Cellular Oncology 26 (2004) 21–29
IOS Press

DNA-ploidy in advanced gastric carcinoma is less heterogeneous than in early gastric cancer

Maria-Chiara Osterheld *, Liette Caron, Mireille Demierre, Ricardo Laurini and F.T. Bosman
Institut Universitaire de Pathologie, Rue du Bugnon 25, 1011 Lausanne, Switzerland

Received 8 August 2003
Accepted 25 September 2003

Abstract. This analysis of DNA-ploidy heterogeneity in advanced gastric carcinomas is consistent with the hypothesis of the emergence of a single aneuploid cell clone as a crucial mechanism in the progression from early gastric carcinoma to advanced gastric cancer.

The prognostic value of DNA-ploidy in gastric cancers has been a matter of controversy. Tumour DNA-ploidy heterogeneity, the presence within the same tumour of multiple stemlines differing in DNA content, has been described in various tumours including gastric cancers. The occurrence of such heterogeneity has been accepted as an explanation for the divergent DNA-ploidy results in this type of tumours.

A previous study of early gastric cancers suggested that in pure diploid superficial carcinomas, genetic instability might lead to a cell clone which has undergone a ploidy shift and is more aggressive. If so, this would initially result in DNA-ploidy heterogeneity. Proliferative dominance of the aneuploid clone could eventually evolve to a homogeneous aneuploid tumour.

In order to test this hypothesis, we studied DNA-aneuploidy and DNA-ploidy heterogeneity in advanced gastric carcinomas. We performed DNA cytophotometry on multiple samples collected from 16 advanced gastric carcinomas and found 15 DNA-aneuploid tumours (94%) and one diploid tumour. Multiple DNA-stemlines were found in 4 cases (26%). Analysis of proliferative activity performed on the same samples revealed higher proliferation rate in DNA-ploidy homogeneous tumours than in aneuploid heterogeneous tumours. Heterogeneous tumours did not overexpress p53. These results confirm that DNA-aneuploidy is frequent in advanced gastric cancer and demonstrate that a majority of these aneuploid tumours are not DNA-ploidy heterogeneous. Furthermore, the higher proliferative activity in homogeneous-aneuploid carcinomas and their more frequent overexpression of p53 support the hypothesis that in gastric cancer tumour progression implies the development of a dominant and more aggressive (higher proliferative activity, p53 overexpression) aneuploid cell clone.

Keywords: Gastric adenocarcinoma, heterogeneity, DNA ploidy, prognostic factors

1. Introduction

Several studies have reported a correlation between DNA-ploidy and prognosis in gastric carcinoma [1,11–13,26,29,34]. Korenaga et al. suggested that DNA-ploidy is a major determinant of survival. Others have indicated that there is no correlation between prognosis and DNA-ploidy [5]. These contrasting results could be explained by intratumoral heterogeneity in DNA-ploidy. The presence of intratumoral heterogeneity in DNA-ploidy is generally accepted, and has been described in various tumours [2,3,6,7,10,14,17–24,30,31,33–35]. Several studies have now been performed on this subject, comparing the DNA content of tumour cell populations in multiple samples of the tumours. DNA-heterogeneity has been estimated to run between 20 to 60% in gastric cancers and 7 to 30% in colorectal carcinomas [7,10,20,30] and to reach 54% in oesophageal carcinomas [35]. Some authors have indicated that DNA content heterogeneity is better correlated to tumour progression in gastric carcinomas than presence of aneuploidy [7,28].

*Corresponding author: Dr. M.C. Osterheld, University Institute of Pathology, Rue du Bugnon 25, 1011 Lausanne, Switzerland. Tel.: +41 21 314 74 11; Fax: +41 21 314 71 15; E-mail: Maria-Chiara.Osterheld@chuv.hospvd.ch.

In a previous study, we determined that ploidy heterogeneity is present in early gastric carcinoma (EGC) and this heterogeneity occurs more frequently in tumours invading the submucosa. This led us to hypothesise that genome instability plays an important role in gastric carcinoma progression [20]. On the basis of these results we considered the possibility that in DNA-diploid early gastric carcinomas, instability of the genome leads to the emergence of aneuploid cell clones, reflected in DNA-ploidy heterogeneity. Overgrowth of a dominant clone during neoplastic progression eventually could lead to DNA-homogeneous aneuploidy.

In order to confirm this hypothesis, a series of advanced gastric carcinomas was analysed for DNA-ploidy. DNA-ploidy heterogeneity was assessed through the analysis of multiple tumour samples. We also studied whether a correlation exists between ploidy and proliferative activity or p53 overexpression.

