Data Article

Cytogenetics data in adult men involved in the recycling of electronic wastes

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A B S T R A C T

In this data article, 146 villagers (exposed group) were randomly selected from the workers who involved in the e-wastes recycling directly as a daily job in Tianjin. Control group, including 121 villagers, came from another town without e-waste disposal sites. Chromosomal aberrations (CA) and cytokinesis blocking micronucleus (CBMN) were performed to detect the cytogenetic effect for each subject. DNA damage was detected using comet assay; the DNA percentage in the comet tail (TDNA%), tail moment (TM), and Olive tail moment (OTM) were recorded to describe DNA damage to lymphocytes and spermatozoa. Routine semen analysis, spermatozoa motility and morphology were analyzed. The RT2Profiler PCR array was used to measure levels of expression of 84 genes related to quality of DNA. It showed significant relationships between CA, CBMN, DNA damage and exposure time in exposure subjects. The alteration of sperm motility rate, abnormality rate and total sperm counts had association with exposure time and age.

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Specifications table

| Subject area | Environment and health |
|--------------|------------------------|
| More specific subject area | Environmental pollution, cytogenetic alteration |
| Type of data | Table and figure |
| How data was acquired | CA and CBMN were acquired using ZEISS MetaSystems (Germany). DNA damage was detected by comet assay. |
| Data format | Analyzed |
| Experimental factors | Semen and blood were sampled from the two groups in our lab. |
| Experimental features | Lymphocytes were cultured in RPMI 1640 medium for CA and CBMN assay. Spermatozoa or lymphocytes were suspended in PBS for comet assay. |
| Data source location | Institute of Radiation Medicine, Chinese Academy of Medical Sciences & Peking Union Medical College |
| Data accessibility | All the data are in this data article. |

Value of the data.

The data were helpful to understand the positive associations between both CA and CBMN and the duration of working with e-wastes. When stratified for age, for each of the age sub-groups, a statistically significant difference was observed between the group exposed to e-waste and the reference group. Semen quality was worse in the workers who recycled e-wastes than that of reference subjects.

1. Data

A largest electronic waste disposal centers in northern China had been found recently years. Components of e-wastes such as electronic circuit boards or microchips were illegally burned or heated for reclaimable materials (Fig. 1).

The exposure and reference group were both divided by age into three sub-groups (20–29, 30–39 and > 40 years old). For each age sub-group, significant differences were found between exposure and reference groups (Fig. 2A-F). No significant difference was observed among age-groups in either the exposure or reference group (Fig. 2A-F).

Fig. 1. Recycling of e-wastes without any protection. Heat the circuit boards to get metals.
The exposure group was stratified into three sub-groups according to their exposure time (≤ 3, 3–6 and > 6-year groups). The statistical significant relationships between DNA damage (TDNA%, TM) and duration of exposure for DNA damage were found in both lymphocytes and spermatozoa (Fig. 3A and B).
For each of the sub-groups divided by age, there was significantly higher of CA and CBMN in the e-waste workers compared to the reference group (Fig. 4A and B). No significant difference was found among sub-groups in either the exposure or reference group (Fig. 4A and B).

Statistically significant was found between CA, CBMN and exposure time (Fig. 5A). A classical micronucleus in a binucleated lymphocyte, a dicentric chromosome and an acentric fragment are shown in Fig. 5B and C.

Sperm motility rate, abnormality rate and total sperm counts were analyzed in the three sub-groups divided by age for exposure and reference groups. For the same age sub-groups, significant difference was found between exposure and reference group (Fig. 6A, B and C). The sperm parameters above also showed significant difference among different sub-groups in exposure or reference group respectively (Fig. 6A1, B1 and C1).

Relationship between semen alteration and exposure time of e-wastes was analyzed in exposure group. For the three sub-groups divided by exposure time (≤ 3, 3–6 and > 6 years groups), semen parameters were analyzed for every two sub-groups by Wilcoxon rank-sum test. Sperm motility rate, semen volume, sperm concentration and total sperm count decreased significantly with exposure time, however, sperm abnormality rate increased significantly with e-wastes exposure time (Fig. 7).

