



## Persistence and intergenerational transmission of differentially expressed genes in the testes of intracytoplasmic sperm injection conceived mice\*

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**Abstract:** Intracytoplasmic sperm injection (ICSI) is commonly used to solve male infertility problems. Previous studies showed that early environmental exposure of an embryo may influence postnatal development. To detect whether ICSI operations affect the reproductive health of a male or his offspring, we established assisted reproductive technologies (ART) conceived mouse models, and analyzed gene expression profiles in the testes of both ICSI and naturally conceived (NC) newborn F<sub>1</sub> mice using micro-array analysis. Among the differentially expressed genes, we focused on the expression of eight male reproduction-related genes. Quantitative real-time reverse transcription-polymerase chain reaction (qRT-PCR) was used to analyze the expression of these genes in the testes of both adult and old F<sub>1</sub> generation mice and adult F<sub>2</sub> generation mice. Our results showed that down-regulated and somatic cell-expressed genes in newborn mice retained their differential expression patterns in adult and old F<sub>1</sub> generation individuals, implying the persistence and fetal origin of the alteration in the expression of these genes. The intergenerational transmission of differential gene expression was observed, but most changes tended to be reduced in adult F<sub>2</sub> generations. Controlled ovarian hyperstimulation (COH) and in vitro fertilization (IVF) mice models were added to explore the precise factors contributing to the differences in ICSI offspring. The data demonstrated that superovulation, in vitro culture, and mechanical stimulation involved in ICSI had a cumulative effect on the differential expression of these male reproductive genes.

**Key words:** Intracytoplasmic sperm injection, Testis, Intergenerational transmission

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### 1 Introduction

Intracytoplasmic sperm injection (ICSI) is a procedure in which a single sperm is injected into an

oocyte for successful fertilization. This procedure is commonly used in assisted reproduction techniques (ART) to solve male infertility problems. The pregnancy rate following ICSI is associated mostly with semen quality and ICSI treatment-induced damage, which are also crucial factors affecting the health of offspring (Lu *et al.*, 2012). Besides ART-induced common birth defects (Davies *et al.*, 2012; Foix-L'Hélias *et al.*, 2012), it was reported that there was a higher risk of hypospadias and lower semen quality in ICSI offspring (Mau *et al.*, 2004; Mau Kai

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*et al.*, 2007). Epidemiological studies found parental subfertility probably leads to a high risk of decreased semen quality in male offspring (Ramlau-Hansen *et al.*, 2008). A father's hypospadias may not only increase the frequency of hypospadias in sons, but also decrease their semen quality. Moreover, most fathers and sons might have the same susceptible genes involved in reproductive dysfunction (Asklund *et al.*, 2007). However, a twin study indicated that genetic factors accounted for 20% of abnormal sperm density, and that environmental influence was the main factor disturbing male reproductive health (Storgaard *et al.*, 2006).

The Dutch famine near the end of World War II provided useful information to study the long-term effects of the early pregnancy environment on the development of offspring. The term 'catch-up growth' refers to the increasing body mass index found in adulthood in individuals with low birth weight. Low birth weight is also associated with many metabolic diseases in adulthood (Prader *et al.*, 1963). Poor maternal nutrition during gestation may restrict fetal growth and increase susceptibility to diseases, such as obesity, diabetes, and coronary heart disease (Roseboom *et al.*, 2006; van Abeelen *et al.*, 2012). Barker (1990) described the 'fetal origins of adult disease', and claimed that the pregnancy environment could influence fetal development. ICSI technology not only changes the intrauterine environment with gonadotropin stimulation before pregnancy, but also disturbs fertilization and the culture environment of embryos. In the entire ART process, the environment to which the embryos are exposed has a profound effect on gene expression and even on the development and subsequent health of the fetus (Rinaudo and Schultz, 2004; Lonergan *et al.*, 2006). Previous studies reported that alternations of gene expression in oocytes and embryos can be found in the postnatal brain (Wang *et al.*, 2011). Gonadotropin can regulate the expression of testicular RNA helicase, an essential post-transcriptional regulator of spermatogenesis (Tsai-Morris *et al.*, 2012). Oxidative stress may decrease semen quality and male reproductive ability (Fatemi *et al.*, 2012), and in vitro culture can increase the amount of free oxygen radicals. A latest study comparing in vitro fertilization (IVF) and ICSI mice showed that ICSI injection could increase apoptosis of spermatocytes in testes (Yu *et al.*, 2011).

In a previous study, we found no differences in semen quality or testes morphology between ICSI mice and naturally conceived (NC) mice (unpublished data). In this study, we firstly compared the gene expression profiles in the testes of ICSI-conceived newborn mice with those of NC mice to find male reproduction-related differentially expressed genes. Then, the persistence and intergenerational transmission of the differential gene expression were analyzed. Our studies provide a detailed analysis of the long-term effects of ICSI treatments on male offspring.

