ESOPHAGEAL CANCER

Comparative genomic hybridization analysis of genetic aberrations associated with development of esophageal squamous cell carcinoma in Henan, China

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Abstract

AIM: To characterize cytogenetic alterations in esophageal squamous cell carcinoma (ESCC) and its metastasis.

METHODS: A total of 37 cases of primary ESCC and 15 pairs of primary ESCC tumors and their matched metastatic lymph nodes cases were enrolled from Linzhou, the high incidence area for ESCC in Henan, northern China. The comparative genomic hybridization (CGH) was applied to determine the chromosomal aberrations on the DNA extracted from the frozen ESCC and metastatic lymph node samples from these patients.

RESULTS: CGH showed chromosomal aberrations in all the cases. In 37 cases of primary ESCC, chromosomal profile of DNA copy number was characterized by frequently detected gains at 8q (29/37, 78%), 3q (24/37, 65%), 5p (19/37, 51%); and frequently detected losses at 3p (21/37, 57%), 8p and 9q (14/37, 38%). In 15 pairs of primary ESCC tumors and their matched metastatic lymph node cases, the majority of the chromosomal aberrations in both primary tumor and metastatic lymph node lesions were consistent with the primary ESCC cases, but new candidate regions of interest were also detected. The most significant finding is the gains of chromosome 6p with a minimum high-level amplification region at 6p12-6q12 in 7 metastatic lymph nodes but

only in 2 corresponding primary tumors ($P = 0.05$) and 20p with a minimum high-level amplification region at 20p12 in 11 metastatic lymph nodes but only in 5 corresponding primary tumors ($P < 0.05$). Another interesting finding is the loss of chromosome 10p and 10q in 8 and 7 metastatic lymph nodes but only in 2 corresponding primary tumors ($P < 0.05$).

CONCLUSION: Using the CGH technique to detect chromosomal aberrations in both the primary tumor and its metastatic lymph nodes of ESCC, gains of 8q, 3q and 5p and loss of 3p, 8p, 9q and 13q were specifically implicated in ESCC in Linzhou population. Gains of 6p and 20p and loss of 10pq may contribute to the lymph node metastasis of ESCC. These findings suggest that the gains and losses of chromosomal regions may contain ESCC-related oncogenes and tumor suppressor genes and provide important theoretic information for identifying and cloning novel ESCC-related oncogenes and tumor suppressor genes.

INTRODUCTION

Advances in diagnostic and therapeutic modalities for malignancies have improved the survival of cancer patients. However, the mortality rate of patients with esophageal squamous cell carcinoma (ESCC) is still very high due to its highly invasive nature and potential to metastasize to lymph nodes and distant organs. ESCC is one of the leading causes of cancer-related death

in Linxian, Henan Province in northern China, with a mortality rate of 161/100 000 for male and 103/100 000 for female. Recent studies by us and other authors have indicated multiple genetic alterations underlying the multistage carcinogenesis of ESCC, such as p53-Rb pathway[1]. However, the mechanisms of human esophageal multistage carcinogenesis in this area, especially the difference in genetic changes between primary ESCC and lymph node metastasis, are largely unknown.

Comparative genomic hybridization (CGH) analysis can provide comprehensive information about relative chromosomal losses and gains in malignant tumors *in vitro*[2]. This technique can detect the changes of recurrent copy number and may highlight chromosomal regions containing genes that contribute to cancer development and/or progression. In this study, we used CGH analysis to examine 37 primary ESCC and 15 pairs of primary ESCC tumors and their corresponding metastatic lymph nodes, to elucidate the genetic pathway of carcinogenesis and to clarify the metastatic mechanisms of genetic aberrations in ESCC.

MATERIALS AND METHODS

The 37 primary tumor samples and 15 pairs of primary ESCC and their matched lymph node metastasis in this study were all from Linzhou, Henan, the high incidence area for ESCC. The primary specimen for each patient was collected at the time of surgical resection at the Department of Surgery, Yiaochun Hospital and Linzhou Hospital. All the patients underwent esophagectomy without preoperative radiotherapy and/or chemotherapy. Tumor tissue specimens were frozen in liquid nitrogen and kept in a freezer at -80℃ until use.

Microdissection and DNA extraction
Tumor tissue was selected by histopathologic examination on the basis of estimated more than 80% cancer cells. The metastatic lymph nodes were embedded in OTC and cryosected into 15 μm serial slides under -20℃. For DNA extraction, we cut 22 serial 15 μm sections. The first and last ones were used for hematoxylin-eosin (HE) staining, and the remain 20 were lightly stained with hematoxylin. Under microscopic (MZ 12, Leica, Bensheim, Germany) observation, tumor tissues were microdissected manually from surrounding stromal tissues and normal cells with a disposable fine needle, and tissue fragments were collected and transferred into a microtube.

Genomic DNA was extracted from tumor specimens by proteinase K/sodium dodecyl sulfate digestion followed by phenol/chloroform/alcohol extraction. Normal reference DNA was prepared from peripheral blood lymphocytes of healthy donors.

Slide preparation
Metaphase chromosome spreads were prepared from peripheral blood leukocytes of healthy donors. Blood cells were cultured for 72 h in RPMI1640 containing 15% fetal bovine serum and penicillin-streptomycin (PHA 5 μg/mL). Blood cells were harvested by arresting with Colcemid

(0.05 g/L) for 1h, followed by hypotonic treatment in KCl (0.075 mmol/L) for 20 min on ice and fixation in cold methanol: acetic acid (3:1).

