**Table 1.** MicroRNA-31 and clinicopathological and molecular features in serrated lesions and non-serrated adenomas

| | | MicroRNA-31 expression (quartile) | | | | |
|---|---|---|---|---|---|---|
| **Clinicopathological or molecular features** | **Total (*N*)** | **Q1 (<1.6)** | **Q2 (1.6–7.3)** | **Q3 (7.4–30.1)** | **Q4 (≥30.2)** | |
| **All cases** | **603** | **152** | **153** | **148** | **150** | ***p*** |
| Gender | | | | | | |
| Male | 362 (60%) | 101 (66%) | 85 (56%) | 80 (54%) | 96 (64%) | 0.069 |
| Female | 241 (40%) | 51 (34%) | 68 (44%) | 68 (46%) | 54 (36%) | |
| Age (mean ± SD) | 62.0 ± 12.1 | 63.1 ± 11.3 | 60.4 ± 12.7 | 62.4 ± 12.8 | 62.3 ± 11.5 | 0.26 |
| Tumor size (mm) (mean ± SD) | 14.1 ± 11.1 | 16.4 ± 13.3 | 13.3 ± 10.8 | 14.0 ± 10.5 | 12.6 ± 9.5 | 0.020 |
| Tumor location | | | | | | |
| Rectum | 78 (13%) | 38 (25%) | 23 (15%) | 6 (4.1%) | 11 (7.3%) | < 0.0001 |
| Sigmoid colon | 149 (25%) | 45 (30%) | 47 (31%) | 29 (20%) | 28 (19%) | |
| Descending colon (including splenic flexure) | 41 (6.8%) | 12 (7.9%) | 11 (7.2%) | 10 (6.8%) | 8 (5.3%) | |
| Transverse colon (including hepatic flexure) | 114 (19%) | 25 (16%) | 37 (24%) | 26 (18%) | 26 (17%) | |
| Ascending colon | 139 (23%) | 25 (16%) | 29 (19%) | 45 (30%) | 40 (27%) | |
| Cecum | 82 (14%) | 7 (4.6%) | 6 (3.9%) | 32 (22%) | 37 (25%) | |
| Histopathology | | | | | | |
| Hyperplastic polyps (HPs) | 132 (22%) | 39 (26%) | 47 (31%) | 27 (18%) | 19 (13%) | < 0.0001 |
| Sessile serrated adenomas (SSAs) | 122 (20%) | 10 (6.6%) | 30 (20%) | 44 (30%) | 38 (25%) | |
| SSAs with cytological dysplasia | 10 (1.7%) | 0 (0%) | 0 (0%) | 2 (1.4%) | 8 (5.3%) | |
| Traditional serrated adenomas (TSAs) | 101 (17%) | 11 (7.2%) | 17 (11%) | 33 (22%) | 40 (27%) | |
| TSAs with high-grade dysplasia | 16 (2.7%) | 3 (2.0%) | 5 (3.3%) | 2 (1.4%) | 6 (4.0%) | |
| Non-serrated adenomas (tubular or tubulovillous adenomas) | 222 (37%) | 89 (59%) | 54 (35%) | 40 (27%) | 39 (26%) | |
| *BRAF* mutation | | | | | | |
| Wild-type | 354 (59%) | 128 (84%) | 95 (62%) | 71 (48%) | 60 (40%) | < 0.0001 |
| Mutant | 249 (41%) | 24 (16%) | 58 (38%) | 77 (52%) | 90 (60%) | |
| *KRAS* mutation | | | | | | |
| Wild-type | 463 (77%) | 105 (69%) | 115 (75%) | 122 (82%) | 121 (81%) | 0.028 |
| Mutant | 140 (23%) | 47 (31%) | 38 (25%) | 26 (18%) | 29 (19%) | |
| CIMP status | | | | | | |
| CIMP-low/zero | 503 (83%) | 138 (91%) | 142 (93%) | 118 (80%) | 105 (70%) | < 0.0001 |
| CIMP-high | 100 (17%) | 14 (9.2%) | 11 (7.2%) | 30 (20%) | 45 (30%) | |
| MSI | | | | | | |
| MSS/MSI-low | 594 (99%) | 151 (99%) | 150 (98%) | 146 (99%) | 147 (98%) | 0.71 |
| MSI-high | 9 (1.5%) | 1 (0.7%) | 3 (2.0%) | 2 (1.4%) | 3 (2.0%) | |

Percentage (%) indicates the number of cases with a specific clinicopathological or molecular feature within a given quartile category (Q1, Q2, Q3 or Q4) of microRNA-31 expression. *p* Values were calculated by analysis of variance for age and tumor size and by chi-square or Fisher's exact test for all other variables. To account for multiple hypothesis testing in association between miR-31 expression and other nine covariates, the *P* value for significance was adjusted by Bonferroni correction to $p = 0.0056$ (= 0.05/9).

Abbreviations: CIMP: CpG island methylator phenotype; HP: hyperplastic polyp; MSI: microsatellite instability; MSS: microsatellite stable; SD: standard deviation; SSA: sessile serrated adenoma; TSA: traditional serrated adenoma.

### Association of microRNA-31 expression and clinicopathological and molecular features in serrated lesions and non-serrated adenomas

Table 1 shows the clinicopathological and molecular features of serrated lesions and non-serrated adenomas according to the miR-31 expression level. miR-31 expression was significantly associated with tumor location, histopathology, *BRAF* mutation and CIMP-high status ($p < 0.0001$). No significant difference was observed between miR-31 expression and *KRAS* mutation ($p = 0.028$) or MSI ($p = 0.71$). When limiting cases to serrated lesions, miR-31 expression was associated with tumor location, histopathology, *BRAF* mutation and CIMP-high status ($p < 0.0001$; data not shown).

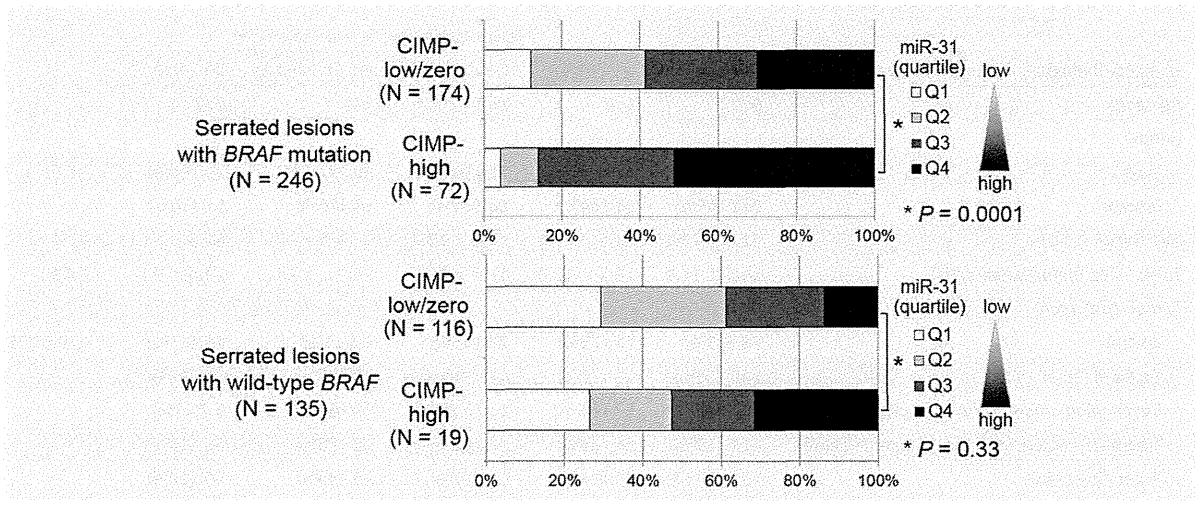

**Figure 2.** Association between miR-31 expression and CIMP status in relation to *BRAF* status in serrated lesions (HPs, SSAs, SSAs with cytological dysplasia, TSAs and TSAs with high-grade dysplasia). A significant association was observed between high miR-31 expression and CIMP-high status in serrated lesions with *BRAF* mutation. However, miR-31 expression was slightly but insignificantly associated with CIMP status in the cases with wild-type *BRAF*. Cases with miR-31 expression were divided into quartiles Q1 (<1.6), Q2 (1.6–7.3), Q3 (7.4–30.2) and Q4 ($\geq$30.2). CIMP: CpG island methylator phenotype; HP: hyperplastic polyp; miR-31: microRNA-31; SSA: sessile serrated adenoma; TSA: traditional serrated adenoma.