2. Material and methods

2.1. Material

Sixteen cases of advanced gastric carcinoma (gastric carcinoma with invasion of at least the muscularis propria) diagnosed in gastrectomy specimens obtained between 1993 and 1999 were used for this study. The nine more recent cases underwent histopathological mapping in detail (cartography), which allowed detailed histological analysis of the tumours and measurement of the size (Fig. 1), following the protocol of Mori [15,16]. The other seven cases were routinely sampled. All available gross and histological material was reviewed. For the nine cases with cartography, one of every two blocks was sampled for cytophotometric DNA-ploidy analysis. For cases without systematic cartographic tissue sampling, the number of blocks for the analysis was calculated as a function of the maximal area of the tumour (one block per 1.5 cm^2) depending on the number of available blocks. In addition, one block of normal gastric mucosa was sampled for each case. When a case presented lymph node metastases, metastatic tumour tissue was also sampled. Hematoxylin and eosin stained slides were screened to identify the different layers of the gastric wall. For selective evaluation of DNA-ploidy, the intramucosal, submucosal components, the muscularis propria and subserosa when available, were separately sampled on the corresponding paraffin block by means of a dissecting microscope to account for the depth of infiltration. Overall 176 paraffin blocks were used resulting microdissection in 425 tumour cell samples.

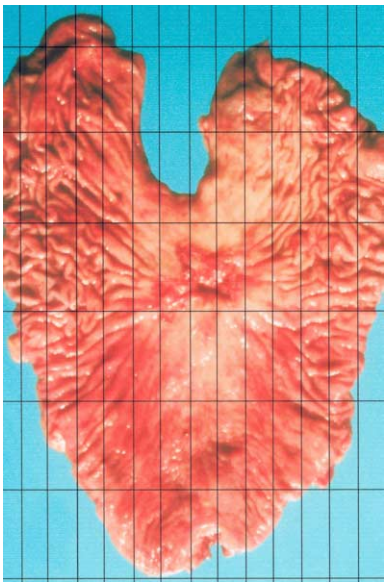

Fig. 1. AGC in the resected specimen prepared for cartography. The lesion is evident in the resected specimen. The tumour containing the surrounding wall was cut into multiple slices parallel to the lesser curvature at interval of 4 to 5 mm.

2.2. DNA-ploidy analysis

All 425 tissue samples were processed following the technique of Hedley, which provided a cytospin of each sample [9]. For Feulgen staining, the cytospins were first hydrolysed in 5 N HCl at 25°C for 45 minutes. The hydrolysis was stopped by rinsing in distilled water. The specimens were then stained with Schiff reagent (Schiff reagent for microscopy, No 1.0933, Merck) for 60 minutes. Sulfite rinse was used. After dehydration in a graded series of alcohols and xylene the cytospins were coverslipped using Eukitt mounting medium. DNA analysis was performed on Feulgen-stained cytospins using an image analysis system (SAMBA, Alcatel TITN Answare, Grenoble, France). A minimum of 200 nuclei was measured per cytospin (300 nuclei for most cases). Only well preserved nuclei were selected by the operator using the gallery program of the SAMBA system. As controls we used 30 to 50 human lymphocytes from a separate slide containing thymus specimen (external reference). At least 6 tissue polymorphonuclear leukocytes were used as internal reference. The coefficient of variation of the DNA index thus measured was below 5%. Histograms exhibiting a G0/1 main peak at 2C were considered to be diploid. DNA index (the mean nuclear DNA content of the G0/1 compartment of a cell population divided by the DNA content of the G0/1 compartment of a similarly

processed group of known diploid cells) for diploidy ranged between 0.85 and 1.15. Considering that in normal tissues and most low-grade or slowly proliferating neoplasms, approximately 85% of the cell population constitute the G0/1 peak and 15% of the cells are in the S-phase and G2/M phases, we only considered as aneuploid the samples in which more than 15% of the cells had a DNA-index in excess of 1.15 [4,20,25]. A sample was considered tetraploid when more than 15% of the cells had a DNA index between 1.70 and 2.30. Similarly, sample was classified as triploid when the main peak had a DNA-index between 1.3 and 1.70. All other samples displaying more than 15% of cells with a DNA-index over 1.15 including single cells with DNA content above the highest possible G2M-region but not corresponding to a defined peak were considered as a cell population with an abnormal content of DNA arbitrary designated hyperploid (Fig. 2). For statistical purposes the tumours were classified into two groups, diploid and non-diploid (aneuploid).

A tumour was considered diploid when all the samples were diploid. A tumour was considered aneuploid when at least one sample was aneuploid (heterogeneous) or all samples were aneuploid (homogeneous). This resulted in different patterns: diploid, aneuploid heterogeneous (Fig. 3) and aneuploid homogeneous (Fig. 4). We assigned a main DNA-ploidy pattern for each case according to the predominant DNA-ploidy pattern.

2.3. Immunohistochemistry

Immunohistochemical analysis was performed on parallel tissue sections, collected from all the blocks before microdissection, using the Mib-1 antibody (1 : 50), for Ki-67 and the D0-7 antibody (1 : 400) for p53.

After deparaffinization and rehydration, the 4 μm sections were treated with 0.5% H_2O_2 in methanol for 10 min to inhibit endogeneous peroxidase. Depending on the antibody, antigen retrieval was performed and the sections were preincubated for 15 min in phosphate buffer saline (PBS) containing 5% albumin from bovine serum (BSA) and then incubated with the relevant antibody at room temperature for 60 min, washed with PBS and subsequently incubated with the second biotinylated antibody at RT for 30 min. Antibody binding was revealed using the streptavidin–biotin-complex-peroxidase (Dako) for 30 min at RT. Sections were then reacted for 10 min in diaminobenzidine tetrahydrochloride dihydrate (DAB) solution, washed in running water, counterstained with hemalun and mounted. The negative control consisted of omission of the primary antibody.