Comparative genomic hybridization(CGH)
CGH was performed essentially as described previously[2]. Briefly, genomic DNA from a tumor sample and a sex-matched normal reference was labeled directly with Spectrum Green-dUTP and SpectrumRed-dUTP (Vysis, Downers Grove, IL, USA) by nick translation. Two hundred nanograms of labeled tumor DNA and normal DNA probes were used in a 10 μL hybridization mixture (containing 55% formamide, 2 × SSC), and 10 μg human CotI DNA, which was denatured at 75℃ for 5 min. The slide containing normal metaphase spreads was treated with RNase (100 mg/L) at 37℃ for 1 h and then denatured at 75℃ in 70% formamide, and 2 × SSC for 5 min. Hybridization with probes was then carried out at 37℃ in a moist chamber for 72 h. The slide was then washed in 0.4 × SSC/0.3% NP-40 at 75℃ for 2 min and then in 2 × SSC/0.1% NP-40 at room temperature for 2 min. After washing, the slide was counterstained with 1 mg/L DAPI in an antifade solution.

Digital image analysis
The hybridized metaphase chromosomes were analyzed using a digital image analysis system containing a Zeiss Axiophot microscope equipped with a Metachrome Ⅱ cool-charged device camera (Photometics, AZ). Three images of each metaphase were captured using filter wheel-mounted, single band excitation Rhodamine, FITC, and DAPI filters. The image analyses were carried out using Quips CGH Analysis software (Vysis). Five metaphases were analyzed to generate fluorescence ratio profiles in each case. Interpretation of the profiles was performed according to the program guidelines. The thresholds used for interpretation of gains and losses of a DNA sequence copy number was defined as a tumor/reference ratio greater than 1.25 or less than 0.75, respectively, by both the standard and the reverse hybridization methods.

Statistical analysis
We analyzed the genetic aberrations of ESCC using the Fisher exact test for independence. Differences with a *P* value less than 0.05 were considered statistically significant.

RESULTS

CGH analysis
A total of 230 DNA copy number gains and 212 DNA copy number losses were found in 37 ESCC samples, with an average of DNA copy number gains of 6.22 and DNA copy number losses of 5.73 per patient. In ESCC, the gain was most frequently detected on chromosome arms 8q (29/37, 78%), 3q (24/37, 65%) and 5p (19/37, 51%), (the chromosomal aberrant frequency on chromosome 6q, 7p and 7q was similar, all 38%), which was followed by (from high to low) 18p (12/37, 32%), 1q (11/37, 30%), 11q (10/37, 27%), 20q (10/37, 27%), 12p (9/37, 24%), 13q (6/37, 16%) and 18q (6/37, 16%). There were 20 cases

