

Original Article

Analysis of semen parameters and sperm numerical chromosome abnormalities in normoteratozoospermic and oligoasthenoteratozoospermic men from Thailand

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Abstract

Sperm from infertile males who desire children is frequently used for intracytoplasmic sperm injection (ICSI). Concerns about the chromosome quality of these donated sperm and the risk for the transmission of genetic defects are under-recognized. We conducted a chromosome study using sperm from 15 Thai men (26-40 years of age; mean, 32 years of age) who were classified as normoteratozoospermia (NT; 7 cases) and oligoasthenoteratozoospermia (OAT; 8 cases). The multi-color FISH (Fluorescence *in situ* hybridization) assay for the analysis of chromosomes 18, X, and Y was used on 13,428 sperm from these donors, and we observed statistically significant differences in numerical chromosome abnormalities between these two groups ($p = 0.011$). The median (range) for numerical chromosome abnormalities were 1.07% (0.18-2.35%) and 9.21% (0.48-29.84%) for sperm from the NT and OAT donors respectively. XY disomy was the most frequent abnormality observed. Correlation with semen parameters indicated that there were significant inverse correlations between sperm chromosomal abnormalities and both normal motile sperm ($r = -0.554$; $p = 0.032$), and normal head sperm ($r = -0.686$; $p = 0.005$). From our data, statistical analyses indicated that semen samples with normal motility of $\leq 60\%$ or normal head morphology of $\leq 85\%$ had an increased risk of sperm chromosomal abnormalities. The results of this study indicated that OAT men were at increased risk for paternal transmission of genetic defects to their offspring. Therefore, sperm chromosome analyses and semen analyses are needed to be carefully evaluated on OAT men before performing the ICSI procedure.

Key words: Multi-color-fluorescence *in situ* hybridization (FISH) assay; Sperm aneuploidy, Semen parameters, Infertility, Chromosome abnormality

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Introduction

The intracytoplasmic sperm injection (ICSI) procedure developed by Palermo et al. (1992) has become a practical way to help infertile couples around the world to have children, especially for males with oligospermia or azoospermia.^{1, 2} However, there are concerns that children born as a result of the procedure may be at increased risk for congenital malformation and genomic imprinting diseases.³⁻⁵ A recent review⁶ indicates a significant increase in urogenital malformations, especially hypospadias, among these children. In addition, abnormalities in pregnancy from the procedure may be associated with the existence of aneuploid sperm.⁷ In some cases, epididymal and testicular spermatozoa may be used but these have aneuploidy frequencies that are significantly higher than those found in ejaculated spermatozoa.⁸ Even with these reports, there is an under-appreciation of the possibility of having abnormal chromosomes in donated sperm and the risk for the transmission of genetic defects.⁹

Thailand has an increasing number of ICSI centers for infertile couples. From our review of the literature, there is only one report of increased aneuploidy in sperm collected by mini-Percoll gradient centrifugation from infertile Thai patients.¹⁰ Among many contributing factors, environmental pollutants have been a major concern for causing chromosome abnormalities in sperm. For instance, studies in Mexico and China found that organophosphorus pesticide and synthetic pyrethroid insecticide exposure increased the frequency of sperm aneuploidy,¹¹⁻¹³ while no such effect was detected in Finland or Canada.^{14, 15} Also, alcohol intake, smoking, and chemotherapy can increase the risk for sperm aneuploidy.^{14, 16-18} The Thai population is exposed to a number of these environmental risk factors that may contribute to infertility and thus the genetic risk to offspring of infertile couples.

To evaluate the potential for genetic risk among ICSI patients in Thailand, we have measured numerical chromosome abnormalities in sperm as detected by the multi-color fluorescence *in situ* hybridization (FISH) assay. Sperm samples were collected from normoteratozoosper-

mic (NT) and oligoasthenoteratozoospermic (OAT) Thai men. In addition, we determined associations between semen parameters and sperm chromosomal abnormalities among these donors in order to identify preliminary prognostic markers for screening genetic risk to the offspring of ICSI patients.

Materials and Methods

Semen samples

All volunteers were recruited at the infertility clinic, Thammasat-Chalermprakit Hospital, Pathumthani, Thailand. The protocol was approved by The research methodology and ethical review committees for research in human subjects, Faculty of Medicine, Thammasat University, Thailand. All participants gave written consent before enrollment. Fresh semen samples were collected by masturbation after 3-5 days of abstinence. After liquefaction at room temperature for 20-30 min, semen samples were analyzed for semen parameters and sperm chromosomal abnormalities.