Fig. 3. Relationship between exposure duration and DNA damage of lymphocytes (A) and spermatozoa (B) in the exposed group. It showed significant relationship between TDNA%, TM and exposure duration for not only lymphocytes but also spermatozoa. *: P < 0.05.
RNA of peripheral blood cells was isolated by use of the RNeasy Mini kit (Qiagen, Hilden, Germany) as instructed by the manufacturer. Integrity of RNA was assessed by means of the Bioanalyzer 2100 (Agilent Technologies, Palo Alto, CA). 84 key genes (Table 1) from Human DNA Damage Signaling Pathway were simultaneously assayed by use of the RT2Profiler PCR array plate (SuperArray Bioscience Corporation, Frederick, MD) according to the manufacturer’s protocol. The detail of gene expression analysis was shown in Ref. [1].

**Fig. 4.** CA (A) and CBMN (B) in lymphocytes of workers recycling e-wastes and in reference group for different age sub-groups. A-B: CA and CBMN in lymphocytes between the group of workers recycling e-wastes and reference group for the sub-groups divided by age. There is no difference of CA and CBMN among the age sub-groups. **: $P < 0.01$. Two way ANOVA was also used to test the interactions between age and CA, CBMN in lymphocytes, respectively. (CA: $F = 2.03, P = 0.18$; CBMN: $F = 1.07, P = 0.39$).
2. Experimental design, materials and methods

2.1. Instruments and reagents

Agarose gels with normal and low melting points were purchased from the BioWest Company (Miami, FL, USA). Tris–HCl, DMSO, NaHCO3, formaldehyde (A.P.), trypan blue and TritonX-100 were purchased from Sigma (St. Louis, MO, USA). The electrophoresis apparatus was purchased from BIO-RAD (Hercules, CA, USA), and the Nikon90i fluorescence microscope was purchased from NIKON (Tokyo, Japan). The comet slides were purchased from Trevigen. Inc. (Gaithersburg, MD, USA).

2.2. Routine semen analysis

The procedure of routine semen analysis was performed according to the standard methods in the WHO manual [2]. Briefly, the semen samples were examined immediately after liquefaction or within one hour of ejaculation. All the semen samples were ensured to be homogeneous by mixing thoroughly. A fixed volume of 10 μl semen was delivered onto a clean glass slide and covered with a coverslip. Scanning the slide and estimating the number of spermatozoa per 400× magnification field gives an approximate sperm concentration in 106/ml. This estimate is used to decide the dilution (1:5, 1:10, 1:20, 1:50) for determining the sperm concentration by hemocytometry. The spermatozoa concentration was determined using the hemocytometer method on two separate preparations of the semen sample. The diluted semen sample was dropped onto the hemocytometer and covered with a coverslip, and was placed in a humid chamber for about five minutes to prevent drying out. The cells sedimented during this time and were then counted. The count only included complete spermatozoa (heads with tails). Any sperm lying on the line dividing two adjacent squares was counted only if it was on the upper or the left side of the square being assessed.
Fig. 6. Sperm motility rate, abnormality rate and total sperm counts for different age sub-groups. A-C: Sperm motility rate, abnormality rate and total sperm counts between the group of workers recycling e-wastes and reference group for the sub-groups divided by age. There is significant difference of sperm motility rate, abnormality rate and total sperm counts between the group of workers recycling e-wastes and reference group in the age sub-groups, respectively. A1-C1: Line chart showed the change of sperm motility rate, abnormality rate and total sperm counts along with age. There is significant difference of sperm motility rate, abnormality rate and total sperm counts among the age sub-groups in exposure or reference group respectively. **: $P < 0.01$, *: $P < 0.05$. Two way ANOVA was also used to test the interactions between age and sperm motility rate, abnormality rate and total sperm counts, respectively. (sperm motility rate: $F = 3.24$, $P = 0.07$; abnormality rate: $F = 3.13$, $P = 0.08$; total counts: $F = 2.89$, $P = 0.12$).
Spermatozoa or lymphocytes were suspended in PBS at a concentration of $1 \times 10^5$/ml. The comet assay, also called single cell gel electrophoresis, was performed as previously reported [3]. Briefly, comet slides were coated with $100 \mu$l of 0.75% (w/v) normal-melting-point agarose. Once the first agarose layer was coagulated, a mixture of 75 $\mu$l of low-melting-point agarose and 25 $\mu$l of spermatozoa suspension was applied as the second layer. The comet slides were immersed in cold lysis buffer (2.5 M NaCl, 0.5 M EDTA, 10 mM Tris HCl pH 10.0 containing 1% Triton X-100, 40 mM dithiothreitol and 100 $\mu$g/ml proteinase K) for 2 h at room temperature to remove any DNA-associated proteins. After lysis, double-distilled water was used to rinse away excess salt. All the comet slides were then placed in buffer for 20 min in a horizontal electrophoresis tank that was pre-filled with cold alkaline buffer (1 mM Na2EDTA and 0.3 M NaOH, pH 13.0) to loosen the tight double-helical structure of DNA for electrophoresis. Electrophoresis was then performed at 25 V and 10 mA for 20 min in electrophoresis buffer at room temperature. The slides were then rinsed twice with distilled water and stained with ethidium bromide (2 $\mu$g/ml). All of the above procedures were carried out in the dark to avoid additional DNA damage. The comets were viewed using a Nikon 90i fluorescence microscope.