Table 1 CGH results of 37 ESCC cases, Linzhou, Henan

Case No.	Gains	Losses
66 908	5p, 10q11-10q21	3p21-3p11, 9,10q23-10qter, 15
66 865	1p31-1qter, 3q, 3q22-3qter, 5p, 6q15-6qter, 7p14-7qter, 8q13-qter, 18p	4pter-4p13, 9q, 5q11-14, 11p, 18q12-18qter
66 867	3q, 5pter-5q12, 6p12-6q12, 7p12-7qter, 8q, 16	3pter-3p13, 4q23-4qter, 8p, 9,11p13-11qter, 13,17p, Xp
66 909	3q, 5p, 7,8q12-8qter,	9p13-9qter, 19
66 755	1q, 2p, 3q, 8q, 9p, 11q13-11q21	1pter-1p31, 3pter-3p13, 8p, 11q22-11qter, 15,16,17,19,21,22
16 182	4p13-4qter, 8p12-8qter, 9p, 16p11-16qter, 16p11-16q21, 18p	1pter-1p32, 3p, 4pter-p14, 11q22-11qter, 18q, 19
66 907	2q14.1-14.3, 2q31-32, 3q23-3qter, 5p, 6q, 7p, 8,12p, 18p	3p, 4,5q, 10,11q21-qter, 12q, 17p, Xp
66 912	2q14-2qter, 3q22-3qter, 5p, 6p12-6q15, 8q, 12q11-12q22, 13,20q	1pter-1p31, 5q, 11pter-11q12, 16,17p, 19
66 910	6p21-6q13, 7q11-7q31, 8q, 13	1pter-1p31, 8p, 16q
66 948	2p, 3q, 3q22-3qter, 7,8q, 10p, 14,16q11-12	1pter-1p31, 3p, 6q, 8p, 11q14-11qter, 13,19,21
16 146	3q, 5pter-5q12, 6p21-6q12, 7q21-7q22, 8q, 17q, 18pter-18q11	8p, 9q, 16,18q12-18qter
16 634	3p12-3qter, 5pter-5q12, 7q21-7qter, 8q, 12p, 18p, 20,20p	1pter-1p33, 4pter-4p15, 9,11pter-11q12, 13,16q, 17,18q, 19p, 21,22
16 179	1q, 3q, 3q22-3qter, 4p13-4q21, 5p, 6p, 7, 8q, 13	1pter-1p31, 3p, 5q, 8p, 9,10,14,19,Y
16 601	5p, 8p12-8qter,Y	3p, 19
16 605	6p, 8q, 11q11-11q21, 14,16pter-16q22, 17p, 20p11-20q13, 22	11q22-11qter, 18q12-18qter
16 609	1q, 2,3q, 3q22-3qter, 5p, 8q, 11p13-11q21, 12p, 13q21-13qter, 16q12-16qter	1p, 3p, 4,5q, 8p, 9p, 10,12q, 18p11-18qter, 21, Xp
16 610	3q, 7p, 8q, 12p12-12q23, 16p11-16q21, 18	1pter-1p31, 8pter-8p12, 11,17,19,Y
16 615	1q31-1qter, 2pter-2q33, 3q13-3qter, 4q12-4q21, 5p, 7q21-7q31, 8q22-8qter, 12,18p	2q34-2qter, 5q13-5q14, 7p11-7q11, 8p, 9,22, X
16 616	6p21-6qter, 7pter-7q21, 8p12-8qter, 10,14	7q22-7qter
16 629	1p32-1p21, 2q11-2q32, 3q22-3qter, 6p, 8q, 9p, 11p, 12q14-12q22, 18,20	2q33-2qter, 6q, 8p, 9q, 10q, 11q, 13,16, X
16 639	1p31-1p13, 3q13-3qter, 11q13-q23, 12pter-12q13, 14	3pter-13, 4pter-12, 5q21-qter, 21,22, Xpter-q13
16 658	3q, 4pter-4q13, 5p, 6p12-6q14, 8q	3p, 8p, 9q21-9qter, 11,19
16 721	1p11-1q22, 7pter-7q31, 14q21-14q23, 19,20	2p, 3p, 5q12-5qter, 6q, 11p, Y
16 740	5p13-5q13, 18pter-18q12	6pter-6p21, 14q13-14qter
19 110	1q21-1qter, 2q, 6,7p, 11p, 11q13-q22, 14, 16p13-16p11	1pter-1p34, 8pter-8q12, 8q23-8qter, 15q22-15qter, 16q, 17, 22
19 315	6p12-6q14, 13,16q11-16q21, 18pter-18q12	1p13-22, 3pter-q21, 8pter-12, 18q21-qter, X
19 419	2q24-2q32, 3q, 8,13,20	3p, 9p22-9q21, 10,16p, 17
16 172	8q22-8qter	13
16 181	3q13-3qter, 7,8,12,17,18p, 20,22	2q14-2q34, 3p, 4q, 5q11-q23, 6q11-24, 13
16 186	3p12-3qter, 5p, 6p21-6q15, 7, 8q, 11p14-11q14, 16,17pter-17q12, 20pter-20q11	13,18q
16 604	1p31-1qter, 3q, 4p12-4q12, 6, 7,8p22-8qter, 10pter-10q11, 11q12-11q23, 14q11-14q31	2pter-2q22, 3p, 5q21-5qter, 9p12-9qter, 13,15,17,18
16 624	1pter-1p31, 3pter-3p21, 3q, 5p, 6p21-6p12, 7p, 8q, 11,18pter-18q12, 19p13-19qter, 20	2p, 3p21-3p11, 4,5q, 8p, 10,14,16q, Y
16 633	8q22-23, 9,12p11-12q21, 21,X	3p, 6,10,11p, 12q21-12qter, 16q23-16qter, 18q,
16 632	1q, 2pter-q32, 3p12-qter, 5pter-q12, 8p22-qter, 9q, 11, 12pter-q13, 15, 16p12-q21, 17p12-q24, 18pter-q12	3pter-3p13, 4,10,13
16 624	3q, 3q22-3qter, 5p, 11p11-11q13	3pter-3p12, 11q14-11qter, 13,18, X
16 625	1q, 3q, 4p14-4q21, 4q26-4qter, 19p11-19q13	1pter-1p319q33-9qter, 15,16,17p
66 945	1p31-1qter, 3q, 5p, 6q14-6qter, 8q12-8qter, 9pter-9q31	3p, 4,5q, 9q31-9qter, 11,13,14

with high copy number amplifications (tumor/reference ratio > 1.5), which were located on chromosome 1pter-1p31, 1p11-1q22, 3q22-qter, 4p13-4q31, 5p, 6p12-6q14, 8q, 9p, 11q12-11q23, 11q13-11q23, 16p11-16q21, 18pter-18q12, 18p and 20p. The chromosomal profile of DNA copy number losses was characterized as follows: the most frequently detected loss was on 3p (21/37, 57%), which was followed in turn (from high to low) by 8p (14/37, 38%), 9q (14/37, 38%), 11q (13/37, 35%), 13q (13/37, 35%), 5q (12/37, 32%), 1p (12/37, 32%), 4p (11/37, 30%), 18q (11/37, 30%), 16q (10/37, 27%), 17p (10/37, 27%) and 19p (10/37, 27%). A summary of genetic aberrations detected by CGH in ESCC is provided in Table 1 and Figure 1.