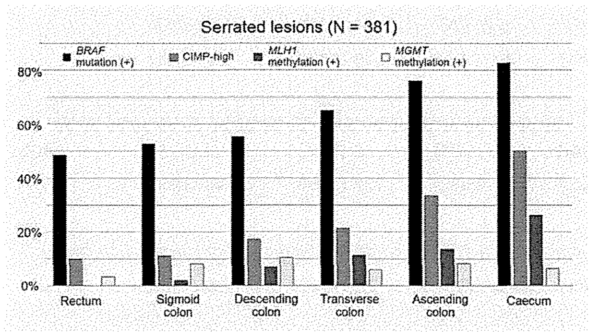

**Figure 3.** Frequency of *BRAF* mutation, CIMP-high and *MLH1* methylation in serrated lesions (HPs, SSAs, SSAs with cytological dysplasia, TSAs and TSAs with high-grade dysplasia). Frequency of *BRAF* mutation, CIMP-high and *MLH1* methylation increased gradually from the rectum to cecum in serrated lesions ($p \leq 0.0002$), but there was no significant difference between *MGMT* methylation and tumor location. CIMP: CpG island methylator phenotype; HP: hyperplastic polyp; SSA: sessile serrated adenoma; TSA: traditional serrated adenoma.

### Association of miR-31 expression and *BRAF* mutation or CIMP status in serrated lesions

Because *BRAF* mutation has been tightly associated with CIMP-high status, we examined miR-31 expression in relation to *BRAF* and CIMP status. High miR-31 expression was associated with *BRAF* mutation and was independent of CIMP status in serrated lesions ($p \leq 0.017$; Supporting Information Fig. 1). In contrast, a significant association was observed between high miR-31 expression and CIMP-high status in serrated lesions with *BRAF* mutation ($p = 0.0001$; Fig. 2). However, miR-31 expression was slightly but insignificantly associated with CIMP status in the cases with wild-type *BRAF* ($p = 0.33$).

### Multivariate analysis to identify association with miR-31 expression in serrated lesions

We also performed multivariate logistic regression analysis to confirm that the association between miR-31 expression and *BRAF* mutation or CIMP status was independent of any other clinical and molecular variables in serrated lesions. Our data showed that miR-31 expression was associated with *BRAF* mutation ($p = 0.0037$) and was independent of other variables (Supporting Information Table 1).

### Molecular characteristics of serrated lesions according to tumor location

The frequency of *BRAF* mutation, CIMP-high status and *MLH1* methylation increased gradually from the rectum to cecum in serrated lesions ($p \leq 0.0002$), but there was no significant association between *MGMT* methylation and tumor location (Fig. 3). Similarly, the number of serrated lesions with high miR-31 expression increased gradually from the rectum to cecum ($p < 0.0001$; Fig. 4). Similar results were observed in non-serrated adenomas ($p < 0.0001$; Fig. 4) and CRCs ($p < 0.0001$; Supporting Information Fig. 2). After serrated lesions and non-serrated adenomas were stratified by *BRAF* mutation, the association between miR-31 expression and tumor location persisted ($p \leq 0.0011$; Supporting Information Fig. 3).

### Association of miR-31 expression and molecular alteration in SSAs with or without cytological dysplasia

High miR-31 expression was conspicuous in SSAs with cytological dysplasia compared to that in SSAs ($p = 0.0079$; Table 2). CIMP-high was well pronounced in SSAs with cytological

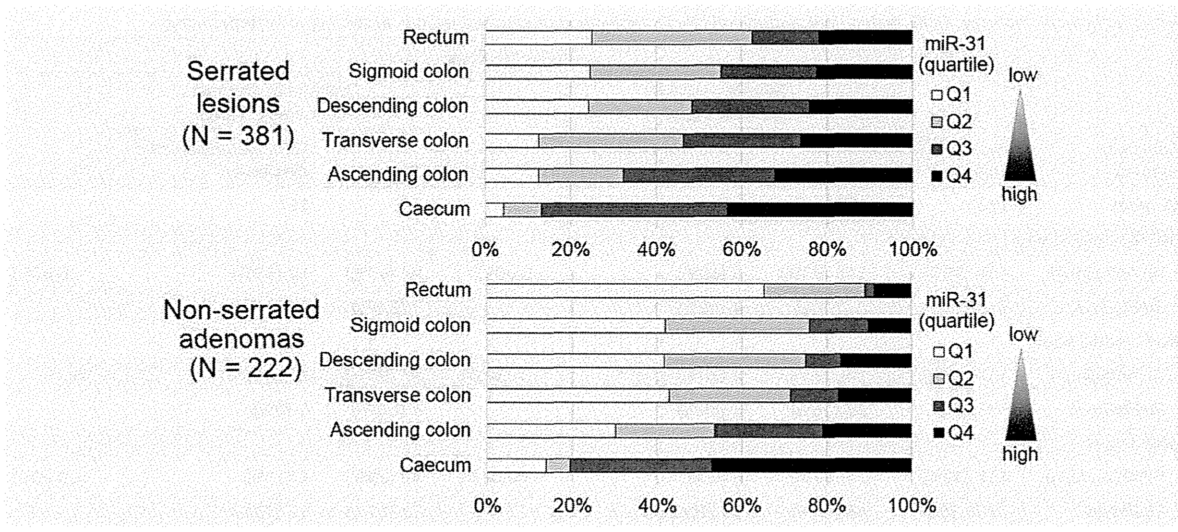

Figure 4. Frequency of miR-31 expression in serrated lesions (HPs, SSAs, SSAs with cytological dysplasia, TSAs and TSAs with high-grade dysplasia) or non-serrated adenomas (tubular or tubulovillous adenomas). The number of cases with high miR-31 expression increased gradually from the rectum to the cecum in not only in serrated lesions ($p < 0.0001$) but also in non-serrated adenomas ($p < 0.0001$). Cases with miR-31 expression were divided into quartiles Q1 (<1.6), Q2 (1.6–7.3), Q3 (7.4–30.2) and Q4 (≥30.2). HP: hyperplastic polyp; miR-31: microRNA-31; SSA: sessile serrated adenoma; TSA: traditional serrated adenoma.

dysplasia (100%, 10/10) compared to that in SSAs (38%, 46/122; $p < 0.0001$). *MLH-1* methylation was more frequently observed in SSAs with cytological dysplasia (80%, 8/10) than in SSAs (16%, 20/122; $p < 0.0001$). Likewise, *MGMT* methylation was more frequently observed in SSAs with cytological dysplasia (40%, 4/10) than in SSAs (7.4%, 9/122; $p = 0.0071$).

### Association of miR-31 expression and molecular alteration in TSAs with or without HGD

With regard to TSAs, no significant difference in miR-31 expression was found between TSAs with HGD and TSAs ($p = 0.23$; Table 2). In contrast, CIMP-high status was more frequently detected in TSAs with HGD (75%, 12/16) than in TSAs (12%, 12/101; $p < 0.0001$). *MGMT* methylation was more frequently observed in TSAs with HGD (38%, 6/16) than in TSAs (3.0%, 3/101; $p < 0.0001$), but no significant difference in *MLH1* methylation was found between TSAs with HGD (0%, 0/16) and TSAs (4.0%, 4/101; $p = 0.27$).

## Discussion

We performed this study to identify the possible association of miR-31 expression with epigenetic features including CIMP status as well as its role in the progression of serrated lesions. High miR-31 expression was associated with CIMP-high status in serrated lesions with *BRAF* mutation. Our data also showed that the association between miR-31 expression and *BRAF* mutation status was independent of CIMP status. Thus, this is the first report to identify an association between miR-31expression, *BRAF* mutations and CIMP status in serrated lesions. Moreover, high miR-31 expression was well pronounced in SSAs with cytological dysplasia than in SSAs, but no significant difference was observed between TSAs and TSAs with HGD. With regard to the colorectal continuum concept, the frequency of high miR-31 expression increased gradually from the rectum to cecum in serrated lesions as did the occurrence of *BRAF* mutation, CIMP-high status and *MLH1* methylation.

miR-31 is located at 9p21.3 and is reportedly up-regulated in CRCs.[31–35,37] We recently reported an association among miR-31 expression, *BRAF* mutation and poor prognosis involving a large CRC sample ($N = 721$); we also reported that high miR-31 expression is frequently detected in the proximal colon (cecum and ascending and transverse colon) compared to that in the distal colon (the descending and sigmoid colon) and rectum.[38] Because the presence of *BRAF* mutation is tightly associated with CIMP status,[20,44–46] we examined the association between miR-31 expression and CIMP status in serrated lesions. With regard to CRCs, Slattery *et al.* reported that miR-31 was the one of the upregulated miRNAs in patients with CIMP-high status; however, they did not examine *BRAF* mutations.[47] Moreover, no previous study has reported the association between miR-31 expression and CIMP status in premalignant colorectal lesions.

