fundamental and applied fields in biology: ecology, evolutionary biology, taxonomy, agronomy, breeding, conservation and forensic identification are mentioned as examples (Karp and Edwards, 1997). There are a variety of genetic markers applied in genome analysis. In the following focus is laid on six DNA marker systems including restriction fragment

length polymorphism (RFLP), single nucleotide polymorphism (SNP), randomly amplified polymorphic DNA (RAPD), amplified fragment length polymorphism (AFLP), minisatellite and microsatellite.

Genetic markers can be generally grouped into two types based on their association with functionality (O'Brien, 1991): Type I markers are these DNA segments encoding for expressed DNA sequences which possess a relatively low degree of polymorphism but high evolutionary conservation, whereas type II markers usually have no identifiable biological function but they are highly polymorphic and not well conserved between species. RFLP and SNP are the most common type I markers in genetic mapping. Type II markers mainly consist of RAPD, AFLP, minisatellite and microsatellite. Alternatively, Dodgson *et al.* (1997) distinguished DNA-based markers into the groups of clone/sequence-based (CSB) markers and fingerprint (FP) markers (Dodgson *et al.*, 1997). CSB markers require the isolation of a cloned DNA fragment and often determination of some, if not all, of its DNA sequence. RFLP, microsatellite and SNP are included in this category. FP markers comprising RAPD, AFLP and minisatellite require no previous knowledge of isolation of a cloned DNA fragment or the sequence of the polymorphic region. Taking both hypotheses into account, FP markers are inherently type II markers while CSB markers include both type I and type II markers. A detailed comparison of the six main genetic markers is listed in Table 1.

Table 1: Summary of main genetic markers (modified based on Dodgson *et al.*, 1997; O'Brien 1991).

	RFLP	Microsatellite	SNP	RAPD	Minisatellite	AFLP
Type of loci (Dodgson)	Clone sequence-based	Clone sequence-based	Clone sequence-based	Fingerprint	Fingerprint	Fingerprint
Type of loci (O'Brien)	I and II	II > I	I and II	II	II	I and II
Genome distribution	Ubiquitous	Ubiquitous	Ubiquitous	Ubiquitous	Heterochromatin	Ubiquitous
PIC*	Low	High	Low	Moderate	High	Moderate
Typical allele no.	2	2 - 30	2	2	2	2
Inheritance mode	Co-dominant	Co-dominant	Co-dominant	Dominant	Dominant	Dominant
Reliability	High	High	High	Low	High	Moderate
Speed of assay	Low	High	High	High	Low	High
Initial investment	Moderate	High	High	Low	Moderate	Low
Automation	Difficult	Yes	Yes	Yes	Yes	Yes
Development costs	Medium	High	Medium	Low	High	Low
Running costs	Medium	High	Medium	Medium	High	Medium

*PIC = polymorphism information content

3.1.2 Isolation of microsatellites

Microsatellites also called simple sequence repeats (SSR) are tandemly repeat motifs of 1-6 bases that are known to be ubiquitous in all eukaryotic genomes analysed to date. They are present with a high probability in non-coding regions (Litt and Luty, 1989; Tautz, 1989; Weber and May, 1989). Specific PCR reactions are performed using genomic DNA as template and two specific primers flanking the repeats. The PCR products that differ in a few nucleotides among individuals are separated through high-resolution electrophoresis by radioactively or fluorescently labelled primers. The most common dinucleotide motif in mammals is (CA)_n. In pigs the number was estimated between 65,000 and 100,000 copies, highly distributed throughout the genome (Winterø *et al.*, 1992; Rohrer *et al.*, 1994). The mutation rate of microsatellites is thought to be high - a rate of up to 10⁻² was observed per generation (Bruford and Wayne, 1993) -and there are often large numbers of alleles that vary in size at a single locus (Beuzen *et al.*, 2000). Microsatellites have the advantages of being abundant, multiallelic, highly polymorphic, co-dominant and assayable by PCR (Dodgson *et al.*, 1997). Therefore, microsatellites have been extensively applied in animal genome mapping, biodiversity and phylogenetic studies. The main disadvantages involve the high cost of generation of microsatellites as microsatellites need to be developed *de novo* for each new species in most cases. In addition, detection of microsatellites sometimes suffers from an inherent weakness in accurately determining the fragment size (Beuzen *et al.*, 2000).

Microsatellite markers became soon after the first description the workhorse to establish genome maps in swine (Archibald *et al.*, 1995; Rohrer *et al.*, 1996) and were subsequently used for the identification of chromosomal regions associated with (quantitative) traits (Andersson *et al.*, 1994; Cassady *et al.*, 2001). To date, more than 1,000 porcine microsatellites have been isolated in cooperative international efforts (Rothschild and Plastow, 1999). Although the current swine linkage maps contain an overall good coverage with an average interval of 2.23 cM (Rohrer *et al.*, 1996), there are still efforts going on to enhance SSR marker densities on so far poorly covered regions or chromosomes like *SSC18* (Campbell *et al.*, 2001). Also, as high-resolution genetic linkage maps are indispensable for positional cloning of economically important quantitative trait loci (QTLs) or major genes (Matisse *et al.*, 1994), microsatellites are also specifically developed in fine mapping approaches to resolve regions associated with important traits (Milan *et al.*, 2000).

Recently, microsatellites have been also widely used - besides the mtDNA D-loop region - to conduct phylogenetic studies in pigs (Paszek *et al.*, 1998; Laval *et al.*, 2000).

Microsatellites have been traditionally isolated from partial genomic libraries selected for small insert size by screening a large number of clones through colony hybridization with repeat-containing probes (Figure 1) (Rassmann *et al.*, 1991). Generally, this method is quite tedious and inefficient, especially for species with low microsatellite frequencies such as birds or plants. According to *Molecular Ecology* primer notes from 1999 to March 2001, the number of positive clones from traditional isolation protocols was in the range of 0.13% to 4.5% with the average of 1.67% in mammals (Zane *et al.*, 2002). Therefore, in order to reduce the time invested in microsatellite isolation and to significantly increase yield, several alternative strategies have been attempted and most of them can be summarized as enhanced protocols with microsatellite-enriched libraries. In fact, these isolation strategies have focused on the improvement of the efficiency of library construction and screening for microsatellite isolation, such as RAPD based, primer extension, selective hybridization and AFLP based selective hybridization methods. As shown in a survey of papers in *Molecular Ecology* primer notes (1999 - March 2001), one third of reports had used enhanced protocols for the isolation of microsatellite loci (Zane *et al.*, 2002). On the other hand, to isolate further microsatellites from known clones of interest and thus to increase microsatellite coverage on the genetic map in predefined regions is also lately receiving massive attention in genetic studies (Wu *et al.*, 1996; Hayden and Sharp, 2001; Fujishima-Kanaya *et al.*, 2003). In Zane *et al.*'s review paper (2002), several methods of microsatellite isolation were discussed and compared with each other. These methods often present slight differences from one another and frequently have not been extensively tested (Zane *et al.*, 2002).

3.1.2.1 'Traditional' strategy of microsatellite isolation

Genomic DNA is fragmented by restriction enzymes or sonication and the small DNA fragments in a range from 300 - 700 bp are usually size-selected prior to construct a partial genomic library using a common plasmid vector either directly or after ligation to specific adaptors (Rassmann *et al.*, 1991). Thousands of recombinant clones can be screened for the presence of microsatellite repeat sequences by Southern hybridization. Radioactive probes (e.g. ^{32}P , ^{33}P) are generally more sensitive, but the manipulation of radioactive materials and their short half life led to the limited use of radiolabelled probes. In contrast, non-radiolabelled probes (e.g. digoxigenin) have become

more popular since the efficiency has greatly improved. After identification of repeat containing clones, specific primers are designed based on the sequencing results and PCR conditions are optimized to amplify microsatellites among individuals.

3.1.2.2 'Enrichment' strategy of microsatellite isolation

3.1.2.2.1 Randomly amplified polymorphic DNA (RAPD)-based

RAPD-based amplification of unknown microsatellites has been proposed using either repeat-anchored random primers or RAPD primers which produce large number of small size fragments by non-library PCR amplification (Wu *et al.*, 1994; Cifarelli *et al.*, 1995; Richardson *et al.*, 1995). The idea behind this approach is that RAPD fragments seem to contain more frequently microsatellite repeats than random genomic clones. PCR fragments can then undergo subsequent Southern hybridization with microsatellite probes and selective cloning of positive bands or through the cloning of all RAPD products followed by screening of arrayed clones (Ender *et al.*, 1996; Lunt *et al.*, 1999). However, the RAPD-based approach has not frequently been used to isolate microsatellites because no sequence information of the regions flanking the microsatellite can be obtained.