## 2 Materials and methods

### 2.1 ART models

All the protocols used in our investigation were approved by the Animal Care Ethics Committee of Zhejiang University. All C57BL/6J mice (6–8 weeks old) were randomly divided into four groups (controlled ovarian hyperstimulation (COH)/IVF/ICSI/NC groups) and raised in a standard environment (room temperature:  $(23\pm 1)$  °C; humidity:  $(55\pm 5)$ %) with a 12-h light-dark cycle.

#### 2.1.1 COH models

Female mice were injected with 7.5 IU pregnant mare serum gonadotrophin (PMSG) (GEN's, Hangzhou, China) and, 48 h later, with 7.5 IU human chorionic gonadotrophin (hCG) (GEN's, Hangzhou, China). After superovulation, the female mice were naturally mated with male mice. COH embryos at the two-cell stage were obtained from the pregnant mice at 1.5 d (the appearance of a vaginal plug was designated as 0.5 d) and transferred to the oviducts of pseudopregnant Institute of Cancer Research (ICR) mice. COH mice were born after about three weeks.

#### 2.1.2 IVF models

Female mice were injected with PMSG and, 48 h later, with 7.5 IU hCG. Metaphase II (MII) oocytes were obtained 14 h after the hCG injection. IVF-fertilized oocytes were obtained after 6 h of co-incubation of MII oocytes with sperm, and the fertilization procedure was performed in human tubal fluid (HTF) medium with 10% serum substitute supplement (SSS) (Irvine Scientific). IVF-fertilized

oocytes were cultured in 10% SSS G1 medium (Vitrolife). IVF embryos at the two-cell stage were transferred to the oviducts of pseudopregnant ICR mice, and IVF mice were born after about three weeks.

### 2.1.3 ICSI models

MII oocytes were obtained after the PMSG-hCG injection procedure. Sperm was injected into the oocytes by ICSI using an Olympus X71 inverted microscope with PIEZO (PrimeTech, Ibaraki, Japan) and micromanipulators (Narishige, Tokyo, Japan) (Wang *et al.*, 2011). The ICSI fertilization procedure was performed in warmed HEPES-buffered modified HTF (mHTF) medium (Irvine Scientific). ICSI-fertilized oocytes were cultured in 10% SSS G1 medium, and ICSI embryos at the two-cell stage were transferred to the oviducts of pseudopregnant ICR mice. ICSI mice were born after about three weeks.

Adult F<sub>1</sub> IVF and ICSI mice were hybridized with the mice in the same group or with the NC mice to obtain F<sub>2</sub> mice. Three types of IVF and ICSI F<sub>2</sub> mice were produced: from ICSI fathers and ICSI mothers (II), from ICSI fathers and NC mothers (IN), and from ICSI mothers and NC fathers (NI). The same terminology was applied to groups in the IVF F<sub>2</sub> generation.

Testes were obtained from newborns, 10-week-old and 1.5-year-old ART (F<sub>1</sub> and F<sub>2</sub>) male mice and NC male mice (F<sub>1</sub> and F<sub>2</sub>). All tissues were stored at -80 °C for RNA extraction. All experiments were repeated three times.

## 2.2 Microarray analysis

Total RNA from the testes was extracted with Trizol (Invitrogen). The gene expression profiles in the testes of ICSI newborn mice were analyzed and compared with those of NC mice, with three mice in each group (every mouse in each group had different parents). GeneChip hybridization for each sample was examined on Affymetrix 3' IVT Expression Arrays (Mouse Genome 430 2.0 Array). The technical procedures and quality controls were performed at the CapitalBio Corporation. Hybridization assay procedures were as described in the GeneChip Expression Analysis Technical Manual (<http://www.affymetrix.com>).

The data were analyzed using Significant Analysis of Microarray (SAM) software to identify the differentially expressed genes. Differentially ex-

pressed transcripts were defined by a fold-change (FC)  $\geq 2$  and a *q*-value  $< 5\%$ . The functional annotation of differentially expressed genes was analyzed using Molecule Annotation System Mas 3.0 (<http://bioinfo.capitalbio.com/mas3/>).

## 2.3 Quantitative real-time reverse transcription-polymerase chain reaction (qRT-PCR)

cDNA was synthesized from purified total RNA using an SYBR PrimeScript™ RT-PCR kit (TaKaRa). qRT-PCR was performed using an SYBR-Green I kit (TaKaRa) and an ABI 7900 thermocycler with five samples (every mouse in each group had different parents) from each group to confirm the differential expression of these genes. *Gapdh* served as an internal control for detecting the level of gene expression. The qRT-PCR primer sequences are shown in Table 1.

