

## CHAPTER 2

### RESEARCH METHODOLOGY

#### Materials

##### Peripheral blood samples

Peripheral blood samples (3-5 ml) were obtained from two study groups and collected in sodium-heparin anticoagulant.

##### 1. Idiopathic mental retardation patients

Idiopathic mental retardation (IMR) patients with and without multiple congenital anomalies (MCA) were recruited by clinicians at Rajanukul Institute. Metaphase chromosomes all patients with normal G-banded karyotypes at the 450-550 band levels was studied with the FISH technique using specific-subtelomeric probes for all chromosome ends.

##### 2. Autistic patients

Peripheral blood of autistic children recruited for the study was tested by high-resolution chromosome analysis, FISH analysis using PWS/AS region, DiGeorge/VCF region and DNA screening for fragile X syndrome. Six randomly selected were also examined with subtelomeric-specific probes.

#### Reagents

Acetic acid

Agarose

Ammonium sulfate

Chelex-100 resin

Chloramphenical  
Colcemid  
Dextran sulfate  
DAPI (4,6-Diamino-2-Phenyl-indole)  
EDTA  
Ethanol  
Ethidium bromide  
Fetal calf serum  
Formamide  
Glucose  
Glycerol  
Human Cot-1 DNA (Invitrogen)  
Human placenta DNA  
IMMOLASE™ DNA polymerase  
Kanamycin  
Magnesium Chloride  
MEM medium  
Methotexate  
Methanol  
NaOH  
Nick translation kit (Vysis)  
phytohemagglutinin  
PN buffer  
Potassium chloride  
Potassium acetate  
p-Phenylenediamine  
Rubber solution  
Spectrum green-dUTP (Vysis)  
Spectrum orange-dUTP (Vysis)  
Sodium chloride  
Sodium citrate

Sodium acetate  
SDS  
Tris-Cl  
TWEEN 20  
Trypsin  
Thymidine  
Tryptone  
Yeast extract  
7-deaza dGTP

### **Equipments**

Applied Spectral Imaging system  
Centrifuge  
Cover slip 24X60 mm  
Centrifuge tube 15 ml  
Diamond pencil  
Fluorescence microscope with light source and appropriate filter sets  
Forceps  
Gel electrophoresis with power supply  
Gloves  
Glass coplin jars  
Hot plate  
Humidified chamber  
Incubator  
Microscope slide  
Microcentrifuge tube 1.5 ml  
Micropipette, range 1-200  $\mu$ l and tip  
Phase contrast microscope  
PCR Thermal cycle (MJ research PTC200)  
Syringe

Timer

Vortex

Water bath

## **Methods**

### **High-resolution chromosome analysis**

Peripheral blood was cultured at 37 °C for 72 hours in MEM medium supplemented with 10% fetal calf serum and PHA (phytohemagglutinin, M-form). After incubating for 48 hours, 0.1 ml of methotrexate was added to the culture and it was incubated at 37 °C for a further 16-18 hours. The culture was washed with plain medium and thymidine was added before incubating at 37 °C for 3 hours and 10 minutes. Ethidium bromide was added into the culture and incubated at 37 °C for a further 1 hour and 45 minutes. Colchicine was added to culture to arrest cells during mitosis. Hypotonic solution (0.075 M potassium chloride) and fixative (methanol and acetic acid in a 3:1 ratio) were then applied sequentially. The cell suspension was placed overnight in a freezer at -20 °C. Finally, the chromosome suspension was dropped onto glass slides on the following day and oven baked at 63-65 °C overnight before the banding procedure.

The banding protocol followed the standard GTG protocol using trypsin and geimsa. The slides were immersed into a trypsin solution for 5-10 seconds (depending on the quality of the chromosomes) and immediately immersed in a serum solution for 30 seconds to stop the trypsin reaction. Then the slide was placed into geimsa stain for 5-8 minutes and washed with distilled water.