Our current study had some limitations due to its cross-sectional nature and the fact that unknown bias (*i.e.* selection bias) may have confounded the results. Nevertheless, our multivariate regression analysis was adjusted for potential confounders including clinical and molecular features. The results demonstrated that high miR-31 expression is independently associated with *BRAF* status in serrated lesions. In contrast, although we found that miR-31 expression was associated with CIMP-high

Table 2. Epigenetic features, CIMP status, MSI and microRNA-31 expression in serrated lesions according to histopathology

| | Histopathology | | | | | | |
|---|---|---|---|---|---|---|---|
| | | Sessile serrated adenomas (SSAs) | | | Traditional serrated adenomas (TSAs) | | |
| Molecular features | Hyperplastic polyps (HPs) | SSAs | SSAs withcytological dysplasia | *P* | TSAs | TSAs withhigh-grade dysplasia | *P* |
| All cases | 132 | 122 | 10 | | 101 | 16 | |
| *MGMT* methylation | | | | | | | |
| Unmethylated | 126 (95%) | 113 (93%) | 6 (60%) | 0.0071 | 98 (97%) | 10 (63%) | <0.0001 |
| Methylayed | 6 (4.6%) | 9 (7.4%) | 4 (40%) | | 3 (3.0%) | 6 (38%) | |
| *MLH1* methylation | | | | | | | |
| Unmethylated | 127 (96%) | 102 (84%) | 2 (20%) | <0.0001 | 97 (96%) | 16 (100%) | 0.27 |
| Methylayed | 5 (3.8%) | 20 (16%) | 8 (80%) | | 4 (4.0%) | 0 (0%) | |
| CIMP status | | | | | | | |
| CIMP-low/zero | 121 (92%) | 76 (62%) | 0 (0%) | <0.0001 | 89 (89%) | 4 (25%) | <0.0001 |
| CIMP-high | 11 (8.3%) | 46 (38%) | 10 (100%) | | 12 (11%) | 12 (75%) | |
| MSI | | | | | | | |
| MSI-low/MSS | 131 (99%) | 121 (99%) | 6 (60%) | <0.0001 | 98 (97%) | 16 (100%) | 0.34 |
| MSI-high | 1 (0.8%) | 1 (0.8%) | 4 (40%) | | 3 (3.0%) | 0 (0%) | |
| MicroRNA-31 | | | | | | | |
| Q1 (<1.6) | 39 (30%) | 10 (8.2%) | 0 (0%) | 0.0079 | 11 (11%) | 3 (19%) | 0.23 |
| Q2 (1.6–7.3) | 47 (36%) | 30 (25%) | 0 (0%) | | 17 (17%) | 5 (31%) | |
| Q3 (7.4–30.2) | 27 (20%) | 44 (36%) | 2 (20%) | | 33 (33%) | 2 (13%) | |
| Q4 (≥30.2) | 19 (14%) | 38 (31%) | 8 (80%) | | 40 (40%) | 6 (38%) | |

Percentage (%) indicates the number of cases with a specific molecular feature according to histopathology. *p*-Values were calculated by chi-square or Fisher's exact test.
Abbreviations: CIMP: CpG island methylator phenotype; HP: hyperplastic polyp; MSI: microsatellite instability; MSS: microsatellite stable; SSA: sessile serrated adenoma; TSA: traditional serrated adenoma.

status in serrated lesions with *BRAF* mutation, the relationship between miR-31 expression and CIMP status did not persist in the cases with wild-type *BRAF*. These results suggested that the association between miR-31 expression and CIMP-high status may have been due to *BRAF* mutation. However, the number of samples of CIMP-high serrated lesions with wild-type *BRAF* was too small ($N = 19$). Moreover, multivariate logistic regression analysis showed that CIMP status was one of the variables associated with miR-31 expression, although no significant association was observed. Therefore, our results imply that epigenetic instability (*i.e.* CIMP-high status) may be related to up-regulation of miR-31 expression. Further functional analysis is needed to clarify the associations between miR-31 expression, *BRAF* mutations and CIMP status in colorectal neoplastic disease.

Accumulating evidence suggests that proximal colon cancers differ from distal cancers in clinical, pathological and molecular features.[18,40,41,47] Yamauchi *et al.* reported that the frequency of CIMP-high, MSI-high and *BRAF* mutation increase gradually along colorectum subsites from the rectum to the ascending colon; these data support the colorectal continuum concept, namely, gradual changes in tumor molecular features, rather than abrupt changes at the splenic flexure (the “Two-colon concept”).[20] Colorectal epithelial cells are constantly in contact with bowel contents, which may play a critical role in cellular transformation and tumor development and progression. Bowel contents (*i.e.* food debris and microbiome) and their interactions with host cells may directly cause cellular molecular changes, or alternatively, may influence tumor progression differentially according to molecular features in premalignant cells.[20] In fact, bowel contents gradually change, and this observation may explain why molecular features of a tumor change gradually. Our current data using serrated lesions and non-serrated adenomas seems to be consistent with a previous study[20] because the frequency of *BRAF* mutation, CIMP-high and *MLH1* methylation increased along the bowel from the rectum to the cecum. These results indicate that gradual changes in tumor molecular features already occur at the early stage of colorectal neoplastic disease.

In the current study, we also found that the frequency of high miR-31 expression increased gradually from the rectum to the cecum in serrated lesions. Similar results were observed in non-serrated adenomas and CRCs. These results show that miR-31 may be a molecule that supports the colorectal continuum concept. To the best of our knowledge, no previous reports have described a specific miRNA associated with this concept. Thus, our data on miR-31 and other molecular features indicate that future studies on colorectal tumors should include information on detailed tumor locations (beyond the proximal colon, distal colon and rectum).

Various authors have reported that SSAs with cytological dysplasia have genetic and epigenetic abnormalities and are at a high risk of progression to CRCs.[4,9,25,27,46] A loss of staining for MLH1 (due to *MLH1* methylation) leads to MSI, and repeat tract mutation in genes such as *TGFβRII* is restricted to the lesions with cytological dysplasia in SSAs.[25,26,48–50] In addition, Dhir *et al.* recently reported that there was a progressive increase in the methylation frequencies of genes from HPs to SSAs to SSAs with cytological dysplasia.[51] Our current data showed that the frequency of high miR-31 expression, *MLH1* and *MGMT* methylation and CIMP-high in SSAs with cytological dysplasia is much higher than in SSAs without. Thus not only accumulating epigenetic alterations but also miR-31 expression may play a role in SSA progression. In contrast, TSAs are much less common than SSAs; therefore, there fewer data is available on their molecular profile.[4,24] TSAs typically do not show *MLH1* methylation or develop into MSI-high CRCs, but they do commonly have *MGMT* methylation.[4,24,25] In addition, the key molecule of the TSA pathway progression remains largely unknown. In the current study, no significant differences in miR-31 expression or *MLH1* methylation were found between TSAs with and without HGD, whereas the frequency of high CIMP status and *MGMT* methylation was much higher in TSAs with HGD than in TSAs without. These results suggest that the molecule controlling serrated lesion progression may distinguish TSAs from SSAs.

In conclusion, miR-31 expression was associated with CIMP-high status in serrated lesions with *BRAF* mutation. Our data also suggest that miR-31 may play an important role in SSA evolution. Moreover, we found that not only *BRAF* mutation and CIMP status but also miR-31 may be a key molecule that supports the colorectal continuum concept. These novel data will improve our understanding of details of the colorectal serrated pathway and may lead to the establishment of a new therapeutic target or a theranostic procedure in some CRC types.

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Data analysis and interpretation: EY, KN, MN, YS, YA, TT, RM, YB

Drafting of the manuscript: MI, KN

Critical revision of the manuscript for important intellectual content: KN, HY, YS

Statistical analysis: KN, MN

Material support: HT, TT,

Study supervision: KN, HS, HY, KI, YS

Final approval of manuscript: all authors.

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RESEARCH ARTICLE

# The effect of IGF-I receptor blockade for human esophageal squamous cell carcinoma and adenocarcinoma

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**Abstract** Insulin-like growth factor-I receptor (IGF-IR) signaling is required for carcinogenicity and tumor development, and this pathway has not been well studied in human esophageal carcinomas. Esophageal cancer is one of the human cancers with the worst prognosis and has two main histologies: squamous cell carcinomas (ESCC) and adenocarcinoma (EAC). Previously, we have reported that detection of the IGF axis may be useful for the prediction of recurrence and poor prognosis of ESCC. We have also shown the successful therapy for several gastrointestinal cancers using recombinant adenoviruses expressing dominant negative IGF-IR (ad-IGF-IR/dn). The aim of this study is to develop potential targeted therapeutics to IGF-IR and to assess the effect of IGF-IR blockade in both of these types of esophageal cancer. We determined immunohistochemical expression of IGF-IR in a tissue microarray. We then assessed the effect of IGF-IR blockade on signal transduction, proliferation, apoptosis, and motility. Ad-IGF-IR/dn, a tyrosine kinase inhibitor, BMS-536924, and adenovirus expressing shRNA for IGF-IR were used. IGF-IR expression was common in both tumor types but not in normal tissues. IGF-IR was detected in metastatic sites at similar levels compared to the primary site. IGF-IR inhibition suppressed proliferation and colony formation in both cancers. IGF-IR blockades up-regulated both stress- and chemotherapy-induced apoptosis and reduced migration. Although IGF-IR/dn blocked ligand-induced activation of Akt-1 mainly, BMS-536924 effectively blocked both activation of Akt and MAPK. The IGF axis might play a key role in tumor progression of esophageal carcinomas. The IGF-IR targeting strategies might thus be useful anticancer therapeutics for human esophageal malignancies.