## 2.4 Statistical analysis

SPSS 16.0 (SPSS Inc., Chicago, IL, USA) was employed for statistical evaluation. qRT-PCR data were analyzed using the  $2^{-\Delta\Delta C_T}$  method ( $\Delta\Delta C_T = (C_{T, Target} - C_{T, Gapdh})_{\text{experimental group}} - (C_{T, Target} - C_{T, Gapdh})_{\text{control group}}$ ). Statistical analysis was performed using the independent-sample *t*-test for comparing two different groups. One-way ANOVA (Dunnet's test) was used to analyze the differences in gene expression between the NC group and the ICSI F<sub>2</sub> groups. Differences were considered to be statistically significant when  $P < 0.05$  (two-tailed).

## 3 Results

### 3.1 Differential gene expression in the testes of ICSI mice

The array analyses showed that there were 474 (150 up-regulated and 324 down-regulated) differentially expressed genes in ICSI newborn mice compared with NC mice (Fig. 1).

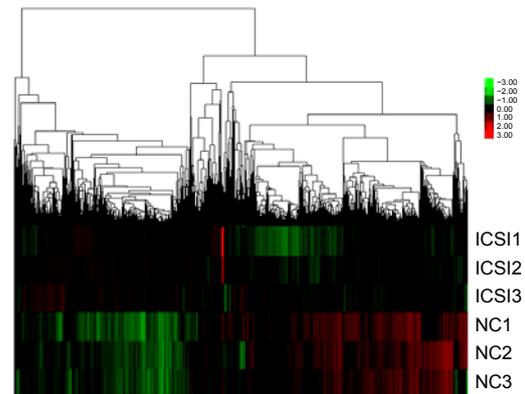
### 3.2 Gene ontology (GO) analysis of male reproductive function

To elucidate the effect of ICSI procedures on the male reproductive system, genes that were differentially expressed in ICSI newborns were classified by GO analysis. Among 152 GO terms for biological functions, six male reproductive function-related GO

terms were related to ICSI-induced gene expression differences (Table 2). These six GO terms included eight genes: five up-regulated genes (*Dmc1*, *Prok2*, *Rec8*, *Spo11*, and *Rhox5*) and three down-regulated genes (*Adcyap1r1*, *Amh*, and *Pdgfra*). Six genes (*Adcyap1r1*, *Dmc1*, *Prok2*, *Rec8*, *Spo11*, and *Rhox5*) are involved in spermatogenesis, male meiosis I, and sperm motility. Two genes (*Amh* and *Pdgfra*) are related to gonad development.

### 3.3 Validation of microarray data by qRT-PCR

We amplified the number of samples to validate the microarray results (Fig. 2). qRT-PCR was used to measure the gene expression in the testes of ICSI and NC newborn mice, and the results were consistent with those from microarray analysis. Thus, the results of qRT-PCR validated the reliability of the microarray analysis.



**Fig. 1 Hierarchical clustering analysis of differentially expressed genes in the testes of ICSI and NC mice**

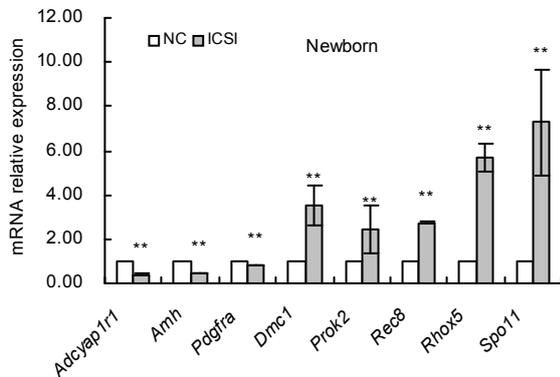
The expression intensities of each gene are represented as a red-green colour spectrum: green for down-regulated genes, red for up-regulated genes and black for genes without changes in expression. According to the analysis, there were 474 (150 up-regulated and 324 down-regulated) differentially expressed genes in the ICSI group