3.1.2.2.2 Primer extension

The primer extension strategy has been proposed for the production of libraries enriched with repeat motifs (Ostrander *et al.*, 1992; Paetkau, 1999). For this approach, the construction of a primary library is essential to obtain a pool of single-strand circular DNA for subsequent enrichment, in which DNA fragments are inserted into phagemids or phage vectors. Following this, a secondary enriched library is produced for specific microsatellite repeats using a primer extension reaction. The resulting library is highly enriched with repeat containing inserts and the following screening steps are similar to the traditional isolation strategy. The primer extension strategy has been proven to be useful for the isolation of dinucleotide repeat microsatellites. For example, the enrichment of (AC)_n repeats could yield from 40% to 50% up to 100% of positive clones (Ostrander *et al.*, 1992; Paetkau, 1999), however it is unclear if this approach is also effective for the isolation of tri- and tetranucleotide repeats. Since it has been found that 0 - 25% positive clones could be isolated using a tetranucleotide repeat primer in the extension step, the usefulness of the method to gain tri- or tetranucleotide containing microsatellites needs more investigation (Paetkau, 1999). In addition, to produce a secondary enriched library only a limited

portion of the genome can be cloned, so the population of inserts undertakes a severe bottleneck that results in loss of rare repeat motifs (Zane *et al.*, 2002). In total, this protocol involves a rather large number of steps which might limit the application of the primer extension strategy for microsatellite isolation.

3.1.2.2.3 Selective hybridization

The selective hybridization strategy is relatively simple and straightforward compared with other methods (Karagyozov *et al.*, 1993; Armour *et al.*, 1994; Kijas *et al.*, 1994). The first step of this strategy produces small genomic fragments which are ligated to vectors or adaptors. After selective hybridization with the repeat nucleotide probe and several washing steps to remove nonspecific binding, microsatellite-containing DNA can be eluted and enriched by PCR amplification. The use of a biotinylated probe in the liquid medium is generally preferable compared with the probe crosslinked to a nylon membrane in the process of the selective hybridization step. Finally, the recovered DNA fragments are cloned and screened for microsatellites by Southern blotting, PCR or direct sequencing. The overall enrichment efficiency of the selective hybridization strategy is in a range of 20% to 90% with respect to di-, tri- and tetranucleotide probes (Zane *et al.*, 2002). Therefore, this approach may be rather efficient and widely applicable.

In addition, Zane *et al.* (2002) suggested a microsatellite isolation strategy based on AFLP-based selective hybridization, which is similar to the selective hybridization strategy except that this method uses AFLP amplification rather than traditional library construction before. Genomic DNA is simultaneously digested with *MseI* and ligated to the *MseI*-AFLP-adaptor followed by PCR. Amplified DNA fragments are selectively hybridized with biotinylated oligonucleotide probes using streptavidin coated beads. The isolation steps are identical to the selective hybridization procedure. The percentage of clones containing dinucleotide repeats varies from 50% to 95% in a variety of species demonstrating a high microsatellite isolation efficiency (Zane *et al.*, 2002).

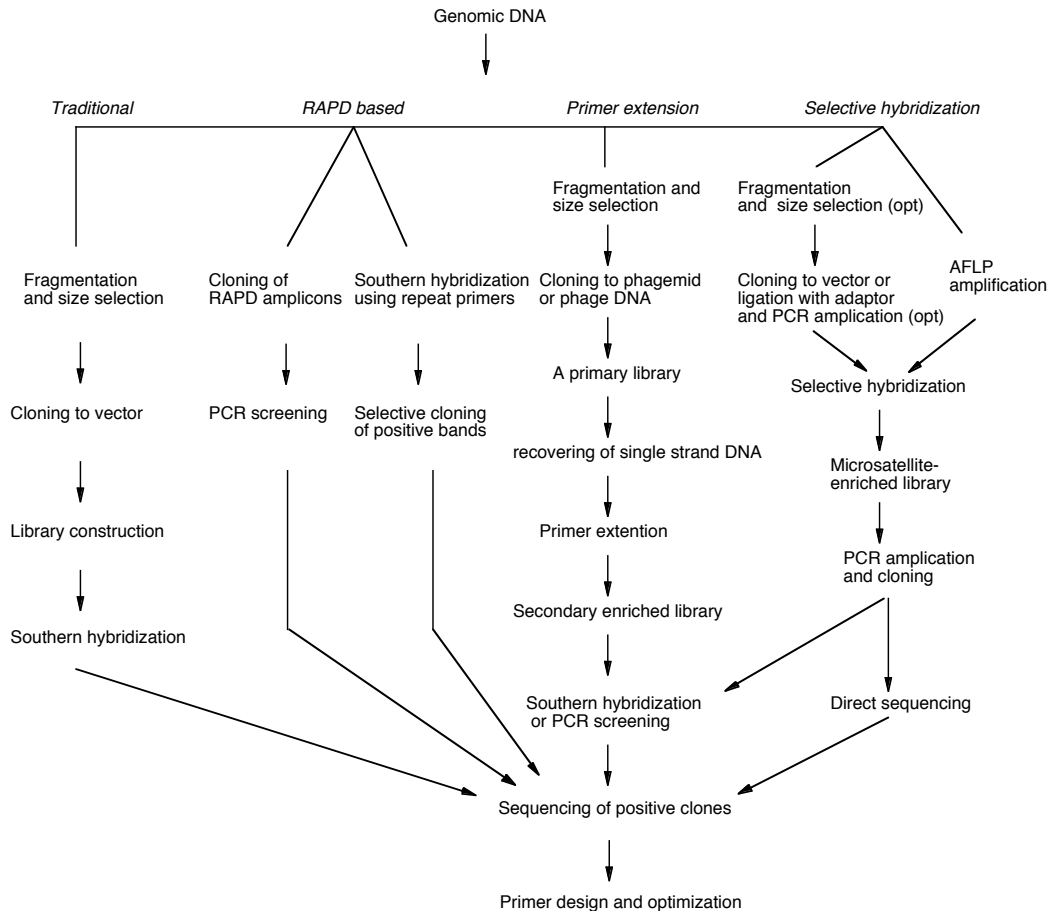


Figure 1: Schematic overview of microsatellite isolation strategies including traditional, RAPD-based, primer selection and selective hybridization methods (opt=optional step).

3.1.2.3 Direct clone-sequencing strategy of microsatellite isolation

Direct clone-sequencing strategies to isolate microsatellites have become more of interest because of the need to generate microsatellites from specific large-insert clones which harbor either functional candidate genes or, which can be used to enrich the already known microsatellite density on so far poorly covered chromosomes.

Recently, Fujishima-Kanaya *et al.* (2003) isolated some gene-associated dinucleotide microsatellites from BAC clones using a direct-sequencing method. Chen *et al.* (2004a) independently developed another rapid and efficient technique to isolate new microsatellite markers from PAC clones. The main difference between the two methods is the larger number of repeats contributing to their primers - (CA/GT)₁₀ instead of (CA/GT)₈ - and the increased number of nucleotides (n = 3) at the 3' end following the repeat motif (e.g. CGA/GCT). Fujishima-Kanaya *et al.* (2003) also determined the primary sequence of the large-insert clone by

setting up two sequencing reactions using a CA-repeat primer as the forward primer and a GT-repeat primer as the reverse primer. So, their averaged initial number of primers to determine sequence information was four compared with two oligonucleotides used by Chen *et al.* (2004a).

3.1.3 Characterization of genes

3.1.3.1 Large-insert libraries in pig genome mapping

Large-insert genomic libraries are required for the straightforward isolation and characterization of genes accomplished by construction of large-insert contigs. Large-insert libraries constructed in bacterial artificial chromosome (BAC), P1-derived artificial chromosome (PAC) and yeast artificial chromosome (YAC) vectors have been gradually established in livestock and extensively used in pigs for positional cloning, physical mapping and functional analysis similar to their impacts in humans and mice (Alexander *et al.*, 1997; Rogel-Gaillard *et al.*, 1997; Rogel-Gaillard *et al.*, 1999; Al-Bayati *et al.*, 1999; Anderson *et al.*, 2000; Suzuki *et al.*, 2000). A comparison of the characteristics of the three vector cloning systems is shown in Table 2 (Amemiya *et al.*, 1999; Giraldo and Montoliu, 2001). The most notable feature of these systems relative to conventional lambda and cosmid systems is their greatly increased insert sizes which may contain full-length genes and therefore allow for expedient characterization of gene structure and functions.