Differences in copy number alterations between 15 pairs of primary ESCC and their matched lymph node metastasis

A total of 102 gains and 90 losses were found in 15 primary ESCC samples, with an average of gains and losses per patient of 6.8 and 6.0, respectively, and 110 gains and 142 losses were found in 15 lymph nodes metastasis samples, with an average of gains and losses per patient

of 7.4 and 9.5. More genetic changes (252) were found in lymph nodes metastasis than in the corresponding primary lesions (192), especially the losses (9.5/case *vs* 6.0/case). The copy-number changes for the entire genome detected in these 15 primary ESCC and their corresponding metastatic lesions are summarized in Table 2 and Figure 2. In primary tumors, the most frequently detected sites of chromosome gain were 3q (15 of 15, 100%), 8q (11 of 15, 73%), 1q (11 of 15, 73%), 12p (8 of 15, 53%), 18p (6 of 15, 40%), 5p (7 of 15, 47%), 6p (7 of 15, 47%), 20p (11 of 15, 73%). In metastatic lymph nodes, the most frequently detected sites of chromosome gain were 3q (14 of 15, 93%), 8q (10 of 15, 67%), 1q (11 of 15, 73%), 12p (8 of 15, 53%), 18p (6 of 15, 40%), 5p (7 of 15, 47%), 6p (7 of 15, 47%), 20p (11 of 15, 73%). High copy-number amplification with a minimum gain 3q24-qter was detected in two primary tumors and six metastatic lymph nodes. The other three high copy-number amplifications of 6p21-6q12 were detected only in metastatic lymph nodes but not in their corresponding primary tumors. The high copy-number amplification of 20p was detected in metastatic lymph node lesions but not in their corresponding primary tumor. In primary tumors, the chromosomal profile of
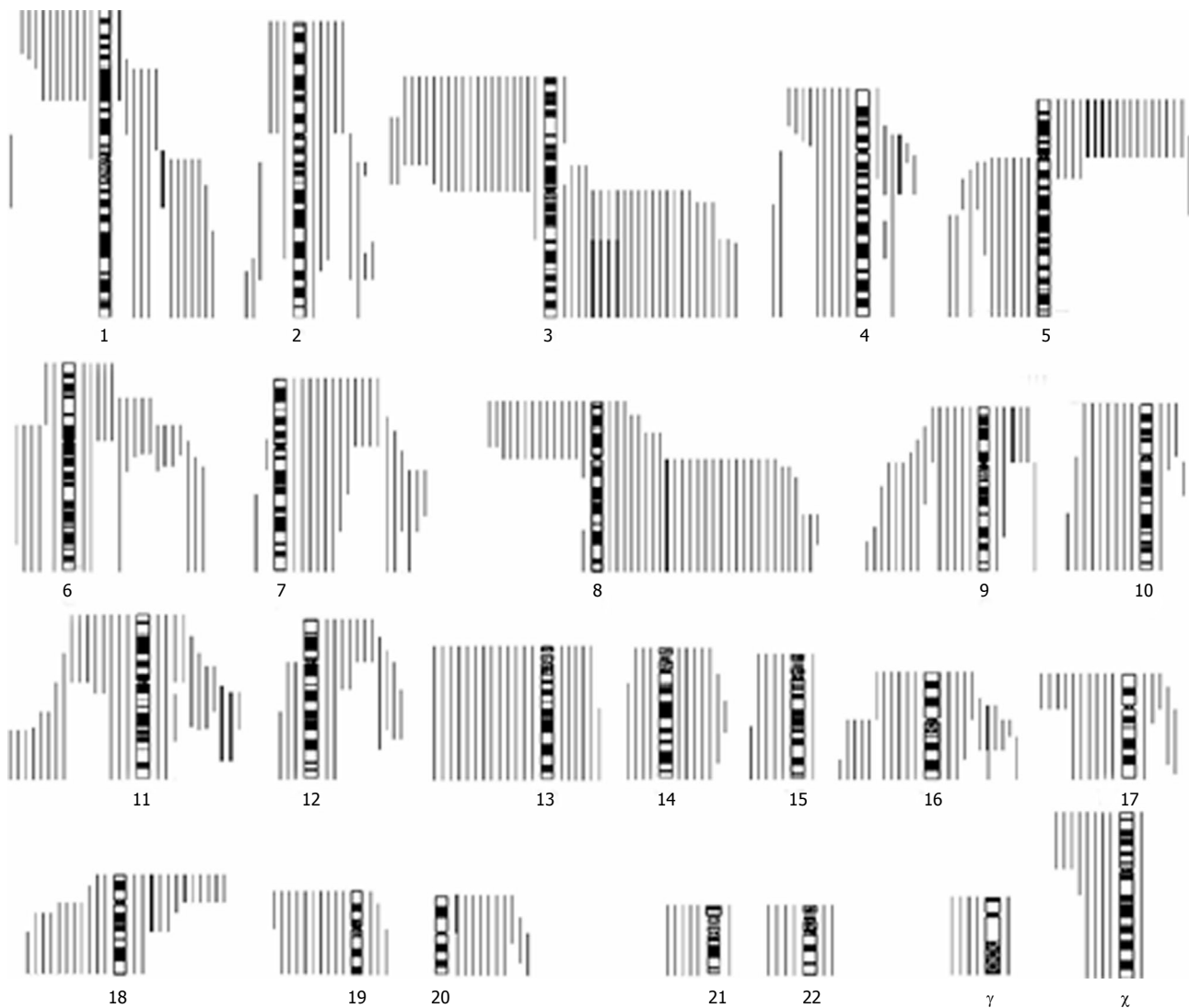
Figure 1 Copy number alterations of 37 ESCC cases analyzed by CGH. Chromosomal regions of gain are on the right side of the chromosome ideograms, and regions of loss are on the left side.