Proliferative activity was established through the Ki-67 (Mib1) labeling index and computer analysis (Immunoquic system, Zeiss). Multiple microscopic fields (200×) of each tumour were analysed. The account from the field with the highest proliferative activity was taken for statistical analysis.

p53 staining results were read semiquantitatively by two independent observers. Samples were classified into two categories according to a distribution proposed by Symmans [32]. The first group comprised the cases without or with rare p53 positive cells (negative), and those with a low proportion of positively stained nuclei (less then 50% positive cells); the second group was formed by cases displaying a high proportion of positively stained nuclei (more than 50% of positive cells).

2.4. Statistical analysis

Possible correlations between DNA-ploidy, intratumoral DNA-ploidy heterogeneity and histological type of tumour, depth of invasion, TNM stage, proliferative activity and p53 overexpression were analysed by means of the Fischer's exact test. A p value of less than 0.05 was considered statistically significant.

3. Results

We studied 16 patients (9 women and 7 men) with an average age at gastrectomy of 65.5 years. The histological pattern for each tumour was determined according to the WHO classification. The depth of infiltration was classified according to the TNM system (Classification of malignant tumours, fifth edition, 1997). The cases are summarized in Table 1.

14 tumours out of 16 were poorly differentiated (grade 3), 1 was moderately differentiated (grade 2) and 1 well differentiated (grade 1). Six were of the intestinal type and 9 of the diffuse type. One tumour showed a mixed type. Only two tumours were free of lymph node metastases; most displayed one or more metastatic lymph nodes (2N0; 6N1, 5N2, 3N3). Seven carcinomas were limited to the muscularis propria (7T2); seven invaded the serosa (7T3) and two extended to the adjacent structures (2T4). The surface area of the tumours varied between 3 × 2.5 and 15 × 17 cm.

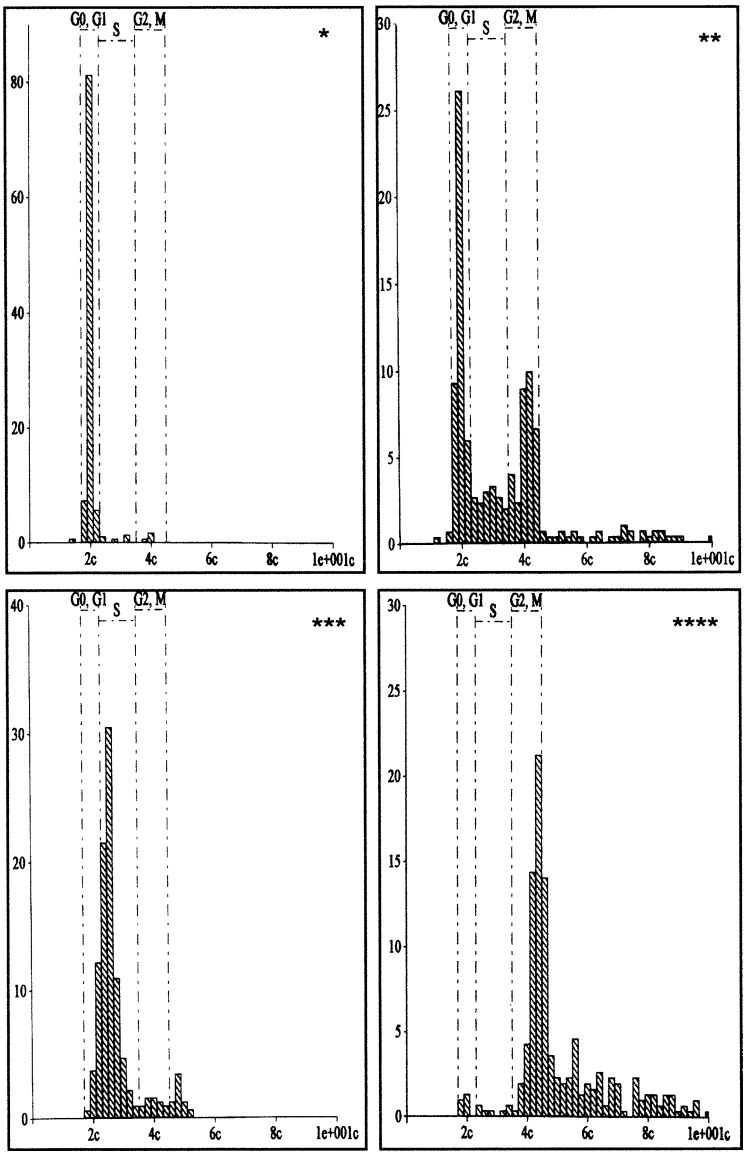

Fig. 2. Histograms illustrating intratumoral DNA-ploidy different results: *a diploid case, **an aneuploid hyperdiploid case, ***an aneuploid triploid case and ****an aneuploid tetraploid case.