Table 2: Comparison of the BAC, PAC and YAC cloning systems (adapted from Amemiya *et al.* 1999; Giraldo & Montoliu 2001).

	BAC	PAC	YAC
Host cells	<i>Escherichia coli</i>	<i>Escherichia coli</i>	<i>Saccharomyces cerevisiae</i>
DNA topology of recombinants	Circular, supercoiled	Circular, supercoiled	Linear
Insert size	Up to 300 kb	Up to 300 kb	Up to 1 – 2 Mb
Transformation method	Electroporation	Electroporation	Spheroplast transformation
Selection for vector	Chloramphenicol	Kanamycin	Drop out media (lacking tryptophan and uracil)
DNA yield	Medium	High	Low
Stability	Very stable	Very stable	Variable, but can be very unstable
Degree of chimerism	Very low (<5% clones)	Very low (<5%)	Variable, but can be very high (>50%)
Purification of intact insert	Easy	Easy	Relatively difficult
Direct sequencing of insert	Relatively easy	Relatively easy	Difficult
Insert rearrangement	Very rare	Very rare	Yes

The BAC system is bacterial plasmid-based and the vectors are essentially an F-factor replicon with a chloramphenicol resistance gene (Shizuya *et al.*, 1992). BAC vectors can maintain genomic DNA fragments of up to 300 kb size. Very little or no rearrangements of the inserts and

hardly any chimeric clones have been observed. BACs appear to be quite stable and can easily be handled and characterized. The PAC cloning system uses a P1 bacteriophage replicon and a kanamycin resistance gene (Ioannou *et al.*, 1994). It can accommodate insert fragments of up to 300 kb and exhibits nearly all the advantages of BACs, and overcomes the drawback of low amount recombinant DNA, but the disadvantage of the PAC system is the larger vector size compared to BACs. The YAC cloning system uses two vector arms, both containing yeast selectable markers and telomere sequences, and one contains a centromere and a yeast autonomously replicating sequence (ARS) (Burke *et al.*, 1987; Nelson and Brownstein, 1994). The development of YAC permits cloning of extremely large fragments of more than 1 Mb size, however, disadvantages of the YAC system including a high degree of chimerism, inherent instability, and an overall difficulty in handling limits its usefulness.

Several large-insert genomic libraries have been constructed for the use in pig gene mapping and have been successfully used to isolate known genes and/or to generate contigs of genomic regions. Their relevant details regarding the respective libraries are provided in Table 3. The average insert sizes of these libraries range from 589 kb down to 119 kb in the order of YAC > BAC > PAC. All the libraries represent from three to five haploid genome equivalents.

Table 3: Large-insert libraries used in pig genome mapping.

	BAC				PAC	YAC	
Institution	INRA, France	CHORI, USA	Roslin Institute, UK	NAI, Japan	IVM, Göttingen Germany	USDA, USA	INRA, France
Pig breed	Large White male	Duroc female	Large White/Meishan boar	Large White/Landrace/Duroc boar	German Landrace male	Meishan boar	Large white male
Tissue	Skin fibroblasts	White blood cell	Blood lymphocytes	Kidney	White blood cell	Blood lymphocytes	Blood lymphocytes
Vector	pBeloBACII	pTARBAC1.3	pBeloBACII	pBAC-Lac	pCYPAC2	pYAC4	pYAC4
Host strain	DH10B	DH10B	DH10B	DH10B	DH10B	AB1380	AB1380
Restriction enzyme	<i>HindIII</i>	<i>MboI</i>	<i>HindIII</i>	<i>HindIII</i>	<i>MboI</i>	<i>EcoRI</i>	<i>EcoRI</i>
No. of Total clones	107,520	98,229	~ 100,000	103,488	90,240	33,120	33,792
Insert size	135 kb	173 kb	150 kb	133 kb	119 kb	589 kb	280 kb
Coverage genome	5 ×	5.7 ×	5 ×	4.4 ×	3.2 ×	5.5 ×	3 ×
Library screening	PCR on pools	PCR on pools (High density filters)	PCR on pools (High density filters)	PCR on pools	PCR on pools	PCR on pools (High density filters)	PCR on pools
Reference	Rogel-Gaillard <i>et al.</i> , 1999	de Jong <i>et al.</i> , 2002*	Anderson <i>et al.</i> , 2000	Suzuki <i>et al.</i> , 2000	Al-Bayati <i>et al.</i> , 1999	Alexander <i>et al.</i> , 1997	Rogel-Gaillard <i>et al.</i> , 1997

* <http://bacpac.chori.org/porcine242.htm>

3.1.3.2 Strategy of positional candidate gene approach

As discussed in later chapters, there are strategies including candidate genes, positional cloning and QTL genome scans to isolate and characterize genes of interest. In this section, the combined strategy of positional cloning and candidate gene approach, the positional candidate gene approach as used in our studies is illustrated (Figure 2).

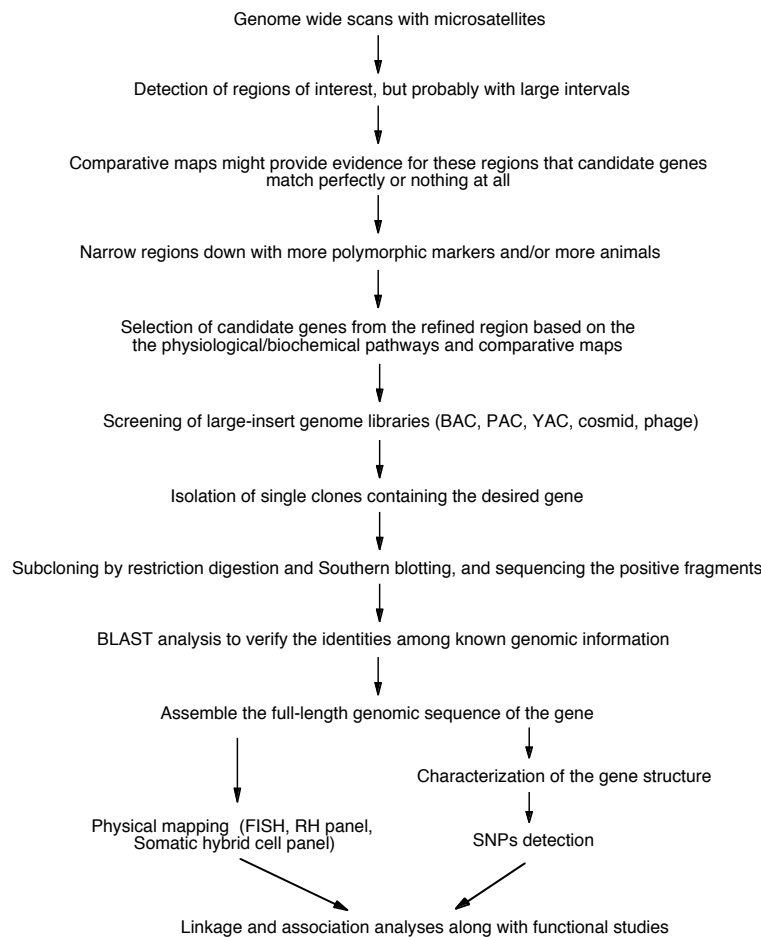


Figure 2: Flow chart of the positional candidate gene strategy

Genome wide scans of QTL mapping normally result in some large chromosomal regions associated with effects on traits of economical importance or on other traits. If the QTL regions are too large to imply direct sequencing and positional cloning, e.g. 10 Mb - 40 Mb (1 Mb = 1,000,000 bp = 1 cM), it is necessary to narrow down QTL regions with large intervals. A finemapping approach normally starts with more animals and/or the inclusion of more suitable markers. However, it might be difficult to find enough and suitable markers in a region of special interest. Thus the approach proposed by Chen *et al.* (2004a) to use already known markers in a

region to isolate additional large-insert library clones to develop some more polymorphic markers is a promising strategy. In addition, analyses of candidate genes in such chromosomal regions can be an alternative or supplement to narrow down QTL regions and further to analyse the causative genes (Collins, 1995). To determine the genomic structure of genes, isolated clones of interest are sequenced and the data processed with bioinformatic tools. After the full-length genomic sequence is assembled, the genomic structure of the gene (exon-intron boundaries, translation part, start codon, poly A) can be determined and all possible SNPs in the coding and non-coding regions can also be identified (e.g. by comparative sequencing of individuals of different breeds or phenotypes). The physical localization of the clone can be mapped alternatively by fluorescent *in situ* hybridization (FISH), somatic cell hybrid panel and radiation hybrid panel analysis. SNPs are detected to evaluate genomic differences between the so-called wild-type and the mutant-type. If an observed SNP is consistent among all mutant animals, this change is probably responsible for the mutant phenotype. Likewise, if a particular nucleotide substitution leads to an obvious non-permissive amino acid change or of a conserved promoter element, this SNP holds the possibility of affecting the structure, and then the function of the corresponding protein (Andersson, 2001). In addition, the characterization of positional candidate genes of desirable traits requires further linkage, association and functional studies. Gene expression such as RT-PCR and Northern blotting should be investigated among the wild-type and mutant animals.