Fig. 7. Relationship among semen parameters and exposure duration. A: Sperm motility rate and semen volume decreased but sperm abnormality rate increased significantly with e-wastes exposure duration. B: Sperm concentration and total sperm count both decreased significantly with exposure duration. *: $P < 0.05$.

2.3. Alkaline Comet assay

Spermatozoa or lymphocytes were suspended in PBS at a concentration of $1 \times 105$/ml. The comet assay, also called single cell gel electrophoresis, was performed as previously reported [3]. Briefly, comet slides were coated with $100 \mu$l of 0.75% (w/v) normal-melting-point agarose. Once the first agarose layer was coagulated, a mixture of 75 $\mu$l of low-melting-point agarose and 25 $\mu$l of spermatozoa suspension was applied as the second layer. The comet slides were immersed in cold lysis buffer (2.5 M NaCl, 0.5 M EDTA, 10 mM Tris HCl pH 10.0 containing 1% Triton X-100, 40 mM dithiothreitol and 100 $\mu$g/ml proteinase K) for 2 h at room temperature to remove any DNA-associated proteins. After lysis, double-distilled water was used to rinse away excess salt. All the comet slides were then placed in buffer for 20 min in a horizontal electrophoresis tank that was pre-filled with cold alkaline buffer (1 mM Na2EDTA and 0.3 M NaOH, pH 13.0) to loosen the tight double-helical structure of DNA for electrophoresis. Electrophoresis was then performed at 25 V and 10 mA for 20 min in electrophoresis buffer at room temperature. The slides were then rinsed twice with distilled water and stained with ethidium bromide (2 $\mu$g/ml). All of the above procedures were carried out in the dark to avoid additional DNA damage. The comets were viewed using a Nikon 90i fluorescence microscope,
| No. | Unigene | GeneBank | Symbol | Description | Gene Name |
|-----|---------|----------|--------|-------------|-----------|
| 1   | Hs.431048 | NM_005157 | ABL1   | C-abl oncogene 1, receptor tyrosine kinase | ABL/JTK7 |
| 2   | Hs.601206 | NM_198889 | ANKRD17 | Ankyrin repeat domain 17 | GTAR/NY-BR-16 |
| 3   | Hs.73722  | NM_080649 | APEX1  | APEX nuclease (multifunctional DNA repair enzyme) 1 | APE/APE-1 |
| 4   | Hs.367437 | NM_000051 | ATM    | Ataxia telangiectasia mutated | AT1/ATA |
| 5   | Hs.271791 | NM_001184 | ATR    | Ataxia telangiectasia and Rad3 related | FRP1/MEC1 |
| 6   | Hs.533526 | NM_00489 | ATRX   | Alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae) | ATR2/MRXHF1 |
| 7   | Hs.194143 | NM_007294 | BRCA1  | Breast cancer 1, early onset | BRCA1/BRCC1 |
| 8   | Hs.519162 | NM_006763 | BTG2   | BTG family, member 2 | PC3/TIS21 |
| 9   | Hs.292524 | NM_001239 | CCNH   | Cyclin H | CAK/p34 |
| 10  | Hs.184298 | NM_001799 | CDK7   | Cyclin-dependent kinase 7 | CAK1/CDKN7 |
| 11  | Hs.24529  | NM_001274 | CHEK1  | CHK1 checkpoint homolog (S. pombe) | CHK1 |
| 12  | Hs.291363 | NM_007194 | CHEK2  | CHK2 checkpoint homolog (S. pombe) | CD5/CHK2 |
| 13  | Hs.135471 | NM_006384 | CIB1   | Calcium and integrin binding 1 (calmyrin) | CIB/CIB |
| 14  | Hs.249129 | NM_001279 | CIDEA  | Cell death-inducing DFFA-like effector a | CIDE-A |
| 15  | Hs.151573 | NM_004075 | CRY1   | Cryptochrome 1 (photolyase-like) | PHL1 |
| 16  | Hs.290758 | NM_001923 | DDB1   | Damage-specific DNA binding protein 1, 127 kDa | DDBA/UV-DDB1 |
| 17  | Hs.505777 | NM_004083 | DDB3   | DNA-damage-inducible transcript 3 | CEBPZ/CHOP |