**Table 1 Primers designed for qRT-PCR**

GenBank accession	Gene	Sequence (5' to 3')	Amplicon size (bp)
NM_008084	<i>Gapdh</i>	5'-TGTGTCCGTCGTGGATCTGA-3' 5'-TTGCTGTTGAAGTCGCAGGAG-3'	150
NM_007407	<i>Adcyap1r1</i>	5'-TGGCTATTGCTATGCACTCTGA-3' 5'-GGAAGACTCATTTAGGCCCATCA-3'	104
NM_007445	<i>Amh</i>	5'-GGTAGGGGAGACTGGAGAA-3' 5'-CCAGAGTATAGCACTAACAGGGC-3'	145
NM_011202	<i>Pdgfra</i>	5'-ATGACATCGCGGAGATGGTTT-3' 5'-GGGTTACTCTTACTGGGCCTT-3'	113
NM_010059	<i>Dmc1</i>	5'-CCCTCTGTGTGACAGCTCAAC-3' 5'-GGTCAGCAATGTCCGAAG-3'	114
NM_015768	<i>Prok2</i>	5'-GCTTGCACAAGGACTCTCAG-3' 5'-CTTGGCCCATAGGTGTGCAG-3'	94
NM_020002	<i>Rec8</i>	5'-TATGTGCTGGTAAGAGTGCAAC-3' 5'-TGTCTTCCACAAGGTACTGGC-3'	133
NM_008818	<i>Rhox5</i>	5'-CATTTTGCAGCGCACTAATTCC-3' 5'-AGCCCTCCTGATCTTAAACCA-3'	106
NM_012046	<i>Spo11</i>	5'-CGTGGCCTCTAGTTCTGAGGT-3' 5'-GCTCGATCTGTTGTCTATTGTGA-3'	112

**Table 2 Significant GO terms of biological function on male reproductive health for differentially expressed genes in the ICSI group**

GO annotation	P-value	Protein	Gene symbol	Fold change
Spermatogenesis	$4.52 \times 10^{-16}$	ADCYAP1R1; DMC1; PROK2	<i>Adcyap1r1</i>	0.35
			<i>Dmc1</i>	2.67
			<i>Prok2</i>	2.52
Male meiosis I	$6.54 \times 10^{-12}$	DMC1; REC8; SPO11	<i>Rec8</i>	2.43
			<i>Spo11</i>	3.71
Spermatid development	$3.64 \times 10^{-11}$	DMC1; REC8; SPO11		
Sperm motility	$1.93 \times 10^{-4}$	RHOX5	<i>Rhox5</i>	5.31
Gonad development	$8.45 \times 10^{-4}$	AMH	<i>Amh</i>	0.19
Male genitalia development	$8.34 \times 10^{-3}$	PDGFRA	<i>Pdgfra</i>	0.47



**Fig. 2** qRT-PCR verification of microarray data  
Values are expressed as mean $\pm$ SD ( $n=5$ ). Significant differences are marked by asterisks: \*  $P<0.05$ , \*\*  $P<0.01$

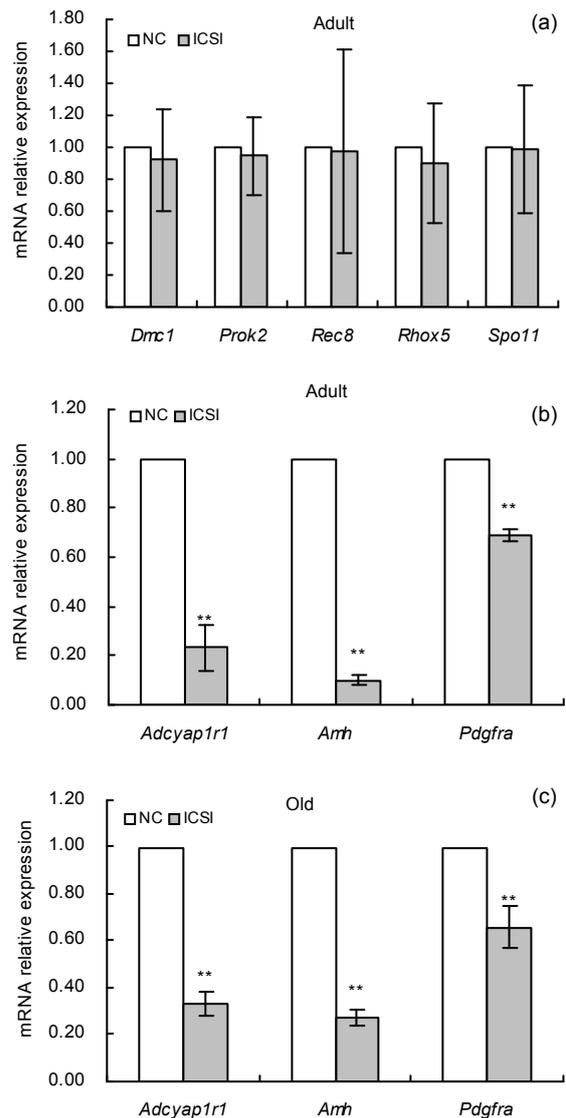
### 3.4 Detection of differentially expressed genes in the male reproductive systems of ART F<sub>1</sub> mice