3.2 Application of DNA markers in pig genetics

With the development of molecular markers porcine genomic maps have been largely enriched in the last few years. The pig genetic linkage map at Roslin (Scotland) has entries for over 3,000 loci including more than 1,000 genes (<http://www.thearkdb.org/browser?species=pig>). A developing AFLP map with about 3,000 AFLP markers is well underway and will provide a great contribution input to map density when finished. However, while the average distance between markers is about 3 - 5 cM, some large gaps still exist in the pig linkage map. The physical map for pigs as for other farm animals lagged behind at the beginning. With the use of a somatic cell hybrid panel (Yerle *et al.*, 1996) and a 7,000 rad (IMpRH) or recently of a 12,000 rad (IMNpRH2) radiation hybrid panel (Yerle *et al.*, 1998; Yerle *et al.*, 2002; Hawken *et al.*, 1999), the physical map has been growing rapidly and contains now over 3,000 genes and markers.

DNA markers can be applied in a variety of different applications, but here the focus will be on the two major basic ways in which they are used in modern pig genetics: (1) as indicators of genetic diversity and in phylogenetic studies, and (2) as genetic markers for QTL mapping and for tagging traits of interests, with special emphases on porcine disease research.

3.2.1 Phylogenetics

The objectives of phylogenetic studies are to reconstruct the correct genealogical ties between species and to estimate the time of divergence between two organisms since they last shared a common ancestor. In phylogenetic studies, a phylogenetic tree is commonly employed to illustrate the evolutionary relationships among a group of organisms.

To date, there are likely over 600 pig breeds or lines worldwide of which two thirds reside in China and Europe and over 200 of them are considered as endangered or critical. In order to meet future challenges in the agricultural and food industries, special efforts are required to conserve the genetic resources. Therefore, phylogenetic studies in pigs aim to evaluate the genetic uniqueness and diversity of pig breeds to assist in developing a rational plan for breed conservation programmes (Ruane, 1999). Ruane (1999) has suggested a set of criteria in an attempt to choose specifically breeds for conservation. The degree of endangerment and genetic uniqueness of the breed are two of seven essential criteria discussed. In addition, the origin and history of domestic pigs can also be explained by phylogenetic analyses. Independent domestication has occurred from wild boar subspecies in Europe and Asia, and introgression of Asian germplasm into European domestic breeds took place during the 18th and early 19th centuries (Giuffra *et al.*, 2000). The divergence of ancestors for European and Chinese Meishan domestic pigs was estimated around ~500,000 years ago using results of mitochondrial DNA.

On the basis of allele frequencies of DNA markers, pairwise genetic distances between breeds can be calculated and applied in diversity analyses among different populations and phylogenetic tree construction. Among at least ten commonly used distance parameters, Cavalli-Sforza and Edward's chord distance (D_C) and Nei *et al.*'s D_A distance generally show higher correct topology values. Nei's standard distance (D_S) and Goldstein *et al.*'s δ_μ^2 are more appropriate to estimate evolutionary times applying computer simulation (Takezaki and Nei, 1996). In the European Community Pig Biodiversity I project (PigBioDiv 1) (<http://databases.roslin.ac.uk/pigbiodiv>), that was completed in 2000, genetic distances represented by Reynold's D_R and Nei's D_S were

used in genetic diversity studies of European pig breeds (SanCristobal *et al.*, 2003). However, there is still no clear consensus opinion regarding which genetic distances are best to estimate phylogenetic relationships among domestic animals as they have undergone complicated genetic changes since the time domestication has started. It is likely that genetic drift and mutation are important factors affecting breed domestication. Moreover, the efficiencies of genetic distance measurements in phylogenetic construction are influenced by the number of animals and molecular loci sampled and by the method used for tree construction such as the neighbour-joining (NJ) and the unweighted pair group method with an arithmetic mean (UPGMA) (Takezaki and Nei, 1996).

To improve the reliability of phylogenetic results, a guideline for genetic distance projects was published by an FAO working group in 1993, recommending that at least 25 animals per breed should be used and that 20 to 30 microsatellite loci, with four to ten alleles each, should be typed (Barker *et al.*, 1993). More recently, several other recommendations have been made public for genetic diversity studies including the use of 2 - 5 microsatellites per chromosome and genotyping of 50 animals (25 of each sex) that are unrelated (Barker *et al.*, 1998). Nevertheless, these guidelines are sometimes ignored and results are published on lower requirements because of the limited budget and availability of some endangered breeds (Paszek *et al.*, 1998). The implication of genetic distances is also very important in genetic biodiversity studies between pig breeds. Diversity measurements such as PIC, effective allele number (N_E), expected heterozygosity, fixation indices of loci, Nei's measure of diversity and allelic richness have been also considered in phylogenetic studies (Petit *et al.*, 1998).

So far, a number of molecular markers have been used for genetic diversity and phylogenetic analyses. These include microsatellites, minisatellites, AFLPs, SNPs, large scale or directed sequencing, mitochondrial DNA (mtDNA) and Y chromosome genotyping (Rothschild, 2003a). Microsatellite markers have been largely used in phylogenetic studies and have some value to measure differences within breeds, however due to their neutral properties, they are poorly correlated with phenotypic changes due to selection. Very recently the use of gene markers has attracted more researchers as variation in these allele frequencies may provide information related to the functional differences between breeds. The phylogenetic studies using major gene markers or SNPs associated with traits of interest would be most relevant for breed conservation and

provide potential breeds efficiently for the future production market. Despite the limited information of gene markers, Ciobanu *et al.* (2001) examined the genetic variation in two conserved local Romanian pig breeds using type I DNA markers. Moreover, mitochondrial DNA maternally inherited is useful for tracing the maternal linkages in populations. Y chromosome consists of a euchromatic non-recombining region (NRY), which makes up 95 percent of its length, flanked by two pseudoautosomal regions (Cooke *et al.*, 1985) and its genotyping can be used for measuring breed history and phylogenetic origins.

The largest ongoing project on biodiversity studies of pig breeds is the European Community Pig Biodiversity II project (PigBioDiv 2), which will evaluate and compare genetic diversity among at least 100 pig breeds originated from China and Europe (Blott *et al.*, 2003). The project will not only determine the relationships between breeds by estimating genetic distances based on microsatellite markers and haplotypic relationships from mtDNA and Y chromosome polymorphisms, but also determine functional differences among breeds by characterizing trait gene loci and QTL regions.

In addition, there are still some technical problems that limit the application of molecular markers in phylogenetic studies (Rothschild, 2003a). Methods such as microsatellites and AFLPs are constrained generally by gel electrophoresis resulting in low throughput. The use of microsatellites or SNPs requires previous identification of a polymorphism, and recognition of the polymorphisms based on size separation can be different among labs, which makes results incompatible and misleading.

3.2.2 Quantitative trait locus (QTL) analysis and disease survey

3.2.2.1 Strategies to identify QTLs

Many economically important traits, such as growth rate, meat quality, milk production, litter size and disease resistance are supposed to be multifactorially influenced by polygenic and environmental factors. The main QTL mapping projects in pigs were summarized by Bidanel and Rothschild (2002) as shown in Table 4. A QTL is defined as a region of the genome covering one or more genes that affect a quantitative trait (Geldermann, 1975). There are usually two main strategies for finding quantitative trait loci including association analysis along with candidate gene typing and genome scans based on linkage mapping (Beuzen *et al.*, 2000; Andersson, 2001; Dean, 2003; Rothschild, 2003b).