| 18  | Hs.339396 | NM_007068 | DMC1   | DMC1 dosage suppressor of mck1 homolog, meiosis-specific homologous recombination (yeast) | DMC1/HisLim15 |
| 19  | Hs.435981 | NM_001983 | ERCC1  | Excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence) | COFS4/UV20 |
| 20  | Hs.487294 | NM_000400 | ERCC2  | Excision repair cross-complementing rodent repair deficiency, complementation group 2 (xeroderma pigmentosum D) | COFS2/EM9 |
| 21  | Hs.498248 | NM_130398 | EXO1   | Exonuclease 1 | HEX1/HEX01 |
| 22  | Hs.591084 | NM_004629 | FANCG  | Fanconi anemia, complementation group G | FAG/RCRC9 |
| 23  | Hs.409065 | NM_004111 | FEN1   | Flap structure-specific endonuclease 1 | FEN-1/MF1 |
| 24  | Hs.292493 | NM_001469 | XRC6   | X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70 kDa) | CTC7/CTCBF |
| 25  | Hs.80409  | NM_001924 | GADD45A| Growth arrest and DNA-damage-inducible, alpha | DDIT1/GADD45 |
| 26  | Hs.9701   | NM_006705 | GADD45G| Growth arrest and DNA-damage-inducible, gamma | CR6/DDIT2 |
| 27  | Hs.661218 | NM_002066 | GML    | Glycophosphatidylinositol anchored molecule like protein | LY6DL |
| 28  | Hs.577202 | NM_005316 | GTF2H1 | General transcription factor IIH, polypeptide 1, 62 kDa | BTF2/BTF2H1 |
| 29  | Hs.191356 | NM_001515 | GTF2H2 | General transcription factor IIH, polypeptide 2, 44 kDa | BTF2/BTF2P44 |
| 30  | Hs.386189 | NM_016426 | GSTE1  | G-2 and S-phase expressed 1 | B99 |
| 31  | Hs.152983 | NM_004507 | HUS1   | HUS1 checkpoint homolog (S. pombe) | Hus1 |
| No. | Unigene   | GeneBank   | Symbol  | Description                                                                 | Gene Name                        |
|-----|-----------|------------|---------|------------------------------------------------------------------------------|----------------------------------|
| 32  | Hs.503048 | NM_002180  | IGHMBP2 | Immunoglobulin mu binding protein 2                                          | CATF1/HCSA                       |
| 33  | Hs.17253  | NM_054111  | IHPK3   | Inositol hexaphosphate kinase 3                                               | INS6K3/IP6K3                     |
| 34  | Hs.61188  | NM_033276  | XRCC6BP1 | XRCC6 binding protein 1                                                       | KUB3                             |
| 35  | Hs.1770   | NM_000234  | LIG1    | Ligase I, DNA, ATP-dependent                                                  | MCC117397                        |
| 36  | Hs.463978 | NM_002758  | MAP2K6  | Mitogen-activated protein kinase 6                                            | MAPK6/MEK6                       |
| 37  | Hs.432642 | NM_002969  | MAPK12  | Mitogen-activated protein kinase 12                                           | ERK5/ERK6                        |
| 38  | Hs.35947  | NM_003925  | MBD4    | Methyl-CpG binding domain protein 4                                           | MED1                             |
| 39  | Hs.195364 | NM_000249  | MLH1    | MutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)                  | COCA2/FCC2                       |
| 40  | Hs.436650 | NM_014381  | MLH3    | MutL homolog 3 (E. coli)                                                      | HNPCC7                           |
| 41  | Hs.509523 | NM_002431  | MNAT1   | Menage a trois homolog 1, cyclin H assembly factor (Xenopus laevis)           | MAT1/RNF66                       |