15 metaphases were counted and 5 metaphases were fully analyzed and karyotyped under a bright field microscope. The images were captured by a cool CCD camera and Applied Spectral Imaging software (Clousto, 2001).

### **Fluorescence *in situ* hybridization (FISH)**

The FISH probes were performed with bacterial artificial chromosome (BAC) and/or P1-derived artificial chromosome (PAC) clones containing 41 different subtelomeric-specific sequences for all human chromosome ends according to the publicly available genome source (NCBI Map Viewer: <http://www.ncbi.nlm.nih.gov/mapview/>). BAC/PAC clones were purchased through the BAC/PAC website at <http://www.bacpac.chori.org>.

Bacterial colonies containing single BAC/PAC clones were inoculated in 5 ml of LB medium containing 25 µg/ml chloramphenicol for the BAC clones and 50 µg/ml kanamycin for the PAC clones. After each clone was incubated at 37 °C overnight the cells were harvested. Plasmid DNA was extracted using the mini-preparation method of Smambrook and Russel (2001) and labeled with spectrum green-dUTP for the p-arm and spectrum orange-dUTP for the q-arm of the chromosome by nick translation.

The nick translation reaction was set up in a total volume of 50 µl and 1 µg of plasmid DNA was used. The calculated volume in µl of plasmid DNA, 2.5 µl of 0.2 mM spectrum green-dUTP or spectrum orange-dUTP, 5 µl of 0.1 dTTP, 10 µl of dNTP mix, 5 µl of 10X nick translation buffer and 10 µl nick translation enzyme were added sequentially into a microcentrifuge tube. Sterile water was added to bring the volume to 50 µl. The reaction was carried out at 15 °C for 16 hours and then the reaction was stopped at 72 °C for 10 minutes. 5 µl of labeled probe was precipitated by adding 1.2 µl of 3 M NaOAc, 1 µg of Cot-1 DNA and 2 µg of human placental DNA. 30 µl of cold ethanol were added into the tube and it was placed in a freezer at -80 °C for 15 minutes, after which it was centrifuged at 13,000 rpm for 30 minutes. After centrifugation, the supernatant was discarded and the pellet allowed to dry. The pellet was then resuspended by adding 10 µl of hybridization solution and incubated at 37 °C for 1 hour.

For the FISH analysis, 3 slides per case were each divided into eight sections with a diamond pencil and 4 µl of metaphase suspension was placed onto each section. Metaphase slides were pretreated with 2XSSC/0.05% TWEEN 20 at 37 °C for 30 minutes and dehydrated with an ethanol series (70%, 80% and 100%) for 2 minutes each at room temperature. The p-arm and q-arm probes of each chromosome were denatured and hybridized to the denatured-metaphase, one chromosome per section, eight chromosomes per slide. The slides were incubated in a humidified box at 37 °C overnight. Excess probes were eliminated by washing with 0.4XSSC at 68 °C for 1 minute, 2XSSC at room temperature for 2 minutes and the chromosomes

were then counterstained with DAPI. The slides were analyzed in a fluorescence microscope and the images were captured by a cool CCD camera and Applied Spectral Imaging software. The presence or absence of p-arm and q-arm signals for each chromosome were recorded for at least five metaphases from each patient's sample. Inverted DAPI staining was used for chromosome identification during the FISH analysis (Kearney and Buckle, 2001)

### **Multiplex PCR for screening *FMRI*, *FMR2* and *SRY* genes**

#### **DNA extraction**

50  $\mu$ l peripheral blood was dropped into a microcentrifuge tube and incubated at 37  $^{\circ}$ C until dried. Dried-blood was added with 500  $\mu$ l of TE buffer, and then vortexed for 2 seconds before incubating at room temperature for 30 minutes. After centrifugation at 12,000 rpm for 2 minutes, the supernatant was discarded, and 50  $\mu$ l of 25% Chelex-100 resin were added to the sample and it was further incubated at 56  $^{\circ}$ C for 30 minutes to 24 hours. The sample was heated at 95  $^{\circ}$ C for 10 minutes and centrifuged at 12,000 rpm before PCR analysis.