Table 4: Main QTL mapping programmes in pigs (Bidanel & Rothschild 2002)

Country	Institution	Population ^a	Animals	Markers	Traits ^b
Belgium	Liege University	LW × PI	1032	11 (SSCr 2)	GR, CC
France	INRA	MS × LW	1103	137	GR, CC, MQ, RE, BE
Germany	Hohenheim University	PI × (MS or WB)	979	121	GR, CC, MQ
Japan		MS × PM	215	318	GR, CC
Netherlands	Wageningen University	MS × LM	800	127-132	GR, CC, MQ
Norway	Agricultural University of Norway	(DU × LR) × LW	305	11 (SSCr 4); 9 (SSCr 6); 9 (SSCr 7)	MQ
Scotland	Roslin Institute	MS × LW	390	9 (SSCr 4)	GR, CC
Spain	IRTA-INIA	LR × IB	500	7 (SSCr 6)	GR, CC, MQ
Sweden	University of Uppsala	WB × LW	191	117-236	GR, CC, MQ, DR, ...
USA	Iowa State University	CH × YO	294	5 (SSCr 4); 10 (SSCr 7)	GR, CC, MQ
USA	Iowa State University	BE × YO	500	125	GR, CC, MQ
USA	University of Minnesota	MS × LW	298	119	GR, CC
USA	USDA	MS × SL	540	157	GR, CC, RE
USA	University of Nebraska	ORL × CL	306	151	RE
USA	University of Wisconsin	HGL × LGL	240	75	GR

^aBE = Berkshire; CH = Chinese breeds; IB = Iberian breed; CL = control line; HGL, LGL = line selected for high and low growth rate, respectively; LR = Landrace; LW = Large White; MS = Meishan; ORL = line selected for ovulation rate and embryo survival; PI = Pietrain; SL = synthetic line; WB = wild boar; YO = Yorkshire

^bBE = behavioral traits; CC = carcass composition; DR = disease resistance; GR = growth; MQ = meat quality; RE = reproduction

Candidate gene analyses have been employed to investigate a variety of traits whose physiology is well understood. This approach can be very powerful and can detect loci even with small effects provided that the candidate gene is the causative gene. To evaluate all possible candidate genes for the trait of interest seems, however, too time-consuming and therefore impractical. In farm animals, linkage disequilibrium is more frequently observed (Farnir *et al.*, 2000) which can increase the probability of finding true associations between genetic markers and trait loci, but it also elevates the risk of false-positive associations.

Genome wide scans are useful to resolve the genetics of traits for which hardly anything is known. Genome scans may also reveal previously unsuspected loci as candidate genes for well understood traits. In order to increase the statistical power in QTL mapping, artificial crosses are often made between divergent populations, e.g. European and Chinese pig breeds intercross (Spelman and Bovenhuis, 1998) or progeny testing using the granddaughter design in dairy cattle (Weller *et al.*, 1990; Heyen *et al.*, 1999). In principle, a sufficiently large number of animals in properly designed populations in combination with a set of polymorphic markers evenly spaced

across the genome (high resolution map) are also required to map a QTL with a major effect. In addition, several other factors can influence the chance to detect a QTL, including the size of the effect, the frequency of the alleles, the heritability of the trait, and the chosen thresholds in the statistical analysis (Haley, 1995). Recently, another approach of using a denser collection of microsatellite markers within and nearby genes involving functional variants has been developed for the human genome project and proved to have an increased power (Collins *et al.*, 2003). Moreover, mappers have to be aware that any potential polymorphisms of the gene must later be confirmed in commercial populations before their wide application in marker-assisted selection in breeding programmes.

The chromosome regions of most QTLs are too imprecise for direct positional cloning (Knott and Haley, 1992; Andersson *et al.*, 1994), and thus positional candidate gene approaches are extensively used to identify the causal genes in QTL regions. So far, there is only one example of successful positional cloning known: *PRKAG3* in porcine skeletal muscle is associated with excess glycogen content (Milan *et al.*, 2000). A missense mutation of R222Q in *PRKAG3* causes poor porcine meat processing quality. Once a QTL has been mapped, the potential candidate genes will be investigated to narrow the region of interest by a stepwise process. By comparing the coding sequences and expression levels of positional candidate genes in populations, the unrelated genes might be eliminated and the causative quantitative trait nucleotide (QTN) can be discovered. QTL mutations were recently also found in regulatory rather than in coding regions. Results from *Drosophila* suggest that some trait loci are too difficult to prove causal relationships with QTLs leading to the demand that all gene regions need careful analysis (Mackay, 2001). This postulate has been further confirmed by the finding that a regulatory mutation of *IGF-2* (*IGF2*-intron3-nucleotide 3072) causes a major QTL effect on muscle growth in the pig (van Laere *et al.*, 2003).

3.2.2.2 Comparative mapping and functional analysis

The large numbers of expressed sequence tags (ESTs) from cDNA clones can assist comparative mapping and large-scale expression analysis using array technologies. At present, there are approximately 171,920 porcine ESTs (update to 14th November 2003) deposited in Genbank (http://www.ncbi.nlm.nih.gov/dbEST/dbEST_summary.html). The largest EST project published to date was initiated by the USDA. As an example, the PathoCHIP project funded by the

European community (<http://www.pathochipproject.com>) aims to use spotted cDNA array for disease organism and immune response gene studies. International cooperative efforts will therefore largely advance the pig transcriptome and functional analyses. Comparative mapping is also an important approach in farm animal genome studies as it allows extensive exploitation of human genetic map. Chromosome painting has been successfully used to establish regions of conserved synteny between mammalian animals and humans with human chromosome-specific probes (Chowdhary *et al.*, 1998). Gene expression researches may be particularly valuable to detect imprinted genes (de Koning *et al.*, 2000). Imprinting is the phenomenon in which only one of the two alleles of a gene may be expressed either on random events or origin of parent effect (Hall, 1997). The above mentioned *IGF-2* linked QTL has been reported to be genetically an imprinted locus affecting body composition in pigs (Georges *et al.*, 2003; van Laere *et al.*, 2003). Therefore, an improved strategy might be to develop a haplotype map of the whole genome which is useful to design the second generation genome scans (Weiss and Clark, 2002).

In the last few years, the mutagenesis strategy has also been proposed and offers a different perspective in finding genes determining complex traits (Nadeau and Frankel, 2000). Mutagenesis which considers all genes in a pathway will identify rare mutations causing disease. In contrast, QTL mapping is more likely to identify genes that encode regulatory proteins or rate-limiting enzymes (Korstanje and Paigen, 2002).

3.2.2.3 Monogenic diseases

Simple monogenic diseases in farm animals have been identified and are catalogued in the Online Mendelian Inheritance in Animals (OMIA) database (<http://morgan.angis.su.oz.au/Databases/BIRX/omia/>) (Table 5). Some diseases may not be apparent to breeders or even associated with benign traits in affected animals, and thus inadvertently selected in animal breeding. Hyperkalaemic periodic paralysis is an example of an autosomal dominant disease in horses. Affected individuals have more muscle because the biochemical defect is due to a mutation in the sodium channel of muscle tissue (Rudolph *et al.*, 1992). An important autosomal recessive disease in cattle is the bovine leucocyte adhesion deficiency (*BLAD*), a severe immunodeficiency syndrome caused by a missense mutation that prevents the production of effective *CD18*. The disease is widely spread in the US Holstein-Friesian cattle because one popular sire with a huge number of progeny was the carrier for this mutation (Shuster *et al.*, 1992). For these cases in

which molecular basis has been revealed, diagnostic tests such as a PCR-RFLP screening test have been developed and applied in breeding programmes to increase animal welfare, to reduce the incidence of diseases and to improve production efficiency.

Table 5: Summary of the OMIA database contents for major species (latest update: 16th October 2003).