| 42  | Hs.459596 | NM_002435  | MPG     | N-methylpurine-DNA glycosylase                                                | AAG/APNG                         |
| 43  | Hs.192649 | NM_005590  | MRE11A  | MRE11 meiotic recombination 11 homolog A (S. cerevisiae)                     | ATLD/HNS1                        |
| 44  | Hs.597656 | NM_000251  | MSH2    | MutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)                  | COCA1/FCC1                       |
| 45  | Hs.280987 | NM_002439  | MSH3    | MutS homolog 3 (E. coli)                                                      | DUP/MPR1                         |
| 46  | Hs.271353 | NM_012222  | MUTYH   | MutY homolog (E. coli)                                                        | MYH                              |
| 47  | Hs.369494 | NM_018177  | N4BP2   | Nedd4 binding protein 2                                                       | B3BP                             |
| 48  | Hs.492208 | NM_002485  | NBN     | Nibrin                                                                       | AT-V1/AT-V2                      |
| 49  | Hs.66196  | NM_002528  | NTHL1   | Nth endonuclease III-like 1 (E. coli)                                         | NTH1/OCTS3                       |
| 50  | Hs.380271 | NM_002542  | OGG1    | 8-oxoguanine DNA glycosylase                                                  | HMM/HOGG1                        |
| 51  | Hs.20930  | NM_020418  | PCBP4   | Poly(rC) binding protein 4                                                    | LIP4/MCG10                       |
| 52  | Hs.14347  | NM_182649  | PCNA    | Proliferating cell nuclear antigen                                             | MCG8367                          |
| 53  | Hs.424932 | NM_004208  | AIFM1   | Apoptosis-inducing factor, mitochondrion-associated, 1                        | AIF/PDCD8                        |
| 54  | Hs.111749 | NM_000534  | PMS1    | PMS1 postmeiotic segregation increased 1 (S. cerevisiae)                      | DKFZp781M0253/HNPCC3             |
| 55  | Hs.632637 | NM_000537  | PMS2    | PMS2 postmeiotic segregation increased 2 (S. cerevisiae)                     | HNPCC4/PMS2CL                    |
| 56  | Hs.225784 | NM_005395  | PMS2L3  | Postmeiotic segregation increased 2-like 3                                   | PMS2L9/PMS5                      |
| 57  | Hs.78016  | NM_007254  | PNKP    | Polynucleotide kinase 3’-phosphatase                                          | PNK                              |
| 58  | Hs.631593 | NM_014330  | PPP1R15A| Protein phosphatase 1, regulatory (inhibitor) subunit 15A                    | GADD34                           |
| 59  | Hs.700597 | NM_006904  | PRKDC   | Protein kinase, DNA-activated, catalytic polypeptide                          | DPKAP/DNPK1                      |
| 60  | Hs.531879 | NM_002853  | RAD1    | RAD1 homolog (S. pombe)                                                       | HRAD1/REC1                       |
| 61  | Hs.16184  | NM_002873  | RAD17   | RAD17 homolog (S. pombe)                                                       | CCYCHRAD17                       |
| 62  | Hs.375684 | NM_002165  | RAD18   | RAD18 homolog (S. cerevisiae)                                                 | RNF73                            |
| 63  | Hs.81848  | NM_006265  | RAD21   | RAD21 homolog (S. pombe)                                                       | HR21/HRAD21                      |