Determination of semen parameters

Semen parameters such as pH, sperm concentration, and sperm motility were analyzed using Computer Aided Sperm Analysis (CASA, Model IVOS; Hamilton Thorn, Beverly, MA). Sperm concentration and sperm motility were evaluated according to the WHO guidelines (WHO 1999). Sperm motility was graded as rapid, medium, slow, or static (no motility). Progressive motility count (PMC: sperm with straight forward and rapid movement) and normal motility (rapid plus medium motilities) were also determined. Sperm morphology was evaluated according to Kruger's strict criteria.¹⁹ Sperm was analyzed for normal head, neck, and tail morphology, including the presence of cytoplasmic droplets (as an indication of sperm immaturity). The criteria for having normal semen were ≥ 20 million sperm/ml, $\geq 50\%$ sperm with normal motility, and $> 14\%$ sperm with normal morphology.

Normoteratozoospermic (NT) men had ≥ 20 million sperm/ml per individual, $\geq 50\%$ sperm with normal motility and $\leq 14\%$ sperm with normal morphology whereas oligoasthenoteratozoospermic (OAT) men had < 20 million

sperm/ml, <50% sperm with normal motility and $\leq 14\%$ sperm with normal morphology.

Fluorescence *in situ* hybridization (FISH) assay

The FISH assay was performed as described previously,²⁰ with slight modification. Briefly, fresh semen samples were washed twice with phosphate buffer saline (pH 7.4), centrifuged at 1,500 g for 10 min, and the volumes were adjusted. Each suspension was spread on a cleaned slide and air dried. The slides were then coded, fixed with methanol-acetic acid (3:1 v/v) for 10 min, washed 3 times with 0.2X SSC (pH 7.5) at 37°C, and allowed to dry in air or using a slide warmer at 40°C for not more than 2 min. Subsequently, the slides were incubated with 50 mM dithiotreitol in 0.1 M Tris-HCl (pH 8.0) for 10 min. The smears were visualized intermittently with a phase-contrast microscope to evaluate the degree of decondensation of the sperm. At optimal decondensation, the slides were washed 3 times with 0.2X SSC (pH 7.5) at 37°C and allowed to air dry. A mixture of centromere-specific DNA probes for chromosomes 18, X, and Y (Vysis, Downer Groves, IL) was prepared according to the company's protocol and applied to the prepared slides in the dark. The slides then were transferred to a Hybrite apparatus, set for denaturation at 75°C for 5 min and hybridization at 42°C for 1 hr. Next, the slides were washed in 0.4X SSC at 72°C for 2 min, followed by a quick wash in 0.2X SSC at 37°C and air-drying in the dark. Finally, slides containing sperm DNA were counterstained with DAPI II (Vysis), covered with coverslips and scored using a fluorescence microscope or otherwise kept in the dark below 0°C until used.

Scoring criteria

Scoring was performed blinded using a fluorescent microscope (Olympus BX50F, Tokyo, Japan) that was equipped with three single band-pass filter sets for fluorescein, rhodamine and aqua and a triple band-pass set for fluorescein/rhodamine/DAPI (Vysis). Chromosome abnormalities were recorded as nullisomy for a specific chromosome e.g. 18-null (without chromosome 18) or sex-null (without chromosome X or Y). Disomy e.g. XX

disomy, XY disomy was defined as two signals for the same chromosome with similar intensity, size, shape, and the distance between the two signals of the same color should be wider than the diameter of the signal. Polyploidy, commonly observed as diploidy, was defined as the occurrence of additional chromosome sets in the cells, e.g. X-X-18-18, Y-Y-18-18. Other types of aneuploidy were classified as miscellaneous (misc), e.g., X-Y-Y-18, X-X-Y-18. Therefore, with our scoring criteria, total aneuploidy was the sum of total nullisomy, total disomy and total miscellaneous, while total polyploidy was the sum of all diploidy. Total numerical chromosome abnormalities were the sum of total aneuploidy and total polyploidy.

Statistical Analysis

All statistical analyses were performed using SPSS 11.0 for windows, module base. The Mann-Whitney test, a nonparametric test for two independent samples, was used for comparisons between groups and to test for significance. Spearman's rho correlation coefficient, a bivariate nonparametric correlation, was also determined for different pairs of parameters.