Fifteen tumours were aneuploid (94%), only one was diploid. Of the aneuploid tumours 7 were hyperploid, 6 triploid and 2 tetraploid. Four tumours were heterogeneous; all were diffuse carcinomas. The lymph node metastases found in three heterogeneous aneuploid cases were diploid in 12 lymph nodes and aneuploid in 2 lymph nodes. Lymph node metastases from all other (homogeneously aneuploid) cases were aneuploid.

Regarding p53 immunohistochemistry, 7 tumours showed more than 50% positive cells and 9 cases presented less than 50% of positive cells. The 4 ploidy heterogeneous cases showed a low proportion of p53 positive nuclei. Of the 11 ploidy homogeneous cases, 7 cases showed a high proportion of p53 positive cells; this difference was statistically significant ($p = 0.05$, Table 2).

Proliferative activity according to the Ki-67 labeling index was lower than 50% in the diploid tumour and in 3 of the 4 ploidy heterogeneous tumours. Of the ploidy homogeneous tumours only one had a labeling index lower than 50%; this difference was statistically significant ($p = 0.03$; Table 3).

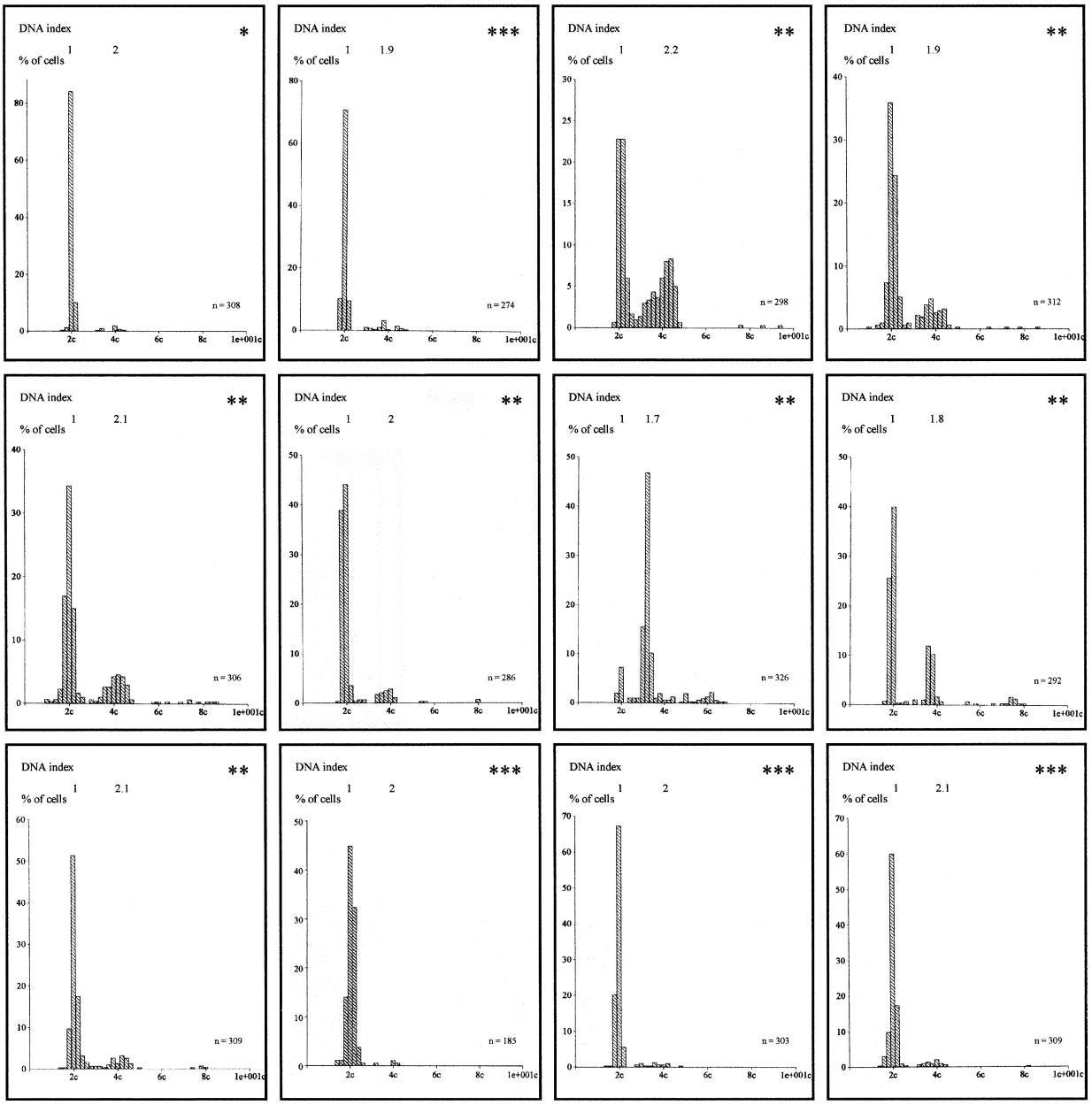

Fig. 3. Histograms illustrating a DNA-ploidy heterogeneous gastric carcinoma: *normal mucosa (diploid), **tumoral sample showing an aneuploid histogram, ***tumoral sample showing a diploid histogram. n = number of cells analyzed.