	Cat	Cattle	Chicken	Dog	Emu	Fox	Goat	Horse	Pig	Quail	Rabbit	Sheep	Turkey	Total
Disorders/traits	263	357	174	451	4	5	66	184	203	34	48	179	28	1996
Single-locus disorder/traits	38	56	63	100	2	3	8	26	33	19	12	59	8	427
Disorder/traits (causative mutation identified)*	7	27	11	38	1	2	5	9	11	2	3	9	1	126
Potential animal models for a human disorder	123	117	34	207	2	3	24	86	65	9	27	62	3	762

*Disorders/traits for which the causative mutation has been identified at the DNA level

3.2.2.4 Disease resistance and immune response traits

Different strategies have been used to identify the genes responsible for multifactorial diseases. Compared with QTL mapping for other traits of economical importance, little progress has been made so far for immune response and disease resistance, primarily owing to the lack of pedigree data with informative disease records and the difficulty to generate dedicated resource populations with a high incidence for the disease. The ryanodine receptor (*RYR1*) encoding the calcium release channel in skeletal muscle was identified as a functional candidate gene. A single missense mutation of R614C was revealed to be responsible for susceptibility to malignant hyperthermia in pigs, which could be triggered by stress or exposure to the anaesthetic gas halothane. This mutation was also associated with increased leanness and appeared to be inadvertently selected by breeders (Fujii *et al.*, 1991). If the genes associated with human or mouse diseases are well studied, candidate gene approaches can be used to identify the genes responsible for these diseases in farm animals and then lead to their functional and association analyses, such as natural resistance associated macrophage protein 1 (*NRAMP1*) and clotting factor IX (Sun *et al.*, 1998; Singer *et al.*, 1996).

To date, QTL scans for immune response and disease resistance are limited in number. Four QTL regions with significant effects on immune capacity were detected on four chromosomes respectively in a Large White × Wild boar cross (Edfors-Lilja *et al.*, 1998). In 2000, additional four QTLs were found on chromosomes 2, 6, 8, and 12 associated with stress-induced alterations

of immune functions in which stress of mixing and transportation was imposed on three-month old pigs (Edfors-Lilja *et al.*, 2000). Two alpha (1, 2) fucosyltransferase genes (*FUT1*, *FUT2*) on porcine chromosome *6q11* have been identified that are closely linked to the blood group inhibitor (S) and *E. coli* F18 receptor (*ECF18R*) loci (Meijerink *et al.*, 1997). Presumably, mechanisms of *FUT1* or *FUT2* gene products are responsible for bacterial adhesion and need to be further determined. A QTL region affecting susceptibility to K88 *E. coli* infection is localized on chromosome 13 (Edfors-Lilja *et al.*, 1995). In addition, Reiner *et al.* (2002) detected QTLs for resistance/susceptibility to pseudorabies virus (*PrV*) in swine by a genome-wide scan (85 microsatellite markers evenly spaced on the 18 pig autosomes and on the pseudoautosomal region of the X chromosome) using a resource family (European Large White × Chinese Meishan pigs) (Reiner *et al.*, 2002). The results revealed that after being challenged, the pure-bred Large White pigs, the F₁ and three-quarters of the F₂ animals, but none of the Meishan pigs, developed the neurological symptoms and died or were euthanized. QTLs for appearance/non-appearance of neurological symptoms were found on chromosomes 5, 6, 9 and 13; QTLs for rectal temperature after *PrV* challenge were found on chromosome 2, 4, 8, 10, 11 and 16. Therefore, fine mapping and association analyses of positional candidate genes are required substantially to identify the causative QTN or genes.

Due to the acceleration of identification of genes from QTL studies, it is suggested that QTL mapping is a promising technique. The harvesting era of QTL genes is beginning (Korstanje and Paigen, 2002). Functional studies and comparative mapping will facilitate the identification of genes associated with immune response and disease resistance. In addition, QTL mapping can be further enhanced by the increasing availability of new markers, the efficiency of genotyping technology, and improved statistical methods for analysing QTL data.

3.3 The phosphoglycerate kinase (PGK) gene family

3.3.1 Members of the PGK gene family

3.3.1.1 Functional loci and pseudogenes of the PGK gene family

Phosphoglycerate kinase (EC: 2.7.2.3) catalyzes the reversible conversion of 1,3-diphosphoglycerate to 3-phosphoglycerate generating one molecule of ATP in the glycolytic pathway, formally known as the Embden-Meyerhof pathway, which converts glucose (or fructose) to pyruvate (Figure 3) (Devlin, 1997). Phosphoglycerate kinase does also modulate sperm metabolism during epididymal transport (Salisbury *et al.*, 1977). It is also critical for tumor expansion and metastasis through the angiogenic process as a disulfide reductase (Lay *et al.*, 2000). Hybridization results of a full-length cDNA encoding for phosphoglycerate kinase indicated the existence of a small family of dispersed *PGK* or *PGK-like* genes in man (Michelson *et al.*, 1983; Michelson *et al.*, 1985; McCarrey and Thomas, 1987): an ubiquitously expressed, X-linked form referred to as *PGK1* (*PGKA*) and a testis-specific, autosomally determined isoform referred to as *PGK2* (*PGKB*) on chromosome *6p21.1-p12* are known besides two pseudogenes. *PGK1P1* is located on *Xq11-q13*, proximal to the expressed *PGK1* gene (Michelson *et al.*, 1985; Willard *et al.*, 1985), whereas *PGK1P2* is assigned to chromosome 19 (Willard *et al.*, 1985; Gartler *et al.*, 1986).

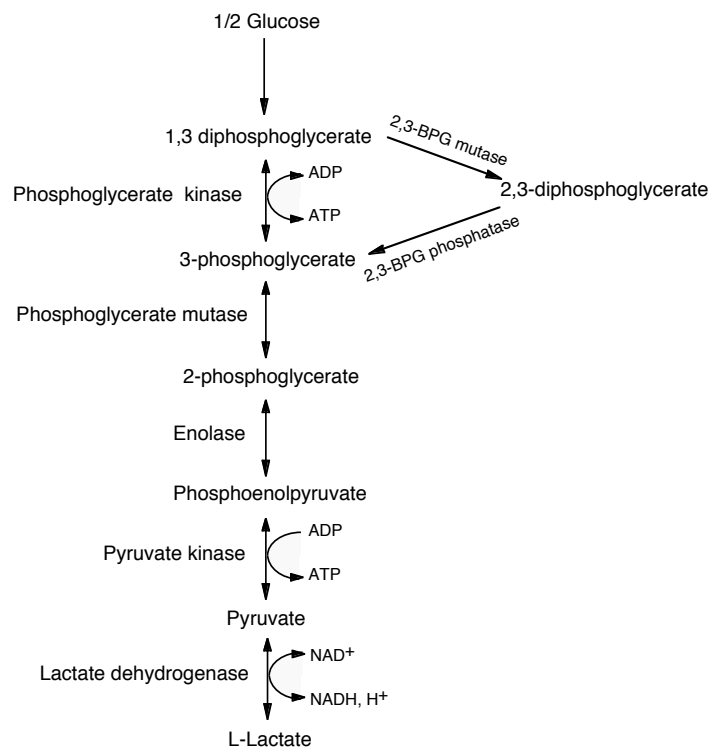


Figure 3: The glycolytic pathway (Devlin 1997) (BPG=bisphosphoglycerate).

PGK is a highly-conserved enzyme in all eukaryotic species, including yeast as the human-yeast chimeric PGK molecules are also functional (Mas *et al.*, 1986). Therefore, it is reasonable to assume that similar functional regions have been conserved in the human PGK proteins. Two isozymes of PGK, each encoded by a separate gene, are differentially expressed during spermatogenesis in mammals (Kramer and Erickson, 1981; VandeBerg, 1985; McCarrey *et al.*, 1996). The PGK1 isozyme is encoded by the X-linked *PGK1* gene and is expressed in premeiotic spermatogenic cells as well as in all somatic cells and in oogenic cells (VandeBerg, 1985), while the PGK2 isozyme is exclusively expressed in meiotic and postmeiotic spermatogenic cells, which was proposed to compensate for reduced expression of the *PGK1* gene in these cells (McCarrey and Thomas, 1987; McCarrey, 1990). By analysis of the cDNA and the encoded proteins of these two functional *PGK* genes, it was suggested that none of the differences in the amino acid sequence between the PGK1 and PGK2 protein contributes to any likely change of catalytic function of these two isozymes. However, a potential difference exists between them suggesting that the PGK2 protein is more stable *in vivo* than the PGK1 protein (McCarrey *et al.*, 1996). To identify some associated genes or markers for male fertility and/or male fertility dysfunction, the porcine functional *PGK* genes were identified by Chen *et al.* (2004b) and Chen *et al.* (2004c). The X-linked *PGK1* on *SSCXq12-q13* and the testis-specific *PGK2* on *SSC7q14-q15*, respectively, coincide with the homology between the X chromosomes in human and pig, and the homology between the p arm of human chromosome 6 and q arm of pig chromosome 7.