Results

A summary of the semen parameters from all fifteen semen samples (7 NT and 8 OAT) was presented in Table 1. The median (range) age for the two groups was 28 (26-36) and 32 (27-40) years, respectively. There was no significant difference in age among these groups ($p=0.414$). There also were no significant differences between these groups for semen volume or pH ($p=0.082$ and $p=0.221$), respectively. Both semen samples had <14% sperm with normal morphology, so all of them were classified as teratozoospermia. No significant difference in the frequency of sperm with normal morphology was observed between these groups, with the median (range) measured at 6% (0-8%) and 0% (0-7%) ($p=0.063$). Nevertheless, significant difference in the frequency of sperm with normal motility between the two groups was observed with the median (range) measured at 75% (52-86%) and 6% (0-33%) ($p = 0.001$).

Table 1 Analysis of semen parameters from 15 Thai volunteer

Donor no.	Age (yr)	Conc. (x10 ⁶ /ml)	Vol. (ml)	pH	%Normal morphology				% Normal motility						
					Overall	Head	Neck	Tail	Cytoplasmic droplet	Overall	Rapid	Medium	Slow	Static	PMC*
Normoterozoospermia (NT)															
1	33	200.9	1.9	8.5	7	85	3	10	1	52	46	6	19	29	29
2	28	171.2	3.3	8.0	6	85	21	6	0	83	78	5	13	3	53
3	27	295.6	1.3	8.5	0	86	17	0	1	68	59	9	24	8	30
4	27	204.7	2.9	8.0	2	93	8	4	0	86	82	4	11	3	58
5	33	85.3	2.9	8.0	5	93	7	1	1	75	70	5	12	13	33
6	26	45.6	3.3	8.5	6	91	14	0	0	76	71	5	9	15	38
7	36	46.1	2.4	8.0	8	90	0	2	0	58	53	5	8	34	28
Median	28	171.2	2.9	8.0	6	90	8	2	0	75	70	5	12	13	33
Oligoasthenoteratozoospermia (OAT)															
8	33	5.6	3.6	8.5	0	85	8	12	0	6	5	1	1	93	2
9	30	6.4	2.3	8.0	5	95	12	0	6	16	16	0	1	83	4
10	34	9.4	3.7	8.0	0	87	6	3	11	33	28	4	5	6.3	17
11	31	13.2	1.6	8.5	7	68	20	9	6	5	3	2	5	85	2
12	32	4.8	4.8	8.0	0	0	86	16	7	5	4	1	2	92	2
13	32	2.2	3.4	8.0	0	91	1	8	3	0	0	0	0	100	0
14	27	4.7	3.2	8.0	3	64	6	23	4	13	12	1	2	84	10
15	40	2.6	5.0	8.0	0	20	0	0	0	6	5	1	1	93	2
Median	32	5.2	3.5	8.0	0	76.5	7	8.5	5	6	5	1	1.5	88.5	2

*PMC: progressive motility count

Table 2 showed a summary of the frequencies of numerical chromosome abnormalities observed for each semen sample in terms of aneuploidy (combination of disomy, nullisomy, and miscellaneous forms of aneuploidy) and polyploidy. The sum of aneuploidy and polyploidy made up the total numerical chromosome abnormality category. There was a significant difference in the total (numerical chromosome) abnormality frequency between NT and OAT groups (median (range) of 1.07% (0.18-2.35%) and 9.21% (0.48-29.84%) ($p=0.011$). The frequency of numerical chromosomal abnormalities from the OAT sperm samples was 6-8 times higher than that from the NT sperm samples.

Among the aneuploid abnormalities, XY disomy had the greatest difference among the three groups ($p=0.011$). No significant differences were observed for 18-18 disomy, XX disomy, YY disomy, total nullisomy or total polyploidy ($p>0.05$). There was, however, a significant inverse correlation between the frequency of sperm chromosomal abnormalities (Table 2) and the frequency of sperm with normal head morphology ($r=-0.686$; $p=0.005$) (Table 1). There was no correlation between the frequency of numerical chromosomal abnormalities and sperm with normal neck morphology ($r=-0.002$; $p=0.995$) or with normal tail morphology ($r=-0.376$; $p=0.166$). Among the sperm motility parameters, there was a significant inverse correlation between sperm chromosomal abnormalities and the frequency of sperm with normal motility ($r=-0.554$; $p=0.032$), specifically sperm with rapid motility ($r=-0.564$;

$p=0.028$) and progressive motility ($r=-0.552$; $p=0.033$). There were no significant correlations with other types of motility ($p>0.05$).