**Keywords** Dominant negative · EAC · ESCC · IGF-IR · TKI

**Abbreviations**

| | |
|---|---|
| ad-IGF-IR/482st | Adenovirus expressing IGF-IR /482st |
| ad-IGF-IR/950st | Adenovirus expressing IGF-IR/950st |
| ad-shIG F-IR | Adenovirus expressing short-hairpin IGF-IR |
| des(1–3)IGF-I | $NH_2$ terminally truncated IGF-I |
| dn | Dominant negative |
| EAC | Esophageal adenocarcinoma |
| ESCC | Esophageal squamous cell carcinoma |
| ERK | Extracellular signal-regulated kinase |
| IGF | Insulin-like growth factor |
| IGFBP | IGF binding protein |
| IGF-IR | IGF-I receptor |
| IGF-IR/482st | Truncated IGF-IR of 482 amino acid long |

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| | |
|---|---|
| IGF-IR/950st | Truncated IGF-IR of 950 amino acid long |
| IGF-IR/dn | Dominant negative form of IGF-IR |
| InsR | Insulin receptor |
| mAb | Monoclonal antibody |
| PI3-K | Phosphatidylinositide 3-kinase |
| TKI | Tyrosine kinase inhibitor |

## Introduction

Esophageal cancer is one of the cancers with the worse prognosis worldwide [1]. At the time of diagnosis, more than half of patients have either unresectable tumors or metastatic ones. Even after a curative-intent surgical operation, the 5-year survival is still limited [2], and the therapy for unresectable esophageal carcinomas is typically minimally effective. Therefore, we must aim to seek new therapeutic options for this disease. The main types of human esophageal tumor are squamous cell carcinoma (ESCC) and adenocarcinoma (EAC).

Recently, advances in molecular research have brought new therapeutic strategies, including small molecule tyrosine kinase inhibitors (TKI) and monoclonal antibodies (mAb), into clinical testing. One group of new targets is the tyrosine kinase receptors. The insulin-like growth factor (IGF) family is a promising candidate [3, 4]. Agents targeting the IGF-I receptor (IGF-IR) pathway are moving into the clinic. Toward that end, we have studied this pathway in esophageal cancers.

IGF-IR is a heterotetramer of two α- and two β-chains [5]. Binding of the ligands IGF-I and IGF-II to IGF-IR causes receptor autophosphorylation and activates multiple signaling pathways, including ras/extracellular signal-regulated kinase (ERK) and the phosphatidylinositide 3-kinase (PI3-K)/Akt-1 axes [6]. Activation of IGF-IR is regulated by multiple factors, including IGF binding proteins (IGFBP) and IGF-2 receptor [7–9]. Elevation of serum IGF-I increases the risk of developing several cancers [10], and IGF-IR is essential for both malignant transformation and progression [3, 4]. Reduction of IGF-IR can induce apoptosis in tumors but produces only growth slowing in untransformed cells, suggesting that it might be an excellent target for therapeutic intervention [3]. IGF-IR knockout mice are viable (though physically small), indicating that relatively normal development and differentiation can occur in its absence [11]. These findings suggest a potential basis for tumor selectivity in therapeutic applications.

Human esophageal epithelial cells express IGF-IR, and IGF-I can stimulate both DNA synthesis and proliferation in these cells [12–14]. Salivary IGF-I continuously bathes the esophageal lumen and is in a free form (not bound to IGFBP, unlike the serum pool), which could enhance its binding ability to receptors on the esophageal mucosal cells [15]. These data indicate that the IGF/receptor may play important roles in homeostasis and esophageal premalignancy [14].

Both IGF-IR and IGFs are overexpressed in esophageal cancer tissues compared to normal ones [16–18]. In addition, IGFBP3 and an IGF-IR antibody suppress cancer cell proliferation [19, 20]. However, the role of the IGF axis in esophageal cancer has not been adequately studied. We reported previously that expression of IGF-IR and IGF-II were detected in 60 and 50% of ESCC, respectively, and were associated with invasion depth, metastasis, advanced tumor stage, and recurrence [21]. Patients with ESCC expressing both IGF-IR and IGF-II had a significantly shorter survival rate than those expressing either alone or neither in both single and multivariate analysis. Dominant negative for IGF-IR (IGF-IR/dn) suppressed proliferation and up-regulating chemotherapy-induced apoptosis through blocking ligand-induced Akt activation in an ESCC cell line, TE-1 [21].

In addition, there is a strong positive association between visceral obesity (metabolic syndrome) and risk of EAC, and the IGF axis is speculated to relate to both obesity and EAC [22]. IGF-IR expression in resected EAC was significantly higher in viscerally obese patients than in those of normal weight. Disease-specific survival was longer in patients with IGF-IR-negative EAC than in those with IGF-IR-positive tumors [23]. Thus, there are several lines of evidence that the IGF axis may play an important role in EAC.

There are several possible approaches to blocking IGF-IR signaling with therapeutic intent [24], including blocking the ligand or receptor using mAbs [25, 26] or TKIs [27, 28]. All of these are complicated by the high homology of this receptor to the insulin receptor (InsR). An approach that is intrinsically specific for IGF-IR is to use dominant negative or soluble IGF-IR receptor approaches to specifically inhibit the function of the wild-type receptor [29, 30]. We have constructed two different adenoviruses expressing IGF-IR/dn (ad-IGF-IR/dn) [31–34]. Ad-IGF-IR/482st encodes a truncated extracellular domain of IGF-IR (without the transmembrane domain) and thus produces a secreted protein that affects neighboring cells in addition to the transduced cells (a bystander effect). Another ad-IGF-IR/950st encodes a receptor that lacks the tyrosine kinase domain and thus remains on the membrane of the transduced cells to form non-functional receptor complexes. We have reported that ad-IGF-IR/dn may be a useful therapeutic strategy against several gastrointestinal tumors [21, 31, 32, 34, 35]. We have also reported that the adenoviral vector-based approach to express a short-hairpin inhibitory RNA of IGF-IR (ad-shIGF-IR) induced effective IGF-IR silencing in gastrointestinal cancers as manifested by effective blockade of the downstream pathway of IGF-IR and antitumor effects [36]. A dual targeting TKI for IGF-IR/InsR, BMS-536924, may have an advantage compared to a single targeting TKI, as transformed cells can also use insulin receptor activation of similar signaling pathways for proliferation in addition to IGFR signals [35, 37].

In order to evaluate the expression of IGF-IR in EAC and in metastatic sites of ESCC, we analyzed an esophageal cancer tissue microarray immunohistochemically. To assess IGF-IR blockade for both esophageal cancers, histologies ESCC and EAC, we used several strategies including IGF-IR/dns, shIGF-IR, and BMS-536924.

## Methods

### Materials, cell lines, and recombinant adenovirus vectors

Anti-Akt1(c-20), anti-ERK1(K-23), anti-phospho-ERK1(E-4), ant-IGF-I(G-17), and anti-IGF-IRβ(2C8) were purchased from Santa Cruz Biotechnology (Santa Cruz, CA, USA) and anti-phospho-Akt(Ser473) was from Cell-Signaling Technology (Beverly, MA, USA). Anti-IGF-IR(Ab-4) was from Oncogene Research Products (Cambridge, MA, USA) and anti-IGF-II was from Peninsula Laboratories (San Carlos, CA, USA). PI3-K inhibitors, wortmannin and LY294002, p38-MAPK inhibitor SB203580, cisplatin (CDDP), and 5-fluorouracil (5-FU) were purchased from Sigma (St. Louis, MO, USA), and MEK1 inhibitor PD98059 was from Cell Signaling. Recombinant human IGF-I and IGF-II were purchased from R&D systems (Minneapolis, MN, USA) and des(1–3)IGF-I from GroPep (Adelaide, Australia). All human esophageal cancer cell lines (Fig. 1) were obtained from the Japanese Cancer Collection of Research Bioresources Cell Bank (Tokyo, Japan), Riken Bioresource Center Cell Bank (Tsukuba, Japan), and European Collection of Cell Cultures (Salisbury, UK). Cells were passaged in RPMI1640 and DMEM, both with 10% fetal bovine serum.

Recombinant adenoviruses expressing IGF-IR/dn (482 and 950 amino acids long, IGF-IR/482st and IGF-IR/950st, Ad-IGF-IR/482st and Ad-IGF-IR/950st, respectively) were generated as described previously by homologous recombination [31]. Recombinant adenovirus vectors expressing shIGF-IR (ad-shIGF-IR) were generated as described previously [38]. An adenovirus expressing β-galactosidase was used as a control (ad-LacZ). Scrambled shRNA adenovirus (ad-Scr) is another control that has a short hairpin sequence but no specific target, also as described previously.

BMS-536924 was kindly provided by Bristol-Myers Squibb (New York, NY, USA). Stock solution was prepared in DMSO and stored at −20°C.