Eight genes showing differential expression were detected in the adult F<sub>1</sub> generation. Five genes that were up-regulated in newborn ICSI mice displayed similar expression levels in ICSI and NC adult mice (Fig. 3a), while the expression levels of three genes down-regulated in newborn ICSI mice were still lower in adult ICSI mice than in adult NC mice (Fig. 3b). In adult mice, pairwise comparisons between NC and COH, COH and IVF, and IVF and ICSI groups were performed to investigate the crucial step that induced the changes in gene expression. *Adcyap1r1*, *Amh*, and *Pdgfra* were expressed at lower levels in the COH group than in the NC group (Fig. 4a). The expression of *Amh* was decreased in the IVF group compared with the COH group (Fig. 4b). The expression levels of *Adcyap1r1* and *Amh* in the ICSI group were lower than those in the IVF group (Fig. 4c). The differences in expression of the three genes among the four old F<sub>1</sub> generation groups were almost the same as those among the adult F<sub>1</sub> generation groups (Figs. 3c and 4d–4f). But *Adcyap1r1* showed no difference in expression between the NC and COH groups, and *Amh* showed no difference between the COH and IVF groups.

### 3.5 Detection of differentially expressed genes in the male reproductive systems of ART F<sub>2</sub> mice

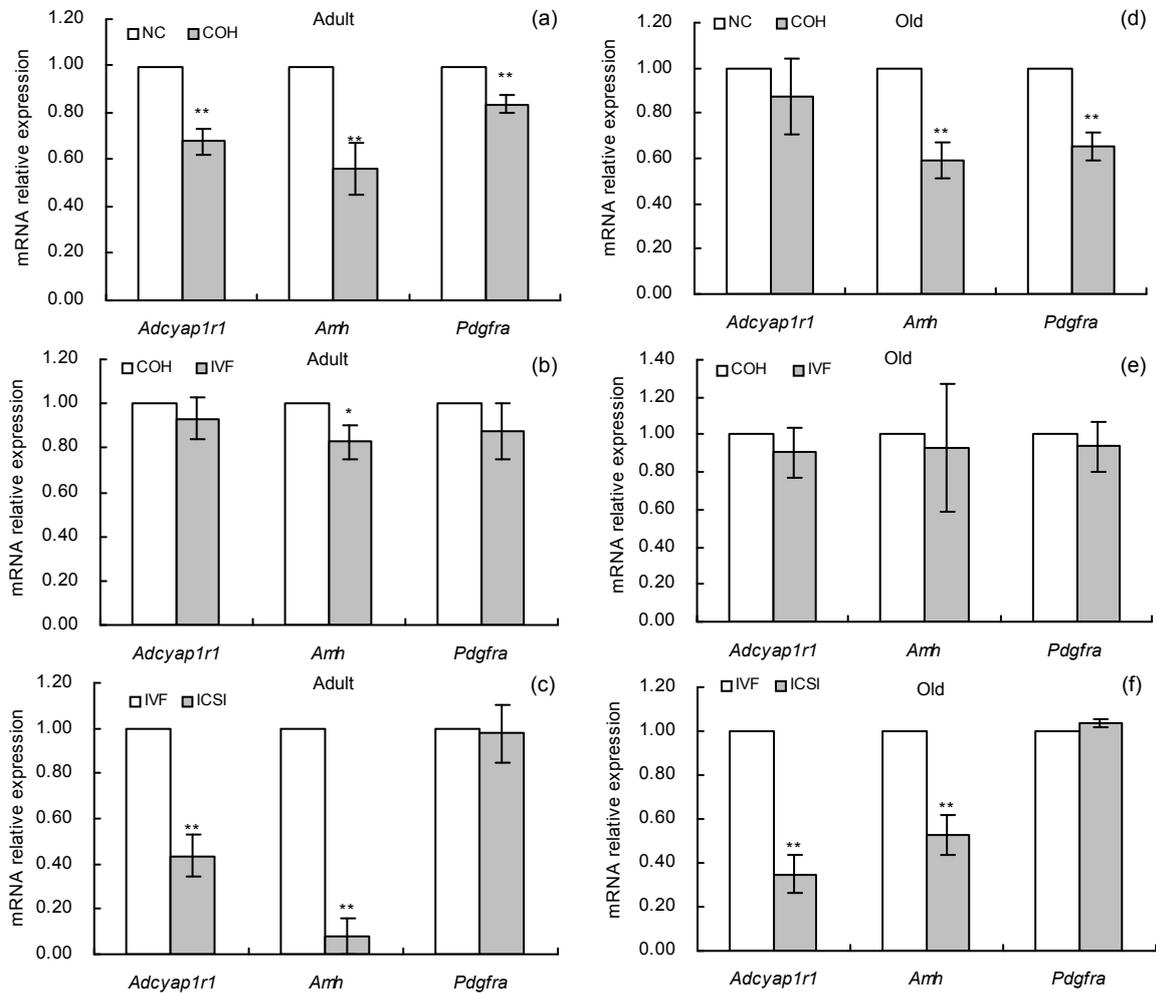
The expressions of the three down-regulated genes were also analyzed in the F<sub>2</sub> generations. Except for *Pdgfra*, the genes were expressed at lower

levels in the ICSI F<sub>2</sub> mice (Fig. 5a). Compared with the expression levels in ICSI F<sub>1</sub> mice, the expressions of *Adcyap1r1* and *Pdgfra* increased, while that of *Amh* decreased in the three types of ICSI F<sub>2</sub> mice (Fig. 5b). The differences in expression between each IVF F<sub>2</sub> generation group and its corresponding ICSI F<sub>2</sub> generation group were similar to those found in the F<sub>1</sub> generation (Fig. 6).