A summary of the statistical analysis for evaluating the cutoff values of the semen parameters relative to estimating the risk of sperm chromosomal abnormalities ($>1.07\%$) was shown in Table 3. This analysis indicated that semen samples were significantly associated with increased frequency of chromosomally abnormal sperm if they possessed at least one of the following parameters: sperm concentration ≤ 20 million cells/ml, sperm with normal motility of $\leq 60\%$ (rapid motility of $\leq 50\%$ or $\leq 25\%$ progressive motility), or normal head morphology $\leq 85\%$. However, if a higher number of sperm would have been analyzed, the results may be somewhat different.

A comparison of the sex (X/Y) ratios among the NT and OAT groups was given in Table 4. The X/Y ratio was defined as the ratio between the total number of sperm containing chromosomes X and 18 and the total number of sperm containing chromosomes Y and 18. No significant differences were observed among the sex ratios of the two groups (median (range) of 1.3 (1.0-1.7), and 1.75 (1.0-15.8), respectively; $p=0.16$). Nevertheless, the sex ratio was significantly correlated with the frequency of total chromosomally abnormal sperm ($r=0.55$; $p=0.034$). The sex ratio was specifically correlated with % polyploidy ($r=0.725$; $p=0.002$) and % XY disomy ($r=0.62$; $p=0.013$).

Table 2 Analysis of numerical chromosomal abnormalities in sperm from 15 Thai men

Donor No.	Aneuploidy										Total aneu ploidy	Polyploidy				Total polyploidy	Chromosomal abnormality
	Disomy		Sex disomy		Total disomy	Nullisomy				Misc*							
						X or Y	18	Total									
	X-X	Y-Y	X-Y	Total													
18-18																	
Normoteratozoospermia (NT)																	
1	0.19	0.19	0.09	0.09	0.38	0.57	0.19	0.09	0.28	0.09	0.95	0.09	0.09	0.19	0.40	1.35	
2	0.06	0.12	0.12	0.78	1.02	1.08	0.36	0.48	0.84	0.06	1.98	0.00	0.00	0.00	0.00	1.98	
3	0.00	0.09	0.00	0.53	0.62	0.62	0.00	0.00	0.00	0.09	0.71	0.27	0.09	0.00	0.39	1.10	
4	0.00	0.00	0.20	0.20	0.40	0.40	0.10	0.50	0.61	0.05	1.06	0.00	0.00	0.00	0.00	1.06	
5	0.00	0.00	0.34	0.11	0.45	0.45	0.56	0.00	0.56	0.00	1.01	0.00	0.00	0.00	0.00	1.01	
6	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.18	0.18	0.00	0.00	0.00	0.00	0.18	
7	0.00	0.08	0.00	0.00	0.08	0.08	2.10	0.17	2.27	0.00	2.35	0.00	0.00	0.00	0.00	2.35	
median	0.00	0.08	0.09	0.11	0.4	0.45	0.19	0.09	0.56	0.06	1.01	0.00	0.00	0.00	0.00	1.07	
Oligoasthenoteratozoospermia (OAT)																	
8	0.35	1.92	0.17	18.67	20.77	28.10	0.87	1.05	1.92	5.41	28.10	0.52	0.17	0.7	1.75	29.84	
9	0.00	0.00	0.00	2.81	2.81	3.51	0.00	0.70	0.70	0.00	3.51	0.00	0.00	0.00	0.00	3.51	
10	0.08	0.00	0.00	1.83	1.83	3.67	1.12	0.56	1.67	0.16	3.67	0.00	0.00	0.00	0.08	3.75	
11	0.00	0.00	0.11	8.89	9.01	9.92	0.23	0.00	0.23	0.68	9.92	0.00	0.00	0.00	0.00	9.92	
12	0.00	0.00	0.00	4.03	4.03	4.03	0.36	4.51	4.86	0.00	8.90	0.00	0.00	0.00	0.00	8.90	
13	0.00	0.00	0.00	0.00	0.00	0.00	0.24	0.24	0.48	0.00	0.48	0.00	0.00	0.00	0.00	0.48	
14	0.00	0.00	0.00	5.71	5.71	5.71	0.00	0.00	0.00	0.95	6.67	2.86	0.00	0.00	2.86	9.52	
15	0.00	0.00	0.00	10.29	10.29	10.29	0.64	0.64	1.29	1.29	12.86	0.00	0.00	0.64	0.64	13.50	
median	0.00	0.00	0.00	4.87	4.87	4.87	0.30	0.44	0.88	0.42	7.78	0.00	0.00	0.00	0.32	9.21	