### Immunohistochemical analysis

The paraffin-embedded esophageal tissue microarray (ES208) was purchased from US Biomax (Rockville, MD, USA). After deparaffinization, endogenous peroxidase activity was blocked. Antibodies were applied after blocking with normal goat serum. Sections were incubated with the anti-rabbit secondary antibody (Santa Cruz Biotechnology) and a strep tavidin-HRP followed by exposure to the diaminobenzidine tetrahydrochloride substrate (Dako). The sections were counterstained in Mayer's hematoxylin and mounted. Immunostaining signals were scored by two independent observers. Semiquantitative scores were given as the score of the percentage of positive cells plus the score of the staining intensity. The scoring criteria of the percentage of positive cells were as follows: score 0, 0–5% positive cancer cells; score 1, 6–25%; score 2, 26–50%; score 3, 51–75%; score 4, 76–100% positive. The intensity score was given as follows: score 0, no staining; score 1, weak/equivocal; score 2, moderate; score 3,

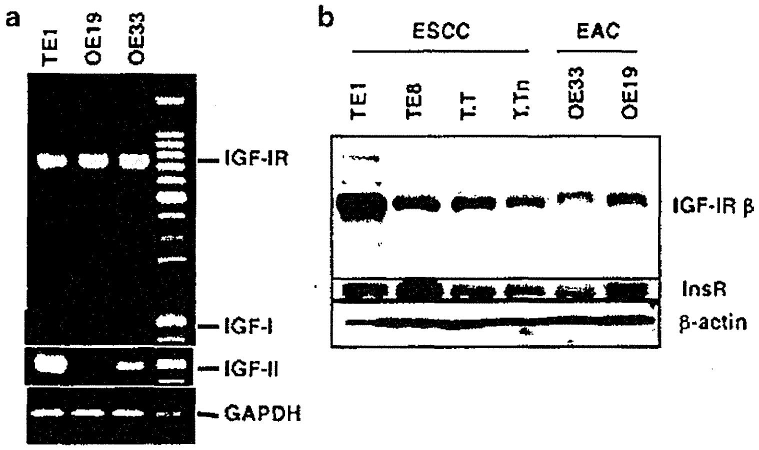


Fig. 1 The expressions of IGF-axis in esophageal carcinoma cell lines. a RT-PCR revealed that three cells express mRNAs of IGF-II and IGF-IR but not IGF-I. b Western blotting showed that two EAC and four ESCC cells express both IGF-IR and InsR

strong staining. The final scores were from 0 to 7 and four or more were considered positive.

### Reverse transcription PCR

Total RNA from cells was isolated by the acid guanidinium thiocyanate–phenol–chloroform method. Primer sets for the amplification of IGF-I cDNA sequences were 5′-CACTGT CACTGCTAAATTCA-3′ and 5′-CTGTGGGCTTGTTGAAA TAA-3′ [39]. Primers for IGF-II cDNA were 5′-AGTCGATGC TGGTGCTTCTCA-3′ and 5′-GTGGGCGGGGTCTTGG GTGGGTAG-3′ [40]. Primers for IGF-IR were 5′-ATTGAG GAGGTCACAGAGAAC-3′ and 5′-TTCATATCCTGTTTT GGCCTG-3′ [40]. Randomly primed cDNAs were prepared from 1 mg of total RNA by M-MLV reverse transcriptase (Takara, Japan) and amplified by PCR. For amplification of these sequences, 35 cycles of PCR was programmed as follows: 94°C, 30 s; 60°C, 30 s; 72°C, 30 s.

### Western blotting

Cells were cultured in serum-free medium for 24 h and then stimulated with 20 ng/ml IGF-I or 10 nM insulin. Cell lysates were prepared as described previously [31]. Equal aliquots of lysate (100 μg) were separated by 4–20% SDS-PAGE and immunoblotted onto polyvinylidene Hybond-P membrane (Amersham, Arlington Heights, IL, USA). Analysis was performed using the indicated antibodies, and bands were visualized by ECL (Amersham).

### Assessment of the effect on in vitro cell growth

Tumor cells were grown to 70% confluence in six-well plates and infected with adenovirus. The number of cells was then assayed by Trypan blue staining.

Four thousand cells were seeded into the wells of a 96-well plate, and each was infected with adenovirus or control. Cell growth was measured using WST-1 reagent (Roche, Basel, Switzerland) as described previously [21].

### In vitro tumorigenicity

Anchorage-independent growth was assessed by soft agar clonogenicity assays. Briefly, cells were detached and plated in 0.2% agarose with 1% underlay ($2\times10^4$ cells/5-cm dish). After 1 week, media were added over the soft agar. The medium overlay was changed after 1 week. Colonies greater than 125 μm were counted after 3 weeks using a calibrated graticule.

Colony forming activity was assessed by plating $3\times10^3$ per plate on 60-mm culture dishes and incubated for 24 h. The cells were then treated with BMS-536924 and were incubated for 14 days. After air-drying, cells were fixed with methanol and stained with Giemsa solution. Colonies containing 50 cells or more were counted.

### Measurement of apoptosis

The DNA fragmentation assay was performed as follows: low molecular weight DNA was extracted with 0.5% Triton X-100, 10 nM EDTA, and 10 mM Tris–HCl, pH 7.4, treated with 400 μg/ml RNase A and then proteinase K for 1 h at 37°C, ethanol-precipitated, and subjected to 1% agarose gel electrophoresis. The gels were stained with 1 μg/ml ethidium bromide. Early apoptosis was quantified by staining with Annexin-V-FITC according to the manufacturer's protocol (BD Biosciences) and measured by flow cytometry. Cells undergoing apoptosis showed an increase in Annexin-V binding but excluded propidium iodide. TUNEL assays were performed with in situ apoptosis detection kit (Takara) following the manufacturer's protocol. Caspase-3 colorimetric protease assay was performed following the manufacturer's protocol (Caspase-3 Colorimetric Protease Assay Kit; MBL). In brief, $3 \times 10^6$ cells were lysed in 100 μl of chilled cell lysis buffer, and total cell lysates (100 μg) were incubated with 4 mM VETD-pNA Substrate (200 μM final concentration) at 37°C for 1 h. Caspase-3 activity was measured by colorimetric reaction at 405 nm.

First, cancer cells infected with Ad-IGF-IR/dns or Ad-LacZ were induced with 10 mJ/cm$^2$ UV light. To assess the efficacy of IGF-IR/dn on chemotherapy-induced apoptosis, tumor cells were treated for 24 h with 1 mM 5-FU or 50 μM cisplatin.

### Migration assay

Wounding assays were performed using a modification of the procedure described by Pennisi et al. [41]. Briefly, six-well chambers were prepared by scratching registration marks onto the slide surface. TE1 cells (infected with adenoviruses) were plated, grown normally for 48 h, and starved overnight. Cells were cut with a cell scraper, and five images were captured

**Table 1** Summary of immunohistochemical expression of IGF-IR

| | IGF-IR (+) | | |
|---|---|---|---|
| Normal esophageal mucosa | 0/7 | 0% | |
| Esophageal carcinoma | 31/57 | 54% | $p = 0.0111$ (Fisher) |
| | IGF-IR (+) | | |
| Squamous cell carcinoma | 23/34 | 68% | |
| Primary sites | 15/23 | 65% | |
| Metastasized sites | 8/11 | 73% | |
| Lymph node | 6/9 | 67% | |
| Skin | 2/2 | 100% | |
| Adenocarcinoma | 8/22 | 36% | |
| Adenosquamous carcinoma | 0/1 | 0% | |