DNA copy number losses were 3p (10 of 15, 67%), 10p (2 of 15, 13%), 10q (2 of 15, 13%), 4q (6 of 15, 40%), 4p (7 of 15, 47%), 19p (8 of 15, 53%), 13q (4 of 15), 1p (7 of 15), 17p and 18q (4 of 15, 27%). In metastatic lymph nodes, the chromosomal profiles of DNA copy number losses were 3p (12 of 15, 80%), 10p (8 of 15, 53%), 10q (7 of 15, 47%), 4q (10 of 15, 67%), 4p (9 of 15, 60%), 19p (10 of 15, 67%), 13q (8 of 15, 53%), 1p (7 of 15, 47%), 17p and 18q (7 of 15, 47%).

Statistically, in DNA copy number gains on chromosome 6p and 20p, there were significant differences between primary ESCC lesions and their corresponding lymph nodes (*P* < 0.05). In DNA copy number losses on chromosome 10pq, differences were significant between primary ESCC lesions and their corresponding lymph nodes (*P* < 0.05), (Table 3).

DISCUSSION

We have identified a genome-wide map of genetic alterations in ESCC, and compared primary tumor and metastatic lymph nodes in this study. The majority of the chromosomal aberrations in both primary tumor and metastatic lymph node lesions were consistent with the previous reports. For example, the gains of 3q, 5p, 8q23-ter and 20q and deletions of 3p25, 4p, 6q21, 9q22.3-q31, 9p, 11q22-qter, 13q12-13, 18q22.3, and 19q had been detected as frequent chromosomal alterations in ESCC in at least one of the previous CGH studies[3-6]. By comparing the primary ESCC with metastatic lymph nodes, we did detect new candidate regions of interest, such as 6p, 20p and 10pq, which may harbor the genes involved in lymph node metastasis.

The highest frequency of DNA gain in ESCC occurred at chromosome 8q (78%), the chromosomal region at 8q harbors MYCC gene (8q24.1) which has been identified with a high frequency of amplification in ESCC[7,8]. Gains of 3q were commonly seen in ESCC [9]. Possible candidate genes involved in tumor development include the genes for ribosomal protein L22 (RPL22), butyrylcholinesterase (BCHE), glucose transporter 2 (SLC2A2), transferring receptor (TFRC), thrombopoietin (THPO) and the phosphatidylinositol-3 kinase catalytic α-polypeptide (PIK3CA). Deletion of 9p and gain of 5p were seen