*Misc. = other types of aneuploidy, e.g., X-X-Y-18, X-X/18-null

Table 3 Statistical analysis of the cutoff values for each specific semen parameter in response to estimating sperm chromosomal abnormalities at the frequency of > 1.07%

Parameters	Value	% Sensitivity	% Specificity	% PPV	% NPV	% Efficiency
Concentration ($\times 10^6$ cells/ml)	≤ 10	60	80	85	50	66.7
	≤ 20	70	80	87.5	57.1	73.3
	≤ 30	70	80	87.5	57.1	73.3
	≤ 50	80	60	80	60	73.3
	≤ 80	70	60	77.8	50	66.7
	≤ 100	80	40	72.7	50	66.7
% Normal motility	≤ 20	60	80	85.7	50	66.7
	≤ 30	60	80	85.7	50	66.7
	≤ 40	70	80	87.5	59.1	73.3
	≤ 50	70	80	87.5	59.1	73.3
	≤ 60	90	80	90	80	86.7
	≤ 70	90	60	81.8	75	80
% Normal rapid motility	≤ 15	46.2	50	65.7	12.5	46.7
	≤ 20	46.2	50	65.7	12.5	46.7
	≤ 30	70	80	87.5	57.1	73.3
	≤ 40	70	80	87.5	57.1	73.3
	≤ 50	80	80	88.9	66.7	80
	≤ 60	90	60	81.8	75	80
	≤ 70	57.1	0	66.7	60	26.7
% Progressive motility	≤ 10	40	80	85.7	50	66.7
	≤ 20	70	57.1	87.5	57.1	73.3
	≤ 25	70	80	87.5	57.1	73.3
	≤ 30	90	60	81.8	75	80
	≤ 40	90	20	69.2	50	66.7
% Normal head morphology	≤ 60	20	100	100	38.5	46.7
	≤ 65	20	100	100	38.5	45.7
	≤ 70	40	100	100	45.4	60
	≤ 80	40	100	100	45.4	60
	≤ 85	70	100	100	62.5	80
	≤ 90	90	80	50.2	80	86.7

% PPV : % positive predictive value; % NPV : % negative predictive value

Table 4 The sex (X/Y) ratio of Thai semen samples in comparison with their sperm chromosomal abnormalities

Donor no.	number of chromosome X	number of chromosome Y	Total number of chromosomes X and Y	The sex (X/Y) ratio	Total number of chromosome analyzed	% Total chromosomal abnormalities
Normoteratozoospermia (NT)						
1	657	382	1039	1.7	1053	1.35
2	936	698	1634	1.3	1667	1.98
3	652	461	1113	1.4	1125	1.10
4	1065	897	1962	1.2	1983	1.06
5	470	409	879	1.2	888	1.01
6	341	227	568	1.5	569	0.18
7	590	572	1162	1.0	1190	2.35
			median	1.3	1125	1.07
Oligoasthenoteratozoospermia (OAT)						
8	303	99	402	3.1	573	29.84
9	339	210	549	1.6	569	3.51
10	696	512	1208	1.4	1255	3.75
11	520	271	791	1.9	877	9.92
12	392	376	768	1.0	843	8.90
13	218	200	418	1.1	420	0.48
14	80	15	95	15.8	105	9.52
15	185	84	269	2.2	311	13.50
			median	1.75	571	9.21

Discussion

Our chromosome analyses of sperm from NT and OAT groups demonstrated that they had significant differences in the frequency of numerical chromosome abnormalities. Our data were consistent with previous reports indicating that chromosome aneuploidy levels were significantly greater in OAT patients than in controls.²¹⁻²⁴ The previous studies showed that OAT patients had higher incidences of sperm chromosomal abnormalities than men with normal semen parameters. The mean frequency of abnormalities observed in men with severe oligozoospermia was 3-4 times the mean frequency of abnormalities in normal men,²⁵ while the mean frequencies of abnormalities observed in normoasthenoteratozoospermic men were only

double that seen in controls.^{26, 27} The differences in the frequency of abnormalities among the groups in our study were more dramatic, with OAT men having 6-8 times the frequency of abnormalities observed in NT subjects.