| 64  | Hs.655835 | NM_005732  | RAD50   | RAD50 homolog (S. cerevisiae)                                                  | RAD50-2-HRAD50                   |
| 65  | Hs.631709 | NM_002875  | RAD51   | RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)                         | BRCC5/HRAD51                     |
| 66  | Hs.172587 | NM_133509  | RAD51L1 | RAD51-like 1 (S. cerevisiae)                                                  | RSLH2/RAD51B                     |
| 67  | Hs.655354 | NM_004584  | RAD9A   | RAD9 homolog A (S. pombe)                                                     | RAD9                             |
| ID     | Gene ID  | Description                                                                 | Symbol |
|--------|----------|-----------------------------------------------------------------------------|--------|
| 68     | Hs.546282| NM_002894 Retinoblastoma binding protein 8 CTIP/RIM                         |        |
| 69     | Hs.443077| NM_016316 REV1 homolog (S. cerevisiae) REV1L                               |        |
| 70     | Hs.461925| NM_002945 Replication protein A1, 70 kDa HSSB/REPA1                        |        |
| 71     | Hs.408846| NM_022367 Sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A CORD10/RP35 |        |
| 72     | Hs.591336| NM_014454 Sestrin 1 PA26/SEST1                                              |        |
| 73     | Hs.211602| NM_006306 Structural maintenance of chromosomes 1A CDLS2/DKFZp686L19178    |        |
| 74     | Hs.81424 | NM_003352 SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae) DAP-1/GMP1 |        |
| 75     | Hs.654481| NM_000546 Tumor protein p53 LFS1/TRP53                                      |        |
| 76     | Hs.697294| NM_005427 Tumor protein p73 P73                                             |        |
| 77     | Hs.694840| NM_016381 Three prime repair exonuclease 1 AGS1/AGS5                        |        |
| 78     | Hs.191334| NM_003362 Uracil-DNA glycosylase DGU/DKFz781L1143                          |        |
| 79     | Hs.654364| NM_000380 Xeroderma pigmentosum, complementation group A XP1/XPAC           |        |
| 80     | Hs.475538| NM_004628 Xeroderma pigmentosum, complementation group C XP3/XPCC           |        |
| 81     | Hs.98493 | NM_006297 X-ray repair complementing defective repair in Chinese hamster cells 1 RCC |        |
| 82     | Hs.647093| NM_005431 X-ray repair complementing defective repair in Chinese hamster cells 2 DKFZp781P0919 |        |
| 83     | Hs.592325| NM_005432 X-ray repair complementing defective repair in Chinese hamster cells 3 XRCC3 |        |
| 84     | Hs.444451| NM_016653 Sterile alpha motif and leucine zipper containing kinase AZK AZK/MLK7 |        |
and images of 100 comets were collected for each subject using a digital imaging system. Cells that overlapped were not counted. All the comet images were analyzed using Comet Assay Software Project (CASP, Wroclaw University, Poland) [4] and the DNA percentage in the comet tail (TDNA%), the tail moment (TM) and the Olive tail moment (OTM) were recorded to describe the DNA damage to the spermatozoa or lymphocytes.

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Transparency document. Supporting information

Transparency document associated with this article can be found in the online version at http://dx.doi.org/10.1016/j.dib.2018.02.051.

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