Table 2 CGH results of lymph node metastasis, Linzhou, Henan

Case No.	Gains	Losses
16148	2p12-2q32, 3p12-3qter, 5p, 9q	3pter-3p13, 5q31-5qter,X
L16148	1q, 2q11-2q31, 3q, 5p, 9p12-9qter, 12,20	2q32-2qter, 3p, 4,5q, 6pter-6p22, 19,X
16668	3q13-3qter, 4q31-4qter, 7pter-1p11, 8q12-8qter, 18p	1p, 4pter-4p14, 4q21-4q28, 7q22-7qter, 9p
L16668	3q, 4p12-4q13, 7p15-7q22, 8p21-8qter, 13,15pter-15q15, 18pter-18q12, 20pter-20q12	3p, 4pter-4p13, 4q13-4q25, 7q31-7qter, 9p, 11q13-11qter
16669	3p12-3qter, 7p, 8q, 12pter-12q13, 14	1p, 3pter-3p12, 4p, 10,11,17,19
L16669	3p12-3qter, 6p12-6q14, 7p, 8p12-8qter, 14,20p11-20qter	1p, 3pter-3p12, 4p, 10,11,19
16v688	1q21-1qter, 3q, 5p, 6p12-6q24, 7q11-31, 8p22-8q23, 11q, 11q11-11q14, 18pter-18q12	3p, 4q13-4qter, 6pter-6p21, 7q32-7qter, 9p12-9qter, 10p, 11p, 16q, 17pter-17p11, 17q22-17qter, 19
L16688	1p13-1qter, 1p13-1q21, 2,3q, 6p21-6q12, 8q11-8q23, 11q, 11q11-11q14, 12p, 18pter-18q11, 18p11-18q11, 20	3p, 4,5pter-5q15, 6pter-6p21, 6q16-6qter, 7p, 7q31-7qter, 8pter-8p12, 9q, 10p, 11p, 13,17p, 17q22-17qter, 19,21
16691	1q, 2pter-2q21, 3q, 11q11-11q13, 13q14-13qter, 16q11-16q13, 17q21.1-21.3, 20	3p, 8q11-8q22, 9q, 11q14-11qter, 13pter-13q14, 16p, 19,21,22
L16691	1q, 2pter-2q21, 3q, 11q11-11q13, 13q14.3-13qter, 16q11-16q13, 17q21.1-17q21.3, 20	1pter-1p32, 3p, 8q11-8q22, 9q, 11q14-11qter, 13pter-13q14.2, 16p, 17p, 19,21,22
16670	3q, 8q, 12p, 14,16p11-16q21, 18p, 20	1pter-1p31, 9p12-9qter, 17,18q, 19,Y
L16670	3q, 8q, 12p, 14,18p, 20	1pter-1p34, 3pter-3p13, 9q, 10,11p11-11q12, 17,19p,Y
16710	1p33-1qter, 2pter-2q32, 3p13-3qter, 5pter-5q12, 6q16-6qter, 7p, 11q11-11q23, 12pter-12q15, 13,16p13-16qter, 17p,	4p, 18pter-18q21
L16710	1q, 2p22-12, 2q22-2q32, 3q, 5p, 6q21-6qter, 7p, 9pter-9p21, 11q11-11q14, 13,16q, 17pter-17q12	1p, 4,6pter-6q16, 8pter-8p12, 10pter-10p12, 10q23-10qter, 11p, 11q14-11qter, 12q, 16p, 18,21
16727	1p13-1q24, 2p24-2p23, 2p14-2p12, 3q13-3qter, 5p, 7q11-7qter, 8q, 12pter-12q12, 14q23-14qter, 18pter-18q12, 20	1p, 2q32-2qter, 3pter-3p21, 4,5q, 8p, 11p, 18q12-qter
L16727	1q, 2p14-2p11, 3q13-3qter, 5p, 7q11-7qter, 8q, 12pter-12q13, 14,17q, 18p, 20p	1p, 2q32-2qter, 3p, 4,5q, 9p, 10p, 11p, 15pter-15q22, 18q12-18qter, 21
16728	3q, 8p12-8qter, 11p11-11q14, 12pter-12q12, 16p, 18pter-18q12, 20	3p,Xp
L16728	1p21-1pter, 3q, 3q24-3qter, 7p12-7q22, 8q, 8q21-8qter, 12p12-12q12, 14q11-14q21, 20p	4q, 8pter-8p22, 10,11,13q12-13q31, 14q23-14qter, 20q,Xp
16730	1q, 3q, 6,7,8,12pter-12q13, 20q12-20qter	3p, 9p, 16q, 19p13-19q13
L16730	1q, 2,3q, 6,6p21-6q13, 12pter-12q14, 18p11-18q12	1p, 3p, 4q26-4qter, 5q, 9,10,13,16,18q21-18qter, 19p, 21
16731	3q, 4p13-4q13, 16q11-16q12, 11p13-11q13, 12	9,13
L16731	3q, 4p13-4q13, 8p12-8qter	3p21-3p11, 9q, 10,17,18q12-18qter, 19
16738	1q, 3p13-3qter, 5p, 8q	1pter-1p31, 3pter-3p14, 4,11,16,17,19,Xpter-q21
L16738	1p13-1qter, 1p13-1q21, 5pter-5q12, 6p21-6q14, 8q, 20	1pter-1q13, 2pter-2p21, 3p, 4,8p, 11pter-11p12, 11q14-11qter, 13,16p, 17,18, Xpter-q21
16742	1q11-1q24, 3q, 3q24-3qter, 5pter-5q12, 8p11-8qter, 9q, 10p, 12p, 19p12-19q12, 20	1p, 3p, 4,6q16-6qter, 8pter-8p12, 9p, 10q22-10qter, 11,13,14q21-14qter
L16742	1q11-1q24, 2p21-2qter, 3q, 3q22-3qter, 5p13-5q13, 7,8q, 9q21-9q32, 10p12-10q11, 12pter-12q13, 20	1qter-1q32, 3p, 4,6q, 8p, 10q21-10qter, 11,12q21-12qter, 13,14q21-14qter, 19
16745	1q, 2q24-2q33, 3q, 5p, 6q13-6q24, 8,9p, 10pter-10q21, 12q14-12q21	1pter-1p32, 2q21-2q24, 2q34-2qter, 3p, 4,5q, 7q31-7qter, 11q14-11qter, 13pter-13q21, 16,18,19,21
L16745	1q, 2q24-2q35, 3q, 5p, 6p21-6q25, 8	2q21-2q24, 2q34-2qter, 3p, 4,5q, 7q31-7qter, 11q14-11qter, 13pter-13q21, 16,18,19,21
16770	3p12-3qter, 8p12-8qter	17p, 19p, 22
L16770	3q, 6p, 16p11-16q21, 18p, 20	11,13,17p, 18q, 19p, 22

commonly in CGH studies of patients with ESCC[3-5,9] and both are related to the progression of ESCC[10,11]. hTERT on 5p is associated with the prognosis of patients with carcinomas of the breast, lung and ESCC as reported previously [10,12,13]. One of the potential candidate genes in the region includes JS-1 and JK-1[13].

Deletion of chromosome 3p is one of the most frequent allelic imbalances in ESCC detected by CGH[3,4]. In our study, loss of 3p was detected in 65% in ESCC. Possible candidate tumor suppressor genes on these region were FHIT (fragile histidine triad)[15], catenin (CTNNB1)[16], and von Hippel-landau gene[17]. Our results of proximal 3p loss mainly in ESSC may indicate a specific tumor suppressor gene at this locus involved in ESSC in high-risk areas. Loss of 8p was found in 38% of ESCC cases. Deletion of 8p22-pter has been reported in patients with ESCC[5]. Mutations of the Fasciculation and elongation protein zeta-1 (FEZ1) gene at 8p22 were found in patients with ESCC[18], and mutations of two other genes in these regions, tumor necrosis factor-

related apoptosis-inducing ligand receptor 1 (TRAIL-R1) and receptor 2 (TRAIL-R2), were found in patients with metastatic breast carcinoma[19]. Loss of 17p was detected in 37% of ESCC. One potentially relevant gene at 17p is TP53, whose product contributes to the control of cell proliferation and malignant transformation. Inactivation of TP53 is the most common defect found in human cancer including ESCC from Henan, China. Loss of 1p occurred in 32%. The minimal common region of deletion encompasses the most distal band 1p36-pter in ESCC. Loss of chromosome band 1p36 is frequently found in many malignancies, including gastric cardia carcinoma, colon cancer, and ESCC[20].