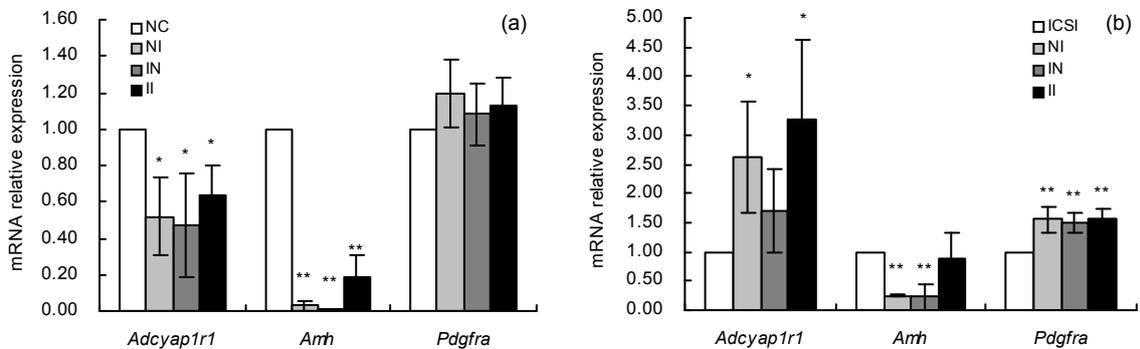


**Fig. 3** Expression of the male reproductive health-related genes in adult ICSI F<sub>1</sub> mice

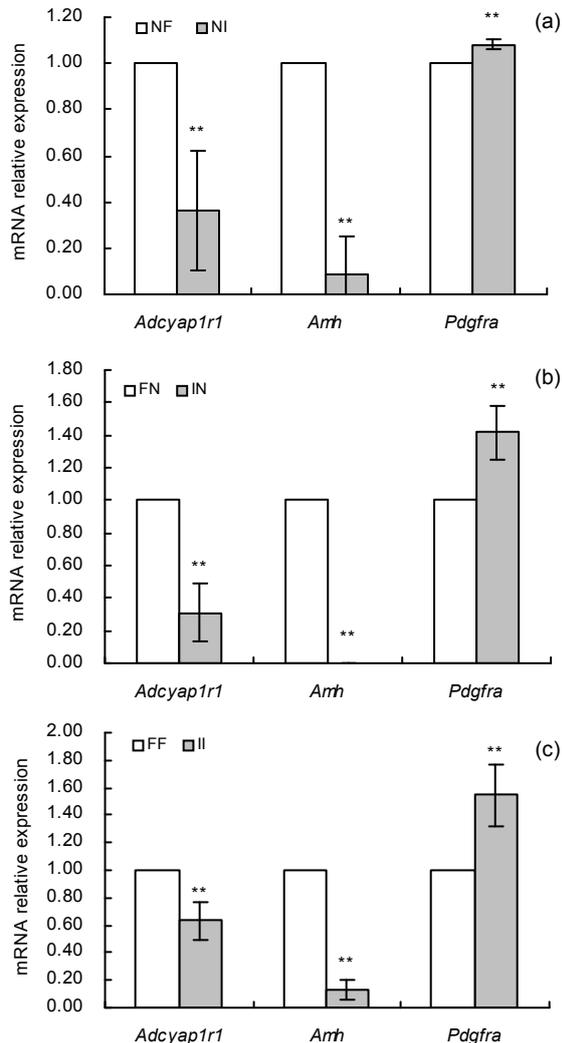
(a) Expressions of *Dmc1*, *Prok2*, *Rec8*, *Spo11*, and *Rhox5* in adult ICSI F<sub>1</sub> mice. (b, c) Expressions of *Adcyap1r1*, *Amh*, and *Pdgfra* in adult and old ICSI F<sub>1</sub> mice, respectively. Values are expressed as mean $\pm$ SD ( $n=5$ ). Significant differences are marked by asterisks: \*  $P<0.05$ , \*\*  $P<0.01$