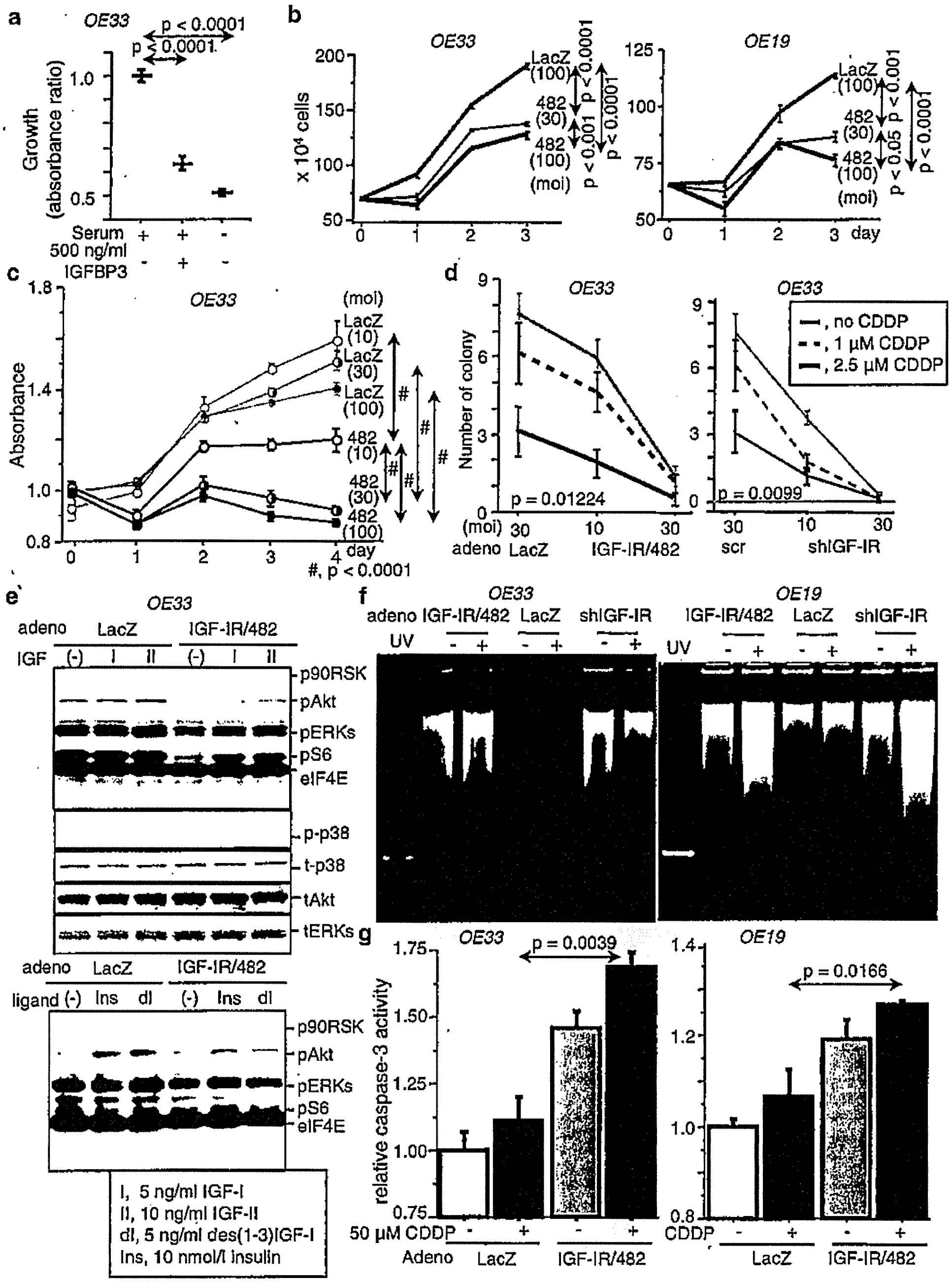


**Fig. 2** The effect of IGF-IR on EAC cells. **a** WST-1 assay showed cell growth of OE33, 48 h of culture with/without IGFBP3. **b** Trypan blue assay showed the number of viable cells. **c** WST-1 assay revealed cell proliferation of adenoviruses-infected OE33. **d** Colony formation assays showed the effect of IGF-IR/dn and cisplatin on colony formation. **e** OE33 was stimulated for 5 min with ligands in serum-free medium. Western blotting showed signal transduction. **f** DNA fragmentation assay detected UV-induced apoptosis. **g** Cells were treated for 24 h with cisplatin. Then, caspase-3 assays were performed

along the cut surface on an Olympus IX-71S1F-2 microscope (Tokyo, Japan) using a ×20 objective. Additional images were captured 24 h later. For each experiment, the number of migrating cells was counted by two independent observers [41].

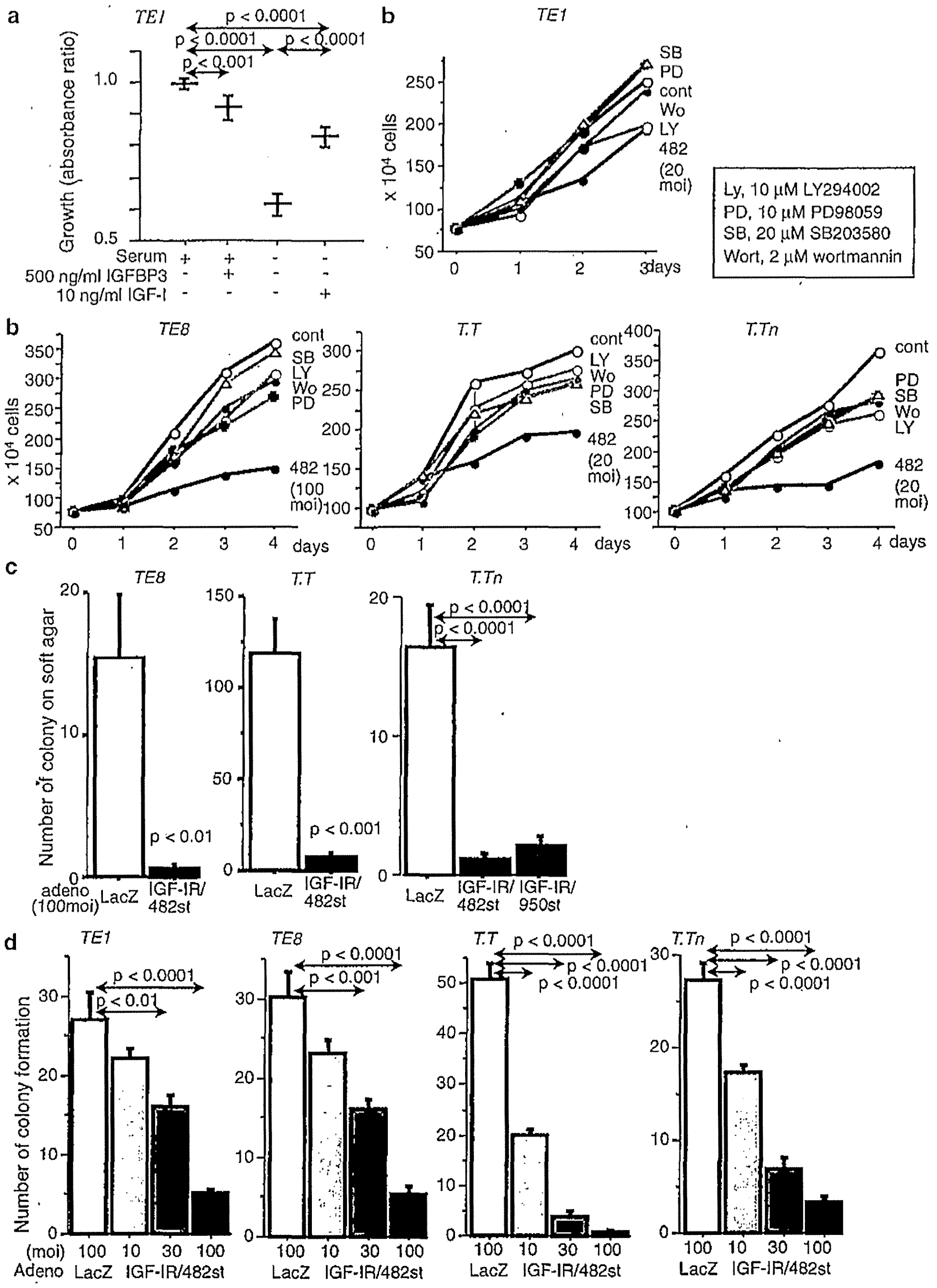


**Fig. 3** The effect of IGF-IR on the growth of ESCC. **a** WST-1 assay showed cell growth after 48 h of culture. **b** Trypan blue assay showed the viable cell number of ESCC cells with several inhibitors or IGF-IR/482st. **c** Soft agar assays detected that ad-IGF-IR/dns blocked colony formation. **d** Colony formation assay showed the effect of IGF-IR/482st on colony number