In 15 pairs of ESCC and their corresponding metastatic lymph nodes, the most interesting finding in this study is the gain of 6p12-6q21 detected in seven metastatic lymph node lesions but only in two corresponding primary tumors (13% vs 47%; P = 0.05). This suggests that 6p may harbor a putative oncogene that plays an important role in the ESCC progression, especially in the lymph
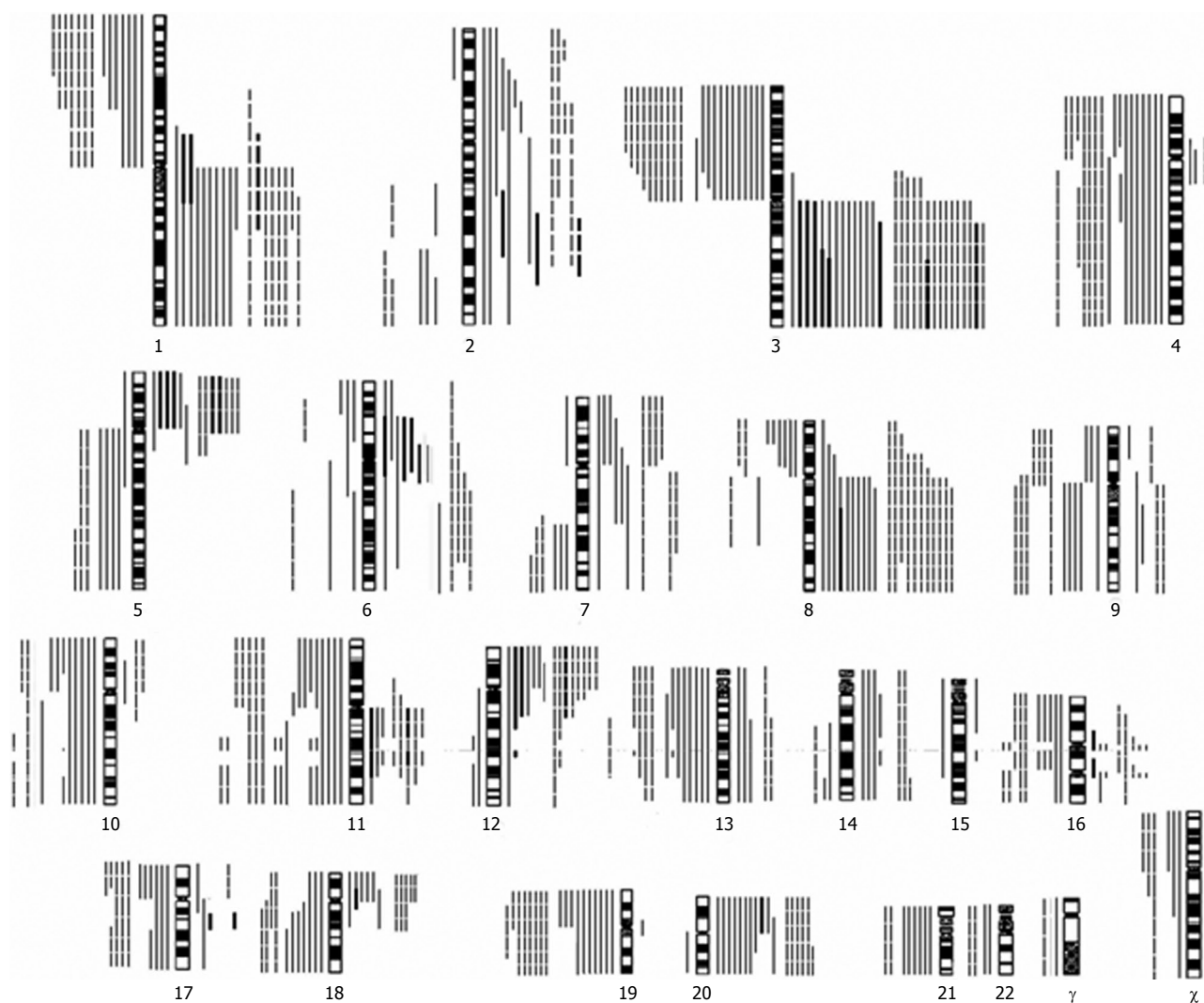
Figure 2 Copy number gains and losses in ESCC by CGH. Chromosomal localization of gains is on the right side of chromosome ideograms and that of losses are on the left side. Thick lines indicate amplified regions. Straight lines indicate lymph nodes metastasis. Conversely primary tumors are indicated by dotted lines.

node metastasis. One study shows that regions 6p12-q14 harbor the CCND3 gene, which shares 53.1% homology to CCND1. The CCND1 gene is amplified in 30% of ESCC[21]. Regions of 6p12 are found to harbor runt-related transcription factor (RUNX) gene, which is associated with cell migration and invasion[22]. The gain of 6p is frequently detected in CGH studies in other tumors including uveal melanoma and Barrett's adenocarcinoma[23,24]. Most interestingly, in three cases, the high-level amplification of 6p12 was detected only in metastatic tumors. This implies that the overexpression of an oncogene(s) at 6p12 confers a selective advantage in ESCC. Moreover, this finding provides a candidate minimum amplification region at 6p12 for further studies and gene cloning. Another interesting finding in this study is the gain of 20p that was detected in 11 metastatic lymph node lesions but only in five corresponding primary tumors. The difference is significant in 20p gain between primary tumors and their metastatic lymph node lesions of ESCC (40% *vs* 73%, $P = 0.03$). This suggests that 20p may harbor an oncogene and play an important part in ESCC progression especially in lymph node metastasis. Little is known about the relationship between 20p and the lymph node metastasis