4. Discussion

The malignant potential of many different tumours has been correlated with DNA ploidy: aneuploid tumours tend to be more aggressive than diploid tumours [3,7,10,14,17–24,27,28,30,31,33,35]. Several authors have reported that DNA-ploidy status has prognostic value in gastric cancer [1,11–13,26,29]. Other studies have shown no correlation between clinicopathological findings or therapy response and DNA-ploidy status [5]. One mechanism responsible for these inconsistencies could be a sampling error due to the presence of ploidy status heterogeneity between different subpopulations of cells in one tumour. In fact, heterogeneous DNA-ploidy, the existence of multiple stemlines differing in DNA content, has been found in 20–60% of gastric cancers [7,10,20,30] and furthermore

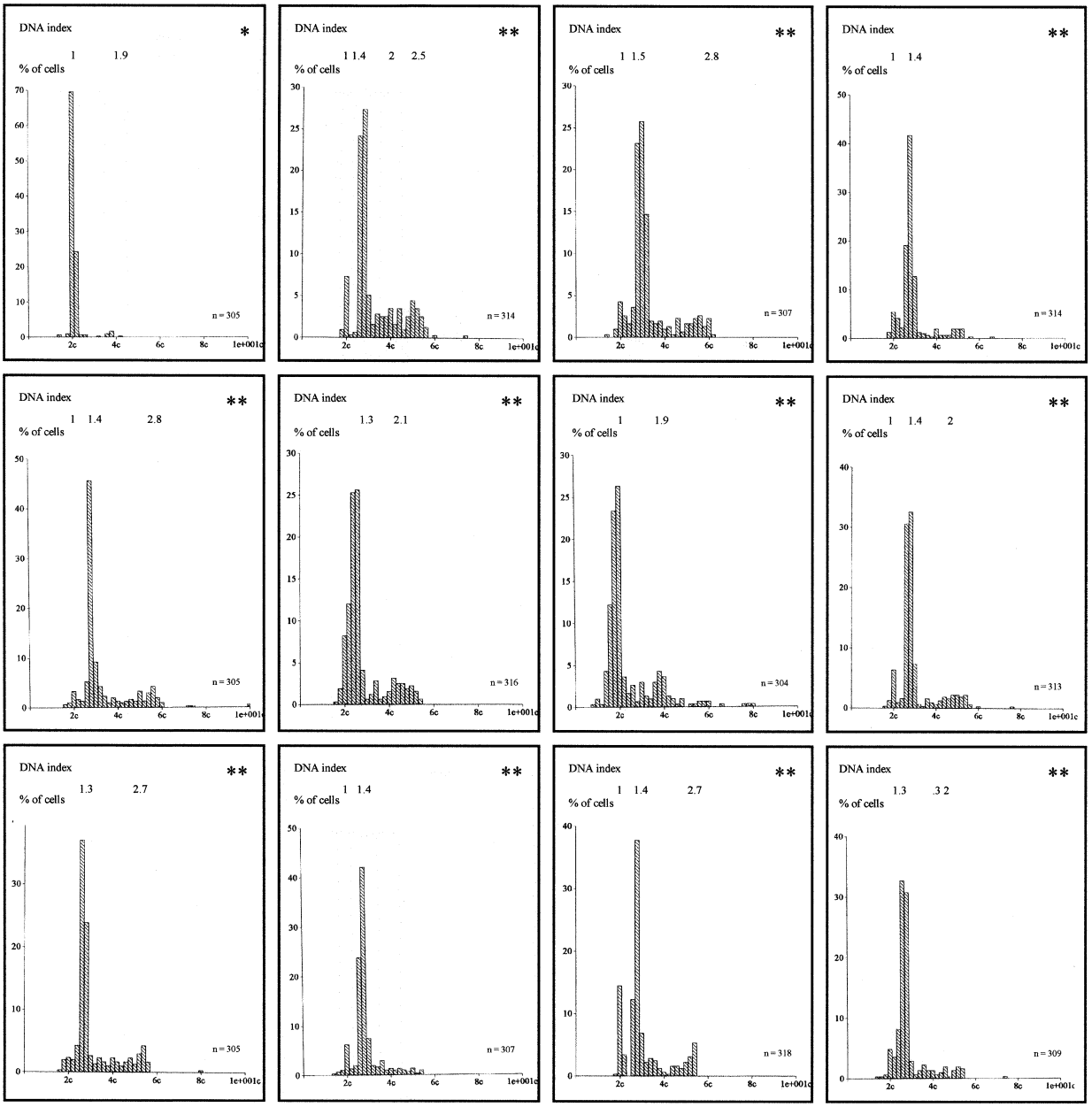

Fig. 4. Histograms illustrating a DNA-ploidy homogeneous gastric carcinoma: *normal mucosa (diploid), **tumoral sample (aneuploid). n = number of cells analyzed.