**Fig. 4** Pairwise comparisons between NC and COH, COH and IVF, IVF and ICSI adult or old F<sub>1</sub> mice (a), (b), and (c) show the gene expression in adult mice; (d), (e), and (f) show the gene expression in old mice. The comparison between the NC and COH groups is presented in (a) and (d). The comparison between the COH and IVF groups is presented in (b) and (e). (c) and (f) show the comparison between the IVF and ICSI groups. Values are expressed as mean±SD (n=5). Significant differences are marked by asterisks: \*P<0.05, \*\*P<0.01



**Fig. 5** Expressions of *Adcyap1r1*, *Arh*, and *Pdgfra* in adults of F<sub>2</sub> generations The comparisons between NC mice and three types of ICSI F<sub>2</sub> mice are shown in (a), while the comparison between ICSI F<sub>1</sub> and F<sub>2</sub> generations are presented in (b). Values are expressed as mean±SD (n=5). Significant differences are marked by asterisks: \*P<0.05, \*\*P<0.01



**Fig. 6 Comparison of the expressions of *Adcyap1r1*, *Amh*, and *Pdgfra* between IVF and ICSI F<sub>2</sub> generations** IVF and ICSI F<sub>2</sub> mice: NF (NC father+IVF mother), NI (NC father+ICSI mother), FN (IVF father+NC mother), IN (ICSI father+NC mother), FF (IVF father+IVF mother), II (ICSI father+ICSI mother). (a) NF vs. NI; (b) FN vs. IN; (c) FF vs. II. Values are expressed as mean±SD ( $n=5$ ). Significant differences are marked by asterisks: \*  $P<0.05$ , \*\*  $P<0.01$

#### 4 Discussion

The use of mouse models successfully avoided the interference of individual differences in genetic and many environmental factors. The testis was used to study the effect of ART methods on the male reproductive system. Microarray analysis showed that there were a large number of genes that were differ-

entially expressed between the ICSI and NC mice. We analyzed differentially expressed genes related to male reproductive function using GO analysis. In total, eight differentially expressed genes were found in newborn mice of the ICSI group, among which *Amh* and *Rhox5* are expressed in Sertoli cells (Hu *et al.*, 2007; Goulis *et al.*, 2008), *Adcy1p1r1* and *Pdgfra* are expressed in Leydig cells (Koh and Won, 2006; Basciani *et al.*, 2010), while the other four genes are mainly expressed in spermatocytes (Lee *et al.*, 2002; Abreu *et al.*, 2010; Bellani *et al.*, 2010; Puverel *et al.*, 2011). There are two essential stages for testicle development: embryonic and pubertal age. Sex determination and phenotype development are completed in the embryonic phase, while spermatogenesis starts well before the pubertal phase, and male meiosis is initiated at pubertal stage. Therefore, we should also detect the expression level of these differently expressed genes in adult mice.

In adult males, the five up-regulated genes returned to normal levels, while the three down-regulated genes were expressed at lower levels. PDGFRA is essential for early embryonic development of Leydig cells (Basciani *et al.*, 2010). Testosterone is produced by the Leydig cells. PDGFRA deficiency can delay the production of testosterone (Schmahl *et al.*, 2008). The decrease in AMH and ADCYAP1R1 in newborn males reflects the maturation status of Sertoli cells (Rey *et al.*, 1993; Koh and Won, 2006; Boukari *et al.*, 2009). Another study reported that the loss of AMH was associated with non-obstructive azoospermia (Fenichel *et al.*, 1999). RHOX5 is an androgen-dependent protein, which regulates spermatogenesis (Domanskyi *et al.*, 2007; Hu *et al.*, 2007). Sertoli cells mediate spermatogenesis by nourishing the development of sperm cells, thus the expression levels of AMH, RHOX5, ADCYAP1R1, and PDGFRA reflect the functions of Sertoli cells (Fenichel *et al.*, 1999; Jamen *et al.*, 2000; Basciani *et al.*, 2002; Denolet *et al.*, 2006). However, if ICSI affects spermatogenesis, why was the down-regulation of *Pdgfra* followed by the increased expression of *Rhox5*? Luteinizing hormone (LH) in male rats may compensate for the dysfunction of Leydig cells as it activates cAMP for testosterone production (Koh and Won, 2006; Nurmio *et al.*, 2008). Therefore, we re-analyzed the results from GeneChip, and found that expression of the LH receptor

(LHCGR) in ICSI mice was 1.61-fold higher than that in NC mice. The increased expression of *Lhcgr* induced by ART might make up for its effect on Leydig cells, and accelerate spermatogenesis in early infancy leading to the observed up-regulation of *Prok2*, *Dmc1*, *Rec8*, and *Spor11*.