Table 3 Chromosomal aberrations with primary ESCC and lymph node metastasis

Chromosomal changes	Primary tumor (%)	Lymph node metastasis %	*P* value
Gain of 6p	2/15 (13)	7/15 (47)	0.05
Gain of 20p	5/15 (40)	11/15 (73)	0.03
Loss of 10p	2/15 (13)	8/15 (53)	0.05
Loss of 10q	2/15 (13)	7/15 (47)	0.05

of ESCC. Heselmeyer *et al* demonstrated that gains of 6p and 20p were connected with advanced-stage cervical carcinomas[25]. Hu *et al* demonstrated the over-expression of CDC25B gene in ESCC[26]. Possible candidate gene on 20p includes CDC25B and proliferating cell nuclear antigen (PCNA), each of which plays an important role at specific stages of cell cycle progression.

Loss of 10p was seen in eight metastatic lymph nodes but only in two corresponding primary tumors. The difference between primary tumors and their metastatic lymph node lesions of ESCC was significant (13% *vs* 53% $P = 0.05$). Loss of 10q was detected in seven metastatic lymph nodes but only in two corresponding primary

tumors. The difference between primary tumors and their metastatic lymph node lesions of ESCC was significant (13% *vs* 47% *P* = 0.05). These alterations had also been found in other carcinoma metastases, such as the head-neck squamous cell carcinoma (HNSCC)[27] and Spitzoid malignant melanoma[28]. A role of the 10q deletion in tumor progression is however conceivable since additional germline mutations in the PTEN gene (on chromosome 10q23) have been shown to be present in Crowden's disease[29].

In this study, more genetic changes were found in lymph node metastasis than in their corresponding primary lesions, especially the losses (9.5/case *vs* 6.0/case). Previous studies showed that DNA copy number losses were more common in the metastases than in the primary larynx tumors and HNSCC[30,31]. In ESCC, DNA losses seem to be more closely associated with metastases than DNA amplification.

In conclusion, using the CGH technique to detect chromosomal aberrations in both the primary tumor and its metastatic lymph nodes of ESCC, gains of 8q, 3q, 5p and losses of 3p, 8p, 9q and 13q were specifically implicated in ESCC in Linzhou population. Furthermore, gains of 6p, 20p and loss of 10pq may contribute to the lymph metastasis of ESCC. These findings suggest that the gains and losses of chromosomal regions may contain ESCC-related oncogenes and tumor suppressor genes. The gains and losses of chromosomal regions identified in this study provide important theoretic information for identifying and cloning novel ESCC-related oncogenes and tumor suppressor genes. Finally, this study provides a practicable model to detect specific genetic change related to tumor metastasis by comparing the primary tumor with its corresponding metastatic tumor using the CGH technique.

COMMENTS

Background
Esophageal squamous cell carcinoma (ESCC) is one of the leading causes of cancer-related death in Linxian, Henan Province in northern China, with a mortality rate of 161/100 000 for male and 103/100 000 for female. However, the mechanisms of human esophageal multistage carcinogenesis in this area, especially the difference in genetic changes between primary ESCC and metastatic lymph nodes are largely unknown.

Research frontiers
In this study, the authors applied comparative genomic hybridization (CGH) to ESCC to elucidate genetic aberrations in carcinogenesis and lymph node metastasis. To the knowledge of the authors, though CGH analysis of ESCC has been reported, no information is available concerning the relationship between genetic changes and the biologic characteristics of ESCC. The gains of 3q, 5p, 8q23-ter and 20q and deletions of 3p25, 4p, 6q21, 9q22.3-q31, 9p, 11q22-qter, 13q12-13, 18q22.3, and 19q had been detected as most frequent chromosomal alterations in ESCC. Our CGH results are generally consistent with other CGH studies.

Innovations and breakthroughs
The present CGH study provides the first record of chromosomal imbalances occurring in ESCC tumors and corresponding lymph nodes in Linxian, Henan Province in northern China. The major findings of this paper are that gains of 8q, 3q, 5p and losses of 3p, 8p, 9q and 13q were specifically implicated in ESCC in Linzhou population, and gains of 6p, 20p and loss of 10pq may contribute to the lymph metastasis of ESCC. These loci may harbor the genes in the development and /or progression of ESCC.

Applications
These loci provide important theoretic information for identifying and cloning novel ESCC-related oncogenes and tumor suppressor genes. Further studies are necessary to identify specific genes of these chromosomal regions and their functions. The target tumor susceptibility genes will be further characterized by mutation analysis. Single strand conformation polymorphism (SSCP) and sequencing analysis will be used to screen the mutation.

Terminology
Comparative genomic hybridization (CGH); Single strand conformation polymorphism (SSCP).

Peer review
This is a nicely written and presented paper with 37 cases of primary esophageal cancer and matched metastatic tissues. Although the number of studied cases is small, it is a useful contribution to the literature.

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