3.3.1.2 Molecular evolution of *PGK* gene family by retrotransposon events

Analysis of the nucleotide sequence of *PGK2* and *PGK1P1* suggested that they originated from the “housekeeping” gene *PGK1* more than 100 million years ago by RNA-mediated gene duplication. It is hypothesized that the *PGK2* gene might then be a transcribed retrotransposon (Boer *et al.*, 1987; McCarrey, 1990). A comparison of the human and murine *PGK* genes indicates that *PGK2* has evolved more rapidly than the *PGK1* gene since the two genes diverged early in mammalian evolution, but the lack of introns in *PGK2* may have diminished the inter-exon variation. Nucleotide sequence characteristics indicate that the *PGK2* retroposon initially included a copy of the endogenous *PGK1* “housekeeping” 5'-regulatory sequences, which facilitated the initial expression of this retroposon (McCarrey, 1987). Therefore, it is implied that the *PGK2* gene initially carried a “housekeeping” promoter sequence that directed ubiquitous

low-level transcription, and has subsequently evolved a tissue-specific promoter that directs high-level transcription (McCarrey, 1990) (Figure 4). With the comparison of the *PGK* genes in human and mouse (Table 6), it was shown that these genes share high homology.

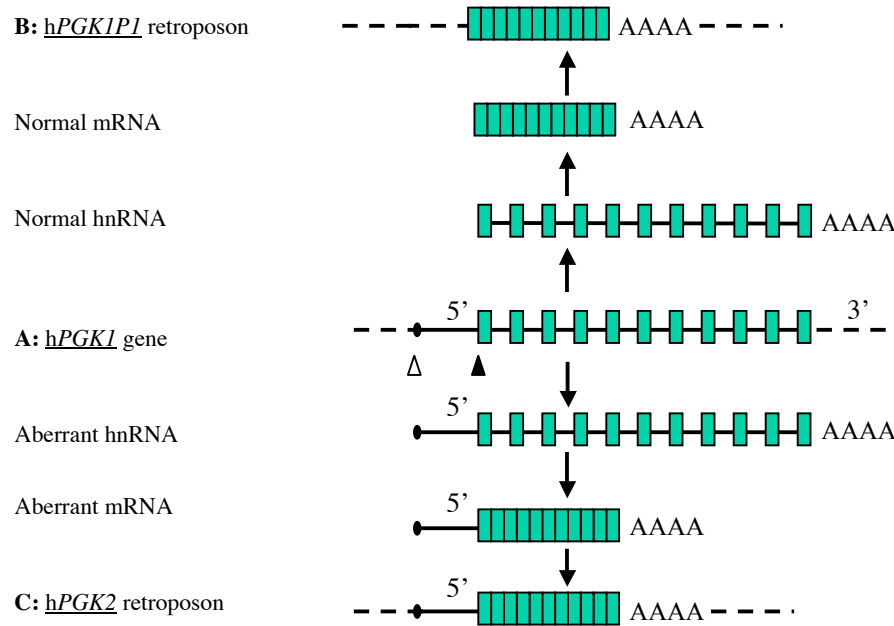


Figure 4: The origin of human *PGK* retroposons (McCarrey 1990). The transcript initiated at the normal start point (solid arrowhead) in *PGK1*; The functional *PGK2* gene is shown originating by similar processing of an aberrant transcript of *PGK1* that initiated at an upstream start point (open arrowhead) and included the endogenous *PGK1* 5'-promoter sequence. hnRNA= heteronuclear RNA.

Table 6: *PGK* gene region homologies in human and mouse (%) (McCarrey 1990).

Genes compared	Promoter (200 bp)	5'-UTR (90 bp)	Coding sequence (1251 bp)		3'-UTR (200 bp)
			N.A	A.A	
h <i>PGK1</i> /m <i>PGK1</i>	48	65.2	92.9	97.6	55.8
h <i>PGK2</i> /m <i>PGK2</i>	63.9	44.8 (67.2)*	84.9	86.1	56.0
h <i>PGK1</i> /h <i>PGK2</i>	44.1	46.2	85.3	87.1	55.9
m <i>PGK1</i> /m <i>PGK2</i>	36.1	24.7 (40.7)*	79.2	84.0	50.5
h <i>PGK1</i> /h <i>PGK1P1</i>	30.9	74.4	94.1	90.0	98.5

* Values in parentheses are based on maximized alignments with deletions excluded. N.A. = nucleic acid, A.A. = amino acid

Evolutionary biologists hypothesized that the earliest life forms contained self-replicating RNA genomes. The advent of polymerases that make DNA copies of RNA templates allowed the conversion of information from unstable ribose-based polymers to more stable deoxyribose-based polymers through the process of reverse transcription. In this way, reverse transcription appears to have a pivotal role in the formation of the first DNA genomes (Kazazian and Moran, 1998). It

is now apparent that reiterative rounds of reverse transcription served to expand both the size and complexity of the mammalian genomes. Retrotransposons of any sequence are potentially threatening to the normal genome function, however, the mechanisms controlling this process remain poorly understood (Curcio and Garfinkel, 1999; Moran *et al.*, 1999; Werle-Schneider *et al.*, 1999). As a result of the human genome project, we now know that only approximately 2-3% of the human genome is comprised of exonic sequences. The remainder, so-called “junk DNA”, is composed largely of introns, simple repeat sequences and mobile elements or their remnants (Figure 5). Mobile elements fall into three major classes: DNA-based transposable elements, autonomous retrotransposons and non-autonomous retrotransposons (Kazazian and Moran, 1998). The non-autonomous retrotransposon is composed mainly of *Alu* elements and processed pseudogenes, both of which end in a poly(A) tail and lacking protein-coding capacity. Their mobilization requires a cellular source of reverse transcriptase, which is mostly likely encoded by retrotransposition-component long interspersed nuclear elements (LINEs or LIs). Mobile elements were firstly recognized as potential causal agents of human disease in 1988 when two separate insertions of truncated LIs retrotransposon were found to disrupt the factor VIII gene, resulting in haemophilia A (Kazazian *et al.*, 1988). Recently, six additional retrotransposed LI insertion were subsequently found, while five of them occurred either in the germ line or during the early development (Woods-Samuels *et al.*, 1989; Miki *et al.*, 1992; Narita *et al.*, 1993; Holmes *et al.*, 1994).

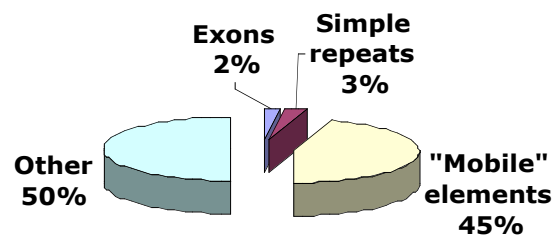


Figure 5: Genome Anatomy

Most pseudogenes have multiple features that confirm their non-functional status. However, there are genes that have many features of pseudogenes, but with the recognition that these genes are potentially functional. Accordingly, experimental design and interpretation across the whole field of molecular genetics must take pseudogenes into careful consideration (Mighell *et al.*, 2000). Processed pseudogenes are probably generated by RNA polymerase II rather than the RNA

polymerase III transcription responsible for other retrotransposons such as either *Alu* or LINE repeats (Maestre *et al.*, 1995).

3.3.2 Biological/physiological function of the PGK

3.3.2.1 Expression and encoded proteins of PGK genes

The mammalian testis is a common location for expression of tissue-specific isozymes of enzymes expressed ubiquitously in somatic cell types (Goldberg, 1977; Hecht, 1993). In many cases, these isozymes are encoded by several autosomal loci. This situation appears to reflect unique requirement in somatic isozyme, thus mandating the need for a specialized testis-specific isozyme. One of the best characterized examples is the *PGK* gene system, encoding the PGK protein which is a two-domain protein; each domain is composed of six repeats of an *alpha/beta* structural motif. In this system, expression of the X-linked somatic form of the enzyme (PGK1) is repressed during the spermatogenesis due to transcriptional inactivation of the single X chromosome in meiotic spermatocytes (McCarrey *et al.*, 1992a; McCarrey *et al.*, 1992b; Kumari *et al.*, 1996). Thus, it has been suggested that the autosomal gene encoding the testis-specific isozyme (PGK2) may be expressed in these cells simply to compensate for this loss, rather than to provide any specialized function in the late spermatozoa (McCarrey, 1994). This suggestion was also supported by enzymological studies of PGK isozymes in humans, mice, and other mammals, and from the evidence of no obvious differences of the molecular size, substrate affinity, energy of activation, coenzyme specificity, catalytic properties, thermal denaturation, as well as K_m and V_{max} values between these isozymes (Pegoraro and Lee, 1978; VandeBerg, 1985).