The most frequently observed abnormality was sex chromosome aneuploidy, especially XY disomy. These data are consistent with a previous report.²⁸ The current hypothesis is that the abnormality is derived from meiotic errors during spermatogenesis, especially from a decrease in XY recombination at the pseudoautosomal regions.²⁹⁻³² Follow-up studies showed that there was a slight but significant increase in *de-novo* sex chromosomal aneuploidy in children born after ICSI.^{33, 34} Additionally, transmission of XY sperm aneuploidy from a father to his child was

observed in a boy with Klinefelter syndrome.³⁵ Therefore, the chromosome abnormality in sperm observed in this study may have genetic consequences.

Comparing the degree of sperm numerical chromosome abnormalities from Thai OAT and NT men with those from other countries indicates that the frequencies are comparable. In our study, the frequencies of disomy sperm in Thai OAT and NT men were 0.5-28% and 0-1.08%, respectively. In the U.S., the frequency was 0.4-18.6% for OAT patients while it was 0.05-0.2% for proven fertile controls.²² In another study, the frequencies of XX disomy sperm from an infertile man with an abortus from ICSI was 18.6%.⁷ Moreover, aneuploidy, especially XY disomy, was significantly higher than other types of aneuploidy.³⁶ All these observations are consistent with our results.

In addition, our data demonstrated that sperm from Thai men with abnormal semen parameters preferentially had X-bearing sperm and that the sex (X/Y) ratio was correlated with the frequency of chromosomally abnormal sperm, especially with the frequency of total polyploidy and XY disomy. The data were consistent with a previous report showing that the sex ratio was different from the expected value in some special cases. In cases of paternal age or of oligospermia that were correlated with the frequency of chromosomally abnormal sperm, the sex ratio was different from the expected value.^{31, 37, 38} Therefore, it is likely that chromosomally abnormal sperm have sex-specific chromosome alterations leading to possible changes in the sex ratio of the offspring.

Previous reports indicated that the frequency of sex chromosome aneuploidy in spermatozoa from healthy men was around 0.2% while that from OAT men was significantly higher. Therefore, studying 500-1,000 spermatozoa per male was considered sufficient to evaluate the overall frequency of chromosomally abnormal sperm in men with abnormal semen parameters as in our study. Giorlandino et al. (1998) studied 600 spermatozoa per male and reported that there were significant differences in autosomal and sex chromosome disomy and nullisomy among couples with recurrent abortion³⁹. Rubio

et al. (1999) studied 1,500 spermatozoa per male and reported that sperm aneuploidy was significantly higher in oligoasthenozoospermia.⁴⁰ In the case of severe oligoasthenoteratozoospermic men we had included data with relatively few analyzed sperm (<500 spermatozoa/male). Although these donors had few sperm, the frequencies of chromosomally abnormal sperm were quite high.

Our study demonstrated specific associations between the frequency of sperm chromosomal abnormalities and semen parameters, especially sperm motility and head morphology. The observations indicated that men were at increased risk of carrying sperm with abnormal chromosomes (>1.07%) when they had sperm concentrations ≤ 20 million cells/ml together with at least one of the following: $\leq 60\%$ sperm with normal motility ($\leq 50\%$ sperm with rapid motility, $\leq 25\%$ sperm with progressive motility), and $\leq 85\%$ sperm with normal head morphology. However, these cutoff values of the semen parameters might be somewhat different if a higher number of sperm and semen samples would be performed. Nevertheless, the results were consistent with previous reports of specific associations between chromosomally abnormal sperm and semen parameters.⁴¹⁻⁴³ In these previous studies, the frequency of total sperm chromosome abnormalities was inversely correlated with total progressive motility⁴¹ and sperm concentration.²⁸ Also, sperm with abnormal head morphology was associated with the incidence of chromosomally abnormal sperm.^{37, 42-44} On the contrary, no correlation has been observed between the frequency of chromosomally abnormal sperm and the overall frequency of morphologically normal sperm.^{45, 46} These data could be indicated that the tail or neck or cytoplasmic morphological abnormalities were not strongly associated to sperm aneuploidy as the head abnormalities was.