Fujimaki et al. (1992) reported that DNA-index-ploidy (multiple clones differing in DNA index in one tumour) heterogeneity was higher than that of DNA-ploidy heterogeneity (multiple clones, either aneuploid or diploid) [7]. In an effort to resolve the controversy we determined DNA-ploidy status and also whether or not heterogeneity existed, by measuring DNA content in multiple samples from a series of resected gastric cancer specimens.

In a previous study [20], we could establish that DNA-aneuploid early gastric carcinomas are frequently heterogeneous for DNA-ploidy and that such heterogeneity occurs more frequently in tumours invading the submucosa (13% in intramucosal tumours and 44%

Table 1
Pathological data and DNA ploidy in advanced gastric cancers

Case	Age/Sex	Type	Grade*	TNM	Surface (cm^2)	Ploidy**	Heterogeneity	Ploidy of N***	Mib1/Ki67****	p53*****
1	82/M	diffuse	3	T2N1Mx	40	D	no	NS	42%	L
2	69/F	diffuse	3	T3N3Mx	77	A, H	yes	9D and 2H	41%	L
3	41/F	intestinal	3	T3N0Mx	22.5	A, T	no	–	64%	H
4	70/M	diffuse	3	T3N1Mx	48	AT	no	NA	72%	L
5	83/F	intestinal	3	T2N1Mx	24.75	A, H	no	1 H	56%	H
6	59/M	mixte	3	T3N2Mx	35.75	A, T	no	1T	75%	L
7	57/F	diffuse	3	T4N2Mx	81	A, T	no	not valuable	32%	H
8	62/M	intestinal	2	T2N0Mx	22.5	A, TT	no	NS	78%	H
9	89/F	intestinal	3	T2N2Mx	81	A, H	no	1T	84%	L
10	55/M	diffuse	3	T3N2Mx	255	A, H	yes	2D	45%	L
11	68/F	intestinal	1	T2N1Mx	7.5	A, T	no	1H	93%	H
12	60/M	diffuse	3	T3N3Mx	177	A, H	no	1H and 1T	81%	L
13	53/F	diffuse	3	T4N1Mx	29.25	A, H	yes	NA	90%	L
14	75/F	intestinal	3	T2N3Mx	27.5	A, TT	no	NA	90%	H
15	55/f	diffuse	3	T3N2Mx	36	A, H	yes	1D	33%	L
16	69/M	diffuse	3	T2N1Mx	14	A, T	no	1T	83%	H

*Grade: 1: well differentiated; 2: moderately differentiated; 3: poorly differentiated.
**Ploidy: D: diploid; A: aneuploid; H: hyperdiploid; T: triploid; TT: tetraploid.
***Ploidy of N (lymph node metastases): NA: not available (usually insufficient material); D: diploid; H: hyperdiploid; T: triploid; TT: tetraploid.
****Mib1/Ki67: per case field with % of maximal proliferative activity.
*****p53: High (H): more than 50% positive cells; Low (L): less than 50% positive cells.

Table 2
Ploidy pattern and p53 expression

	Low expression p53	High expression p53	Total of cases
Heterogeneous cases	4	0	4
Homogeneous cases	4	7	11
Total of cases	8	7	15

$p = 0.05$.

Table 3
Ploidy pattern and proliferative activity

	Ki67, LI* > 50%	Ki67, LI* < 50%	Total of cases
Heterogeneous cases	1	3	4
Homogeneous cases	10	1	11
Total of cases	11	4	15

$p = 0.03$.
*Labeling index.
Statistical evaluation: Fischer's exact test p-value of less than 0.05 is considered statistically significant.

in submucosally infiltrating cases). This study suggested the possibility of genome instability, as reflected in DNA-ploidy heterogeneity of early gastric cancers. Overgrowth of a more aggressive dominant clone of tumour cells would eventually lead to homogeneously aneuploid tumour. Results of some recent studies are consistent with this hypothesis. Notably Furuya et al. [8], studied the relationship between chromosomal instability and intratumoral regional DNA-ploidy heterogeneity in primary gastric cancers. They found that chromosomal instability is a necessary prerequisite for developing intratumoral DNA ploidy heterogeneity with DNA aneuploidy.

In our 16 cases of advanced gastric carcinoma only one case was diploid (6%). DNA-ploidy heterogeneity was found in 4 aneuploid cases (26%). This heterogeneity for DNA-ploidy was not significantly correlated with grade ($p = 0.5$), or depth of invasion ($p = 0.09$), or histological type ($p = 0.09$) as previously described [8].

We earlier reported that early gastric carcinomas are more frequently diploid (53%) [20]. This finding is consistent with our hypothesis of stepwise ploidy progression: from diploid in most early gastric cancer to aneuploid but heterogeneous in infiltrating early gastric cancer to aneuploid but homogeneous in advanced gastric cancer.

The analysis of lymph node metastases also supports this hypothesis: metastases were aneuploid and homogeneous. DNA measurements in lymph node metastases revealed a heterogeneous ploidy pattern only in primary tumours heterogeneous for DNA-ploidy.