By analysis of the specific activities and synthesis of the ubiquitous isozyme PGK1 and the testis-specific isozyme PGK2 in spermatogenic cells of the mouse, it was demonstrated that there is a five-fold increase of total PGK specific activity between immature and adult testes. The increase in total PGK is entirely due to the appearance and increase of the PGK2 isozyme (Kramer and Erickson, 1981; Erickson, 1990). The occurrence of the transcripts produced from the ubiquitously expressed X-linked *PGK1* gene and the testis-specific autosomal *PGK2* gene during spermatogenesis in mouse, revealed that the transcription of *PGK2* is initiated coincidentally with the onset of meiosis in male germ cells, and then continues to increase in the later spermatocytes and postmeiotic round spermatids.

3.3.2.2 *PGK transcript switch and PGK methylation*

The spermatogenic pathway consists of complex developmental events, such as differentiation of spermatogonial stem cells, meiotic cell division, and morphogenic maturation of sperm (Hecht, 1986). Many genes undergo altered expression during this process, and the resulting repertoire of testis-specific proteins are believed to be required both for advancing the spermatogenic pathways and for maintaining the architectural organization of germ cell. Although the molecular basis for the spermatogenic pathway remains to be elucidated, changes in gene expression at both the transcriptional and translational levels are proposed to play important roles (Willison and Ashworth, 1987; Prospst *et al.*, 1988; Erickson, 1990). In the testis, PGK1 exists in spermatogenic cells only during the early stages of spermatogenesis, and the PGK isozyme switches from PGK1 to PGK2 as the pathway proceeds (Kramer, 1981). It was later proposed that the isozyme switch of murine PGK occurs at the transcriptional level during the pachytene spermatocyte stage (Goto *et al.*, 1990; Singer-Sam *et al.*, 1990; McCarrey *et al.*, 1992a). The spermatogenic expression of the murine *PGK2* gene was thought to be regulated by both positive and negative *cis*-acting DNA elements (Goto *et al.*, 1991; Goto *et al.*, 1993; Mizuno *et al.*, 1992). Some of the *cis*-elements could be responsible, at least partly, for the PGK transcript switch in the testis. The negative *cis*-element functions as a silencer (Mizuno *et al.*, 1992), which consists of two separate DNA regions (Nishiyama *et al.*, 1994). By analysis of the upstream region of the *PGK2* gene, the proper expression of the mouse *PGK2* gene requires an upstream region longer than that required by the human gene suggesting the presence of one or more negative *cis*-elements that suppress murine *PGK2* expression in non-testicular organs (Ando *et al.*, 2000).

DNA methylation is thought to play a role in the regulation of tissue-specific genes in animal cells (Cedar, 1988). Most tissue-specific genes are fully methylated in sperm and in almost all somatic tissues of the adult organism (Yisraeli and Szyf, 1984). In the respective tissue of expression, however, these tissue-specific genes undergo a striking “demethylation” that could either be necessary for gene transcription or represent a secondary response to induction which serves to maintain the new active state (Ariel *et al.*, 1991). *PGK2*, a non-CpG-island containing gene is highly methylated in nonexpressing cell types but undermethylated in pachytene spermatocytes and round spermatids, where it is actively transcribed. At later stages of spermatogenesis, however, the gene becomes remethylated and thus acquires the full modification pattern in sperm DNA. It was revealed that the sperm DNA emerging from the testis

does not contain any germ-line-specific unmethylated sites and thus carries the methylation pattern typical for that in somatic tissues (Ariel *et al.*, 1991). A further investigation observed a specific demethylation event in the *PGK2* gene in prospermatogonia at about time of birth. Approximately 10 days before the onset of transcription which occurs for the first time in primary spermatocytes, the *PGK2* gene was unmethylated in adult spermatogenic testicular cells, but was remethylated in mature spermatozoa in the vas deferens. Surprisingly, this remethylation is part of the process of sperm maturation which occurs in the epididymis (Ariel *et al.*, 1994).

3.3.3 Direct effects and associations of the PGKs

3.3.3.1 *PGK and diseases*

PGK1 isozyme deficiency was found to be associated with hemolytic anemia, mental disorder and myoglobinuria in human (Fujii and Yoshida, 1980; Tonin *et al.*, 1993). Recently, Lay *et al.* (2000) found that the administration of phosphoglycerate kinase to tumour-bearing mice caused an increase in plasma levels of angiostatin, and a decrease in tumour vascularity and rate of tumour growth (Lay *et al.*, 2000). It was indicated that phosphoglycerate kinase not only functions in glycolysis, but is also secreted by tumour cells and participates in the angiogenic process as a disulphide reductase.

3.3.3.2 *PGK and male reproduction*

Studies for PGK2 deficiency are limited to date, mainly due to its solely expression in testis, but the concerns for the testis-specific PGK2 are now growing for its putative function related to male reproductive traits (e.g. sterility and fertility) in mammals. The mature spermatozoa requires significant amounts of phosphoglycerate kinase to participate in the metabolism of fructose which is an essential component in semen and which is secreted in both the male and female reproductive tracts (Mann, 1964). Moreover, the inactivation of the single X-chromosome in spermatogenic cells before meiosis may have contributed to the need for a functional autosomal *PGK* locus (McCarrey and Thomas, 1987). According to the presence or absence of different gene transcripts associated with various spermatogenic defects, *DAZ* (Deleted in AZoospermia), *PGK2* and protamine 2 genes have been detected by RT-PCR in patients with nonobstructive azoospermia (Figure 6). The PCR diagnosis was employed to predict the testicular spermatozoa (Song *et al.*, 2000).

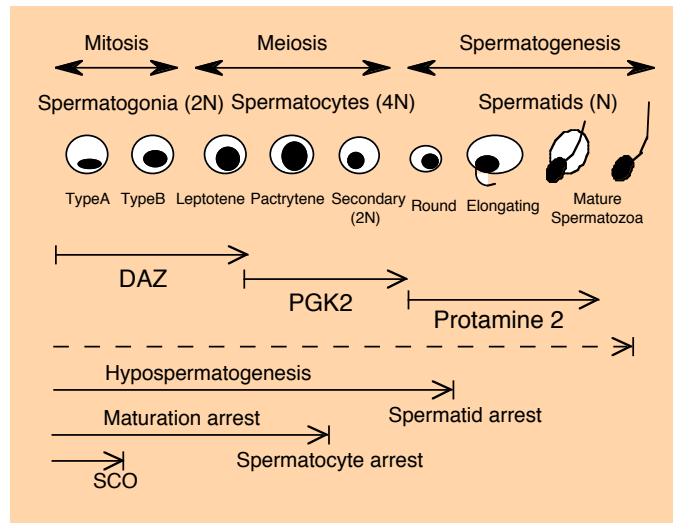


Figure 6: Nuclear status and gene expression during the spermatogenesis. (*PGK2* gene is transcribed in the pachytene spermatocyte.) (Song *et al.* 2000).

Koizumi *et al.* (1990) concluded that the relative *PGK2* quantity provided information on the testicular development and is therefore useful as an indicator of testicular function, such as sperm production capacity. A good correlation was observed between the relative *PGK2* quantities and sperm/spermatid counts. This correlation was also supported by further evidence that in case of sterility-associated with chromosomal abnormality (chromosomal translocation between chromosome X and chromosome 16), a relative *PGK2* quantity was not detected in any of the seven abnormal adult mice. Recently, both the equine and the murine *PGK2* gene were identified within the cysteine-rich secretory protein (*CRISP*) gene family, which are expressed in the male genital tract and that are thought to be involved in sperm-egg fusion (Kasahara *et al.*, 1989; Richards *et al.*, 1989; Giese *et al.*, 2002). Therefore, these genes are supposed to be of interest as candidate genes for inherited male fertility dysfunction and as putative QTL region for male fertility traits.

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