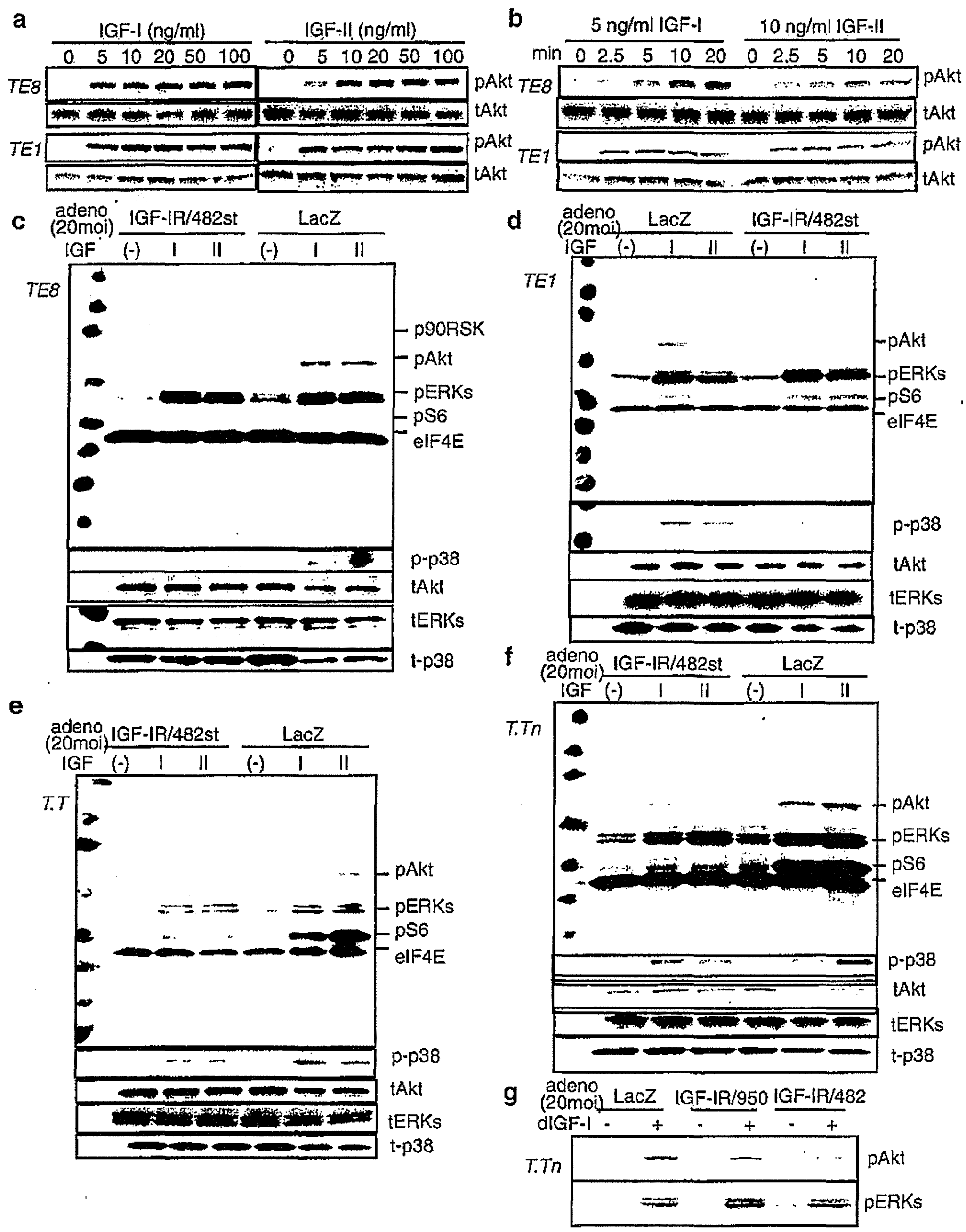
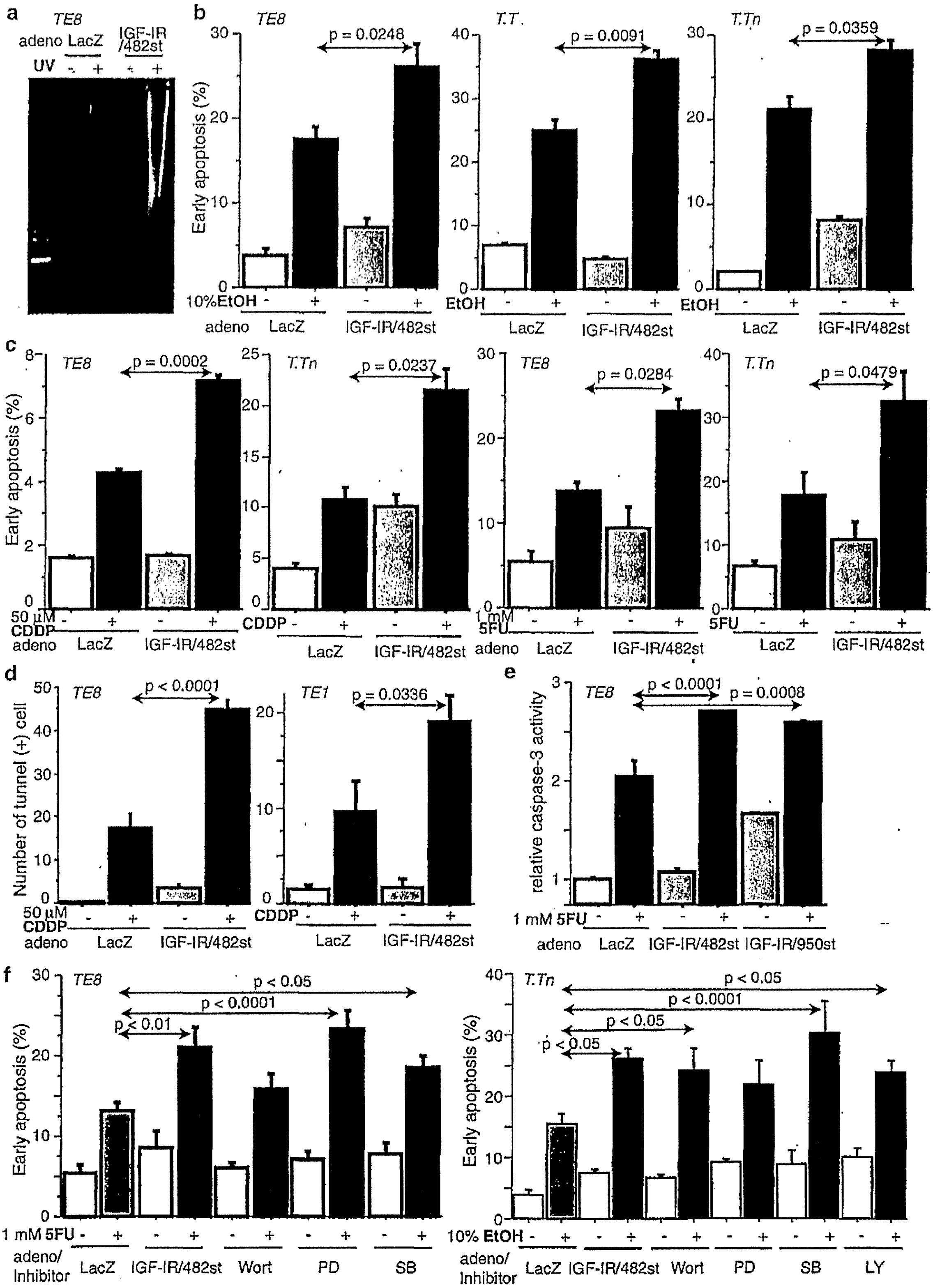


**Fig. 4** The down-stream signals from IGF-IR by Western blotting. **a** Both TE8 and TE1 cells were stimulated for 5 min with IGFs, and then whole cell lysates were extracted. **b** Both cells were stimulated from 0 to 20 min with IGFs. **c–f** Four cell lines infected with adenoviruses were stimulated for 5 min with IGFs. **g** Adenoviruses-infected T.Tn cells were stimulated for 5 min with 5 ng/ml des(1–3)IGF-I


a
TE8
adeno LacZ IGF-IR /482st
UV - + - +
b
TE8
T.T.
T.Tn
p = 0.0248
p = 0.0091
p = 0.0359
Early apoptosis (%)
0 10 20 30
0 10 20 30 40
10%EtOH - + - +
EtOH - + - +
adeno LacZ IGF-IR/482st
c
TE8
T.Tn
TE8
T.Tn
p = 0.0002
p = 0.0237
p = 0.0284
p = 0.0479
Early apoptosis (%)
0 2 4 6 8
0 5 10 15 20 25
0 10 20 30
0 10 20 30 40
50 µM CDDP - + - +
CDDP - + - +
1 mM 5FU - + - +
5FU - + - +
adeno LacZ IGF-IR/482st
d
TE8
TE1
p < 0.0001
p = 0.0336
Number of tunnel (+) cell
0 10 20 30 40 50
0 10 20
50 µM CDDP - + - +
CDDP - + - +
adeno LacZ IGF-IR/482st
e
TE8
p < 0.0001
p = 0.0008
relative caspase-3 activity
1 2 3
1 mM 5FU - + - + - +
adeno LacZ IGF-IR/482st IGF-IR/950st
f
TE8
T.Tn
p < 0.05
p < 0.0001
p < 0.01
p < 0.05
p < 0.0001
p < 0.05
p < 0.05
Early apoptosis (%)
0 10 20 30
0 10 20 30 40
1 mM 5FU - + - + - + - + - +
10% EtOH - + - + - + - + - + - +
adeno/ Inhibitor LacZ IGF-IR/482st Wort PD SB
adeno/ Inhibitor LacZ IGF-IR/482st Wort PD SB LY

◀ **Fig. 5** Apoptotic induction in ESCC. **a** DNA fragmentation assay showed UV-induced apoptosis. **b** Annexin-V assay revealed ethanol (EtOH)-induced early apoptosis. **c** Cells were treated with chemotherapy for 24 h. Then, annexin-V assay detected early apoptosis. **d** TUNEL assay revealed cisplatin-induced apoptosis. **e** Caspase-3 assays demonstrated 5-FU-induced apoptosis. **f** Annexin-V assay detected early apoptosis in ESCC cells with several inhibitors or IGF-IR/dn

### Statistical analysis

Statistical significance of difference between IGF-IR expressions was determined by Fisher's exact probability test.