#### **Polymerase Chain Reaction analysis**

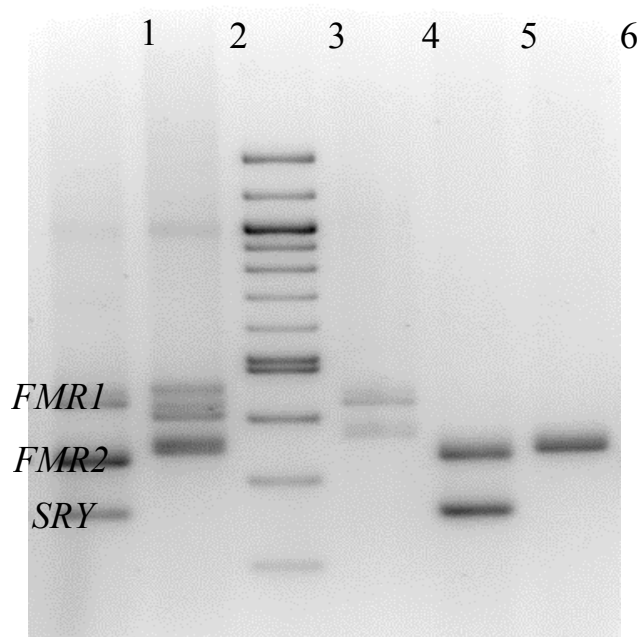
Multiple DNA amplifications were performed; for the *FMRI*, *FMR2* and *SRY* gene, a final reaction volume of 20  $\mu$ l was used with multiplex buffer (50.25 mM Tris pH 8.8, 12.45 mM  $(\text{NH}_4)_2 \text{SO}_4$ ); 1.0 mM Magnesium Chloride; 200  $\mu$ M each dATP, dTTP, dCTP; 10% dimethylsulfoxide (DMSO); 150  $\mu$ M of dGTP, 50  $\mu$ M 7-deaza dGTP; 0.25  $\mu$ M primer SRY; 0.25  $\mu$ M primer FRAXE and 0.5  $\mu$ M primer FRAXA and 1U of IMMOLASE<sup>TM</sup> DNA polymerase.

PCR was carried out following an initial hot start at 95  $^{\circ}$ C for 10 min, 10 cycles of 95  $^{\circ}$ C for 60 seconds, 66  $^{\circ}$ C for 60 seconds, 72  $^{\circ}$ C for 60 seconds, 25 cycles of 95  $^{\circ}$ C for 60 seconds, 64  $^{\circ}$ C for 60 seconds, 72  $^{\circ}$ C for 60 seconds and a final extension of 72  $^{\circ}$ C for 5 minutes.

The PCR products were separated on 2.5% agarose gel and visualized by ethidium bromide staining under a UV transilluminator.

**Table 3 Description of oligonucleotide, summary of amplification results**

Primer name	Primer sequence	Amplified fragment length (bp)
SRY forward	5'CAT GAA CGC ATT CAT CGT GTG GTC3'	254
SRY reverse	5' CTG CGG GAA GCA AAC TGC AAT TCT T 3'	
FRAXA-PSU forward	5' CAGCGTTGATCACGTGACGTGGTTTCAGTG 3'	429 (30 repeat)
FRAXA-PSU reverse	5' GATGGGGCCTGCCCTAGAGCCAAGTAC 3'	
FRAXE-PSU forward	5'AAG CGG CGG CAG TGG CAC TGG GC 3'	384 (30 repeat)
FRAXE-PSU reverse	5' CGCCCCCTGTGAGTGTGTAAGTGTGTGATG 3'	



**Figure 5** An example of Multiplex PCR results. Lane 1 shows the PCR product of a normal male. Lanes 2 and 4 show the PCR product of a normal female. Lane 3 is a 100 bp DNA ladder. Lane 5 shows the PCR product of a full mutation *FMR1* male. Lane 6 shows the PCR product of a full mutation *FMR1* female.