In adult mice, the continuing down-regulation of *Amh* and *Adcyap1r1* indicated that their differential expression in newborn mice may not be associated with testosterone secretion, but with the decreased function of Sertoli cells. Moreover, we detected these three down-regulated genes in old mice, and again found decreased expression in the ICSI group. These results suggest that ICSI treatments had a persistent effect on the three genes and that the changes were of fetal origin. To find the precise factors that induced the differences in ICSI mice, we included data from COH and IVF models of adult and old mice. Comparisons between the NC and COH, COH and IVF, and IVF and ICSI groups were made to analyze the effects of superovulation, in vitro culture and ICSI mechanical stimulation. Our results showed that superovulation was the only factor that induced the down-regulation of *Pdgfra*, while the decreases in *Adcyap1r1* and *Amh* resulted mainly from both hormonal and ICSI mechanical stimulation. These three factors had a cumulative effect on the changes in *Amh*.

Intergenerational transmission of differential gene expression has been demonstrated in many studies (Jimenez-Chillaron *et al.*, 2009; Hoile *et al.*, 2011). We built three types of ICSI F<sub>2</sub> models by hybridizing ICSI and NC F<sub>1</sub> mice to simulate the phenomenon in human beings and observed the effects of the parents. *Amh* and *Adcyap1r1* were still down-regulated in ICSI F<sub>2</sub> mice compared with the control NC group, but *Pdgfra* showed no difference. Compared with ICSI F<sub>1</sub> mice, *Adcyap1r1* and *Pdgfra* showed higher expression, while *Amh* showed lower expression in ICSI F<sub>2</sub> mice, which implies that most of the differences induced by ART treatments tended to be reduced during intergenerational transmission. In F<sub>2</sub> offspring, we also compared the expression of *Amh*, *Adcyap1r1*, and *Pdgfra* between each pair of groups of IVF and ICSI F<sub>2</sub> mice. The results were similar to those of F<sub>1</sub> offspring, except that significant differences in the expression of *Pdgfra* were found in F<sub>2</sub> mice, indicating that ICSI mechanical stimulation can also induce intergenerational transmission of differential gene expression.

## 5 Conclusions

In summary, we found that the differential expression of genes in ICSI adult mice might originate from the newborn period or even earlier. Superovulation, in vitro culture and mechanical stimulation had a cumulative effect on the differential expression of male reproductive genes in the ICSI mice. ICSI treatments, or the mechanical stimulation involved in ICSI, can induce the intergenerational transmission of differential gene expression in the F<sub>1</sub> generation. The effect of the F<sub>1</sub> generation groups that induced the differential gene expression tended to be reduced during intergenerational transmission. However, differences in *Amh* expression, which were maintained from ICSI newborn to old age, showed a more significant difference in F<sub>2</sub> than in F<sub>1</sub> mice. The potential effect of its decreased expression in ICSI testes on male reproductive health needs further investigation. Our studies provide a detailed analysis of the effect of ICSI procedures on the expression of male reproductive genes, which will be a useful reference for future studies on ART methods.

## Compliance with ethics guidelines

Li-ya WANG, Ning WANG, Fang LE, Lei LI, Le-jun LI, Xiao-zhen LIU, Ying-ming ZHENG, Hang-ying LOU, Xiang-rong XU, Xiao-ming ZHU, Yi-min ZHU, He-feng HUANG, and Fan JIN declare that they have no conflict of interest.

All institutional and national guidelines for the care and use of laboratory animals were followed.

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### Recommended paper related to this topic

#### **Different sperm sources and parameters can influence intracytoplasmic sperm injection outcomes before embryo implantation**

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**Abstract:** To evaluate the effects of sperm with different parameters and sources on the outcomes of intracytoplasmic sperm injection (ICSI), 1972 ICSI cycles were analyzed retrospectively. Groups 1 to 5 were composed of cycles using ejaculated sperm and were grouped according to sperm quantity, quality, and morphology into normal (288 cycles), or mild (329 cycles), moderate (522 cycles), severe (332 cycles), and extremely severe (171 cycles) oligozoospermia and/or asthenozoospermia and/or teratozoospermia (OAT) groups. Group 6 was composed of 250 cycles using testicular or epididymal sperm, and Group 7 consisted of 80 cycles using frozen-thawed sperm. We found that fertilization rates were gradually reduced from Groups 1 to 6, and reached statistical difference in Groups 5 and 6 ( $P < 0.05$ ). The high-quality embryo rate was higher in Group 1 than in Groups 2, 3, 5, 6, and 7 ( $P < 0.05$ ). No statistical differences were observed in the rates of embryo cleavage, clinical pregnancy, miscarriage, live-birth, premature birth, low birth weight, weeks of premature birth, average birth weight, or sex ratio for all seven groups ( $P > 0.05$ ). A total of nine cases of malformation were observed, with a malformation rate of 1.25% (9/719). In conclusion, different sperm sources and parameters can affect ICSI outcomes before embryo implantation. A full assessment of offspring malformation will require further study using a larger sample size.