To explore more in detail the relationship between the pattern of intratumoral heterogeneity for DNA-

ploidy and genome instability, we have correlated different DNA-ploidy patterns with the Ki-67 labeling index and the degree of p53 immunoreactivity. Our results show that homogeneous-aneuploid cancers have a higher proliferative index than heterogeneous-aneuploid cancers. These findings support the hypothesis that a single more aggressive neoplastic cell clone is responsible for progression of the tumour. This is also supported by the observation that p53 expression was higher in homogeneous-aneuploid tumours.

In conclusion, this study: (1) confirms that most advanced gastric cancers are aneuploid; (2) demonstrates that these tumours are rarely heterogeneous for DNA-ploidy.

These findings are consistent with the hypothesis of the emergence of a single aneuploid cell clone as a crucial mechanism in the progression from early to advanced gastric cancer. More frequent p53 overexpression and higher proliferative activity is in agreement with the notion that this dominant clone is more aggressive.

References

[1] Y. Adachi, M. Mori, M. Haraguchi, K. Sugimachi and M. Tsuneyoshi, Cytophotometric study of nuclear DNA content in scirrhous gastric carcinoma, *Pathology* **27** (1995), 5–7.

[2] C. Arnerlov, S.O. Emdin, S. Cajander, N.O. Bengtsson, B. Tavelin and G. Roos, Intratumoral variations in DNA ploidy and s-phase fraction in human breast cancer, *Analyt. Cell. Pathol.* **23**(1) (2001), 21–28.

[3] E. Bergers, P.J. Van Diest and J.P. Baak, Tumour heterogeneity of DNA cell cycle variables in breast cancer measured by flow cytometry, *J. Clin. Path.* **49**(11) (1996), 931–937.

[4] R. Bowman, G. Angelini, C. Cabral, O. Datuin, M. Ota and D. Heustis, Interobserver and intraobserver variation in tumor DNA index as analyzed by static image cytometry: a pilot study, *Cell Vision* **3** (1996), 291–296.

[5] M.J. Brito, M.I. Filipe, H. Thompson, M.G. Ormerod and J. Titley, DNA ploidy in early gastric carcinoma (T+): a flow cytometric study of 100 European cases, *Gut* **34** (1993), 230–234.

[6] L.G. Dodd, B.-J. Kerns, R.K. Dodge and L.J. Layfield, Intratumoral heterogeneity in primary breast carcinoma: study of concurrent parameters, *J. Surg. Oncol.* **64** (1997), 280–288.

[7] E. Fujimaki, O. Nakano, S. Chiba, H. Tazawa, H. Yamashiki, S. Orii and T. Sugai, DNA ploidy heterogeneity in early and advanced gastric cancers, *Cytometry (Communication in Clinical Cytometry)* **26** (1996), 131–136.

[8] T. Furuya, T. Uchiyama, T. Murakami, A. Adachi, S. Kawauchi, A. Oga, T. Hirano and K. Sasaki, Relationship between chromosomal instability and intratumoral regional DNA ploidy heterogeneity in primary gastric cancers, *Clin. Cancer Res.* **6**(7) (2000), 2815–2820.

[9] D.W. Hedley, M.L. Friedlander, I.W. Taylor, C.A. Rugg and E.A. Musgrove, Method for analysis of cellular DNA content of paraffin-embedded pathological material using flow cytometry, *J. Histochem. Cytochem.* **31** (1983), 1333–1335.

[10] T. Imada, Y. Yamamoto, K. Fukuzawa, Y. Rino, T. Suda, Y. Moriwaki, H. Akiyama, T. Doi, F. Kito and H. Takemura, Flow cytometric analysis of nuclear DNA heterogeneity in gastric cancer, *Jpn. J. Clin. Oncol.* **7**(4) (1997), 221–226.

[11] D. Korenaga, M. Haraguchi, T. Okamura, H. Baba, A. Saito and K. Sugimachi, DNA ploidy and tumor invasion in human gastric cancer, *Arch. Surg.* **124** (1989), 314–318.

[12] D. Korenaga, T. Okamura, A. Saito, H. Baba, A. Saito and K. Sugimachi, DNA ploidy is closely linked to tumor invasion, lymph node metastasis and prognosis in clinical gastric cancer, *Cancer* **62** (1988), 309–313.

[13] D. Korenaga, A. Watanabe, H. Anai, Y. Maehara and K. Sugimachi, Development of gastric cancer with special reference to growth and DNA content. Slow and rapid growing types, *Europ. J. Surg. Oncol.* **19** (1993), 463–467.

[14] B. Ljungberg, C. Mehle, R. Stenling and G. Roos, Heterogeneity in renal cell carcinoma and its impact on prognosis – a flow cytometric study, *Br. J. Cancer* **74** (1996), 123–127.

[15] M. Mori, Y. Adachi, K. Nakamura, S. Kuroiwa, M. Enjoji and K. Sugimachi, Advanced gastric carcinoma simulating early gastric carcinoma, *Cancer* **65** (1990), 1033–1040.