In conclusion, OAT men had significantly abnormal semen parameters, especially sperm motility and sperm head morphology, as well as numerical chromosome abnormalities, although the etiology (genetic and/or environmental) of these abnormalities is unknown.

Our data suggest that men with these abnormal semen parameters especially with abnormal motility and abnormal head morphology are at increased risk for paternal transmission of genetic defects to their offspring. Analysis of serum parameters could be a rapid method for providing valuable preliminary data regarding genetic risk. For those with high abnormalities, analysis of sperm chromosomes and the selection of the healthiest sperm should be considered before performing ICSI in order to minimize the transmission of genetic defects to children.

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บทคัดย่อ

การตรวจวิเคราะห์ความผิดปกติของโครโมโซมในด้านจำนวนและพารามิเตอร์ของน้ำอสุจิในกลุ่มชายไทยที่มีความผิดปกติของอสุจิแบบ normotatozoospermia (NT) และ oligoasthenotatozoospermia (OAT)

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การใช้อสุจิจากกลุ่มชายที่มีบุตรยากเพื่อผลิตผสมกับไข่ในการเพาะเลี้ยงตัวอ่อนนอกมดลูกพบได้บ่อย แต่การศึกษาคุณภาพของอสุจิในระดับโครโมโซมเพื่อตรวจสอบความเสี่ยงในการถ่ายทอดความผิดปกติให้แก่รุ่นลูกหลานยังมีน้อยมาก ในการนี้จึงทำการศึกษาโครโมโซมของอสุจิในชายไทย ๑๕ ราย (อายุ ๒๖-๔๐ ปี, เฉลี่ย ๓๒ ปี) แบ่งเป็นกลุ่ม normotatozoospermia (NT) ๗ ราย และ oligoasthenotatozoospermia (OAT) ๘ ราย การตรวจวิเคราะห์โครโมโซม ๑๘, X, และ Y ด้วยวิธี multi-color FISH (fluorescence *in situ* hybridization) ครั้งนี้ทำการศึกษากับจำนวนอสุจิทั้งหมด ๑๓,๕๒๘ ตัว ผลการศึกษาพบว่ามีความแตกต่างของความผิดปกติของโครโมโซมในด้านจำนวนระหว่าง ๒ กลุ่มที่ศึกษาอย่างมีนัยสำคัญ (ค่า $P = 0.001$) ค่าเฉลี่ยมัธยฐานร้อยละ ๑.๐๗ (ร้อยละ ๐.๑๘-๒.๓๕) และร้อยละ ๙.๒๑ (ร้อยละ ๐.๔๘-๒๙.๘๔) สำหรับกลุ่ม NT และ กลุ่ม OAT ตามลำดับ โดยพบความผิดปกติแบบ XY disomy มากที่สุด กลุ่มอสุจิที่มีความผิดปกติของโครโมโซมมีความสัมพันธ์เป็นส่วนกลับกับกลุ่มอสุจิที่ไม่มีความผิดปกติในการเคลื่อนไหว ($r = -0.554$; ค่า $P = 0.032$) และเป็นส่วนกลับกับกลุ่มอสุจิที่มีส่วนหัวปกติ ($r = -0.686$; ค่า $P = 0.005$). โดยผลการศึกษาพบว่า น้ำอสุจิที่มีค่า motility \leq ร้อยละ ๖๐ หรือ มีรูปร่างส่วนหัวปกติ \leq ร้อยละ ๘๕ จะมีความเสี่ยงในการที่จะมีจำนวนโครโมโซมผิดปกติด้วย ผลการศึกษานี้แสดงให้เห็นว่ากลุ่ม OAT มีความเสี่ยงที่จะถ่ายทอดความผิดปกติของบิดาไปยังรุ่นลูกหลาน ดังนั้นการตรวจวิเคราะห์ความผิดปกติในระดับโครโมโซมของอสุจิและการตรวจพารามิเตอร์ต่างๆ ของน้ำอสุจิโดยเฉพาะกลุ่ม OAT เป็นสิ่งสำคัญที่ควรพิจารณาให้ถี่ถ้วนก่อนการทำ ICSI

คำสำคัญ: ฟลูออเรสเซนซ์ อินไซท์ ไฮบริไดเซชัน แอสเสย์, ความผิดปกติของโครโมโซมด้านจำนวนของอสุจิ, พารามิเตอร์ของน้ำอสุจิ, ผู้มีบุตรยาก, ความผิดปกติของโครโมโซม