[16] M. Mori, Y. Adachi, Y. Kakeji, D. Korenaga, K. Sugimachi, M. Motooka and T. Ooiwa, Superficial flat-type early carcinoma of the stomach, *Cancer* **69** (1992), 306–313.

[17] S. Moriwaki and O. Kimura, Correlation of DNA content between endoscopic biopsy and surgically resected specimens in gastric and colorectal cancer, *J. Gastroenterol.* **30** (1995), 162–168.

[18] K. Nakamura, T. Yeyama, T. Yao, Z. Xin Xuan, K. Ambe, Y. Adachi, Y. Yakeishi, A. Matsukuma and M. Enjoji, Pathology and prognosis of gastric carcinoma, *Cancer* **70** (1992), 1030–1037.

[19] H. Nenning, J. Rassler and D.H. Minh, Heterogeneity of DNA distribution pattern in renal tumors, *Analyt. Cell. Pathol.* **14**(1) (1997), 9–17.

[20] M.C. Osterheld, R. Laurini, E. Saraga and F.T. Bosman, Evaluation of heterogeneity of DNA ploidy in early gastric cancers, *Analyt. Cell. Pathol.* **19** (1999), 67–72.

[21] R. Palmqvist, A. Oberg, C. Bergtrom, J.N. Rutegard, B. Zackrisson and R. Stenling, Systematic heterogeneity and prognostic significance of cell proliferation in colorectal cancer, *Br. J. Cancer* **77**(6) (1998), 917–925.

[22] S.E. Petersen, P. Bichel and M. Lorentzen, Flow cytometric demonstration of tumor-cell sub-population with different DNA content in human colo-rectal carcinoma, *Europ. J. Cancer* **15** (1978), 383–386.

[23] S.E. Petersen, M. Lorentzen and P. Bichel, A mosaic subpopulation structure of human colorectal carcinomas demonstrated by flow cytometry, in: *Flow Cytometry*, Vol. IV, O.D. Laerum, T. Lindmo and E. Thornd, eds, Universitets forlaget, Oslo, 1998, p. 412.

[24] P. Rosenberg, S. Wingren and C. Guerrieri, Flow cytometric DNA-heterogeneity in paraffin-embedded endometrial cancer, *Acta Oncol.* **36** (1997), 23–26.

[25] J.S. Ross, *DNA Ploidy and Cell Cycle Analysis in Pathology*, Igaku-Shoin, New York, Tokyo, 1996, p. 2.

[26] M. Rugge, F. Sonego, M. Panozzo, R. Baffa, J. Rubio, F. Farinat, D. Nitti, V. Ninfo and S.-C. Ming, Pathology and ploidy in the prognosis of gastric cancer with no extranodal metastasis, *Cancer* **73** (1994), 1127–1133.

[27] J.L. Ruiz-Cerda, M. Hernandez, A. Sempere, J.E. O'Connor, B.F. Kimler and F. Jimenez-Cruz, Intratumoral heterogeneity of DNA content in renal cell carcinoma and its prognostic significance, *Cancer* **86**(4) (1999), 664–671.

[28] A. Saito, D. Korenaga, M. Haraguchi, Y. Maehara and K. Sugimachi, Heterogeneity in gastric carcinoma with special reference to DNA content and mitotic activity: histopathologic differentiation, *J. Surg. Oncol.* **51** (1992), 14–18.

[29] M. Sakusabe, M. Kodana, Y. Sato, T. Kikuchi and K. Koyama, Clinical significance of DNA ploidy pattern in stage III gastric cancer, *World J. Surg.* **20** (1996), 27–31.

[30] K. Sasaki, T. Hashimoto, K. Kawachino and M. Takahashi, Intratumoral regional differences in DNA ploidy of gastrointestinal carcinomas, *Cancer* **62** (1988), 2569–2575.

[31] O. Sasaki, K. Soejima and Y. Haraguchi, Intra-tumor DNA ploidy distribution pattern and its relation to histologic type in gastric carcinoma, *Path. Res. Pract.* **188** (1992), 545–549.

[32] P.J. Symmans, J.M. Linehan, M.J. Brito and M.I. Filipe, P53 expression in Barrett's oesophagus, dysplasia, and adenocarcinoma using antibody DO-7, *J. Pathol.* **173**(3) (1994), 221–226.

[33] H. Tomoda and T. Inoue, Flow cytometric analysis of the DNA content in primary and metastatic lesions of colorectal cancer, *J. Surg. Oncol.* **59** (1995), 101–104.

[34] P. Tosi, L. Leoncini, M. Cintorino, C. Vindigni, C. Minacci, S. Nuti, E. Pinto, A. de Stefano and G. Cevenini, Flow cytometric analysis of DNA ploidy pattern from deparaffinized formalin-fixed gastric tissue, *Int. J. Cancer* **42** (1988), 868–871.

[35] L.S. Wang, L.H. Wu, C.J. Chang, W.Y. Fahn, M.H. Huang, and J.H. Chiu, Flow-cytometric DNA content analysis of oesophageal carcinoma. Comparison between tumour and sequential non-tumour mucosae, *Scand. Cardiovasc. J.* **32**(4) (1998), 205–212.