The results of in vitro experiments are presented as means ± SE for each sample. The statistical significance of difference was determined by one-way ANOVA or two-factor factorial ANOVA. *P* values less than 0.05 were considered to indicate statistical significance.

## Results

### The expressions of IGF axis in esophageal cancers

In the previous paper, we reported that many ESCC cell lines express both IGF-IR and IGF-II, but a few cells express IGF-I [21]. We evaluated the mRNA expression of both IGF-IR and its ligands in two esophageal adenocarcinoma cell lines using RT-PCR (Fig. 1a). Like the control ESCC, TE1, both IGF-IR and IGF-II messages were identified. However, none expressed IGF-I mRNA. Then, we assessed the protein expressions of both IGF-IR and InsR using Western blotting (Fig. 1b). Both receptors were expressed in the two adenocarcinoma cell lines, and those expression levels were less than those of four ESCC lines.

Tissue array data showed that IGF-IR was expressed in cancer tissue more frequently than the normal mucosa (54 and 0%, respectively, $p = 0.0111$; Table 1). The expression of IGF-IR tended to be lower in EAC compared to ESCC (eight out of 22 primary EAC and 15 of 23 primary EACC). In ESCC, the IGF-IR expression ratio of metastatic sites tended to be higher, but not significantly so than that of the primary sites (73 and 65%, respectively).

These results indicate that both ligands and receptors are expressed in many esophageal carcinomas, implying that the IGF/IGF-IR axis might play some role in not only ESCC but also EAC.

### The effect of IGF-IR blockade on EAC cell lines

The natural inhibitor of IGFs, IGFBP3, suppressed the growth of OE33 to a similar level as that observed when they are cultured in serum-free media (Fig. 2a). Ad-IGF-IR/dn could reduce in vitro cell growth of both OE33 and OE19 (Fig. 2b). WST-1 assay showed that IGF-IR/dn blocked the growth of OE33 on plastic in a dose-dependent manner (Fig. 2c). IGF-IR/dn also reduced the number of colonies in a dose-dependent manner and strengthened the suppressive effect of cisplatin on colony formation of OE33 (Fig. 2d). Moreover, silencing IGF-IR by ad-shIGF-IR reduced colony number in a dose-dependent manner and enhanced cisplatin-induced suppression of colony formation in OE33 tumor cells.

Signaling analysis by Western blotting showed that ad-IGF-IR/dn could block both IGF-I- and IGF-II-induced phosphorylation of Akt in OE33 (Fig. 2e). IGF-IR/dn also reduced phosphorylation of both ERKs and S6. IGF-IR/dn could block des(1–3)IGF-I induced downstream signal transduction but not insulin-derived signals.

DNA fragmentation assays showed that IGF-IR/dn induced apoptosis in OE33 (Fig. 2f). In addition, IGF-IR/dn could enhance UV-induced apoptosis in OE33. The results were confirmed in another EAC cell, OE19. Moreover, ad-shIGF-IR showed almost the same effect as ad-IGF-IR/dn in both cell lines. Caspase-3 assays revealed that IGF-IR/dn up-regulated cisplatin-induced apoptosis in both OE33 and OE19 (Fig. 2g).

The results indicate that blockade of IGF-IR suppressed growth and colony formation and induced apoptosis in EAC cells.

### The effect of IGF-IR/dn on ESCC cell growth

In the previous report, we showed the effects of IGF-IR/dn mainly for the ESCC cell line, TE1, so here we assessed the effect of IGF-IR blockade on several other ESCC cell lines as well [21].

IGF-BP3 suppressed proliferation of TE1 cultured in conditioned media with serum (Fig. 3a). The cell growth was markedly suppressed in the media without serum and IGF-I partially overcame this suppression. IGF-IR/482st suppressed in vitro growth of other ESCC cell lines, TE8, T.T, and T.Tn, in addition to TE1 (Fig. 3b). In every cell line, IGF-IR/dn was the most effective for growth suppression among tested inhibitors, wortmannin, LY294002, PD98059, and SB203580.

Soft agar assays revealed that IGF-IR/482st inhibited in vitro tumorigenicity in three ESCC cells: TE8, T.T, and T.Tn (Fig. 3c). In addition to IGF-IR/482st, another dominant negative, IGF-IR/950st, suppressed the carcinogenicity of T.Tn. Colony formation assays showed that IGF-IR/482st suppressed colony formation in a dose-dependent manner (Fig. 3d).

### IGF-IR/dn blocked signal transduction in ESCC cell lines

Both IGF-I and IGF-II could induce phosphorylation of Akt-1 in both TE1 and TE8 cells (Fig. 4a). Effective concentrations of IGF-I were from 5 to 100 ng/ml, and IGF-II was also effective from 5 to 100 ng/ml. In both cell lines, 5 ng/ml IGF-I and 10 ng/ml IGF-II resulted in the activation of Akt-1 in 2.5 to 20 min (Fig. 4b).

Both Akt-1 and ERKs were phosphorylated by the ligands, IGF-I and IGF-II, in TE8 infected with control virus; however, Akt activation was blocked in the cells infected with IGF-IR/482st (Fig. 4c). The same results were observed in the other cell lines, TE1, T.T, and T.Tn (Fig. 4d–f). In the latter two cell lines, IGF-IR/482st inhibited the ligand-induced phosphorylation of S6. In T.Tn, des(1–3)IGF-I phosphorylated both downstream of Akt-1 and ERKs (Fig. 4g). In addition to IGF-IR/482st, IGF-IR/950st blocked phosphorylation of Akt-1 but not ERK in T.Tn.

### Up-regulation of apoptotic induction on ESCC cell lines by IGF-IR/dn

DNA fragmentation assays revealed that the expression of IGF-IR/dn induced up-regulation of UV-induced apoptosis in TE8 (Fig. 5a). Annexin-V assays showed that IGF-IR/dn up-regulated 10% ethanol-induced early apoptosis in three cell lines, TE8, T.T, and T.Tn (Fig. 5b). Moreover, IGF-IR/dn increased apoptosis induced by both chemotherapies (cisplatin and 5-FU) in both TE8 and T.Tn (Fig. 5c). TUNEL assays confirmed the result that IGF-IR/482st enhanced cisplatin-induced apoptosis in both TE8 and TE1 (Fig. 5d). Both IGF-IR/482st and IGF-IR/950st up-regulated 5-FU-induced apoptosis in TE8 as detected by caspase-3 assays (Fig. 5e).

Both PD98059 and SB203580 up-regulated 5-FU-induced apoptosis in TE8 but wortmannin could not, as detected by annexin-V assays (Fig. 5f). Three inhibitors, wortmannin, LY294002, and SB203580, enhanced 10% ethanol-induced early apoptosis in T.Tn, but PD98059 did not.

### The effect of IGF-IR on the migration of ESCC cell lines

T.T cells exhibited high mobility when cultured on plastic in a conditioned medium, but migration was reduced when these cells were cultured without serum (Fig. 6a). IGF-I stimulated the mobility of T.T in a dose-dependent manner, and IGFBP-3 reduced the migration ability of T.T cultured in conditioned media with FCS. The results indicated that the IGF/IGF-IR axis might play a part in the mobility of ESCC.

Both IGF-IR/dns suppressed the migration of T.T significantly (Fig. 6b). Moreover, both forms of IGF-IR/dn reduced the mobility of the other two cell lines, TE8 and T.Tn.

### The effect of BMS-536924 for both types of esophageal carcinoma

The IGF-IR/InsR inhibitor, BMS-536924, blocked IGF-I-induced IGF-IR auto-phosphorylation and its down-stream signals, pAkt and pERKs, in an ESCC cell, TE8 (Fig. 7a). The same results were detected in an EAC cell, OE33. Compared to IGF-IR/dn, BMS-536924 could also block the phosphorylation of ERKs clearly in both cell lines.

BMS-536924 inhibited insulin-induced InsR autophosphorylation and activation of not only Akt but also ERKs in both cell types (Fig. 7b), unlike IGF-IR/482st and IGF-IR/950st.

The kinase inhibitor suppressed colony formation of TE8 completely and blocked that of OE33 in a dose-dependent manner (Fig. 7c). Caspase-3 assay showed that BMS-536924 enhanced 5FU-induced apoptosis in a dose-dependent manner (Fig. 7d).

The results indicate that IGF-IR target therapy might be a candidate strategy for both types of esophageal carcinomas.

## Discussion

We show here that EAC cell lines express both IGF-II and IGF-IR, but not IGF-I, similar to ESCC. We also showed that IGF-IR was expressed in metastatic deposits in addition to the primary ESCC tumors. EAC expressed IGF-IR but tended to do so less frequently than ESCC. These results are compatible with the recent report in which higher IGF-IR protein expressions were observed in ESCC cells compared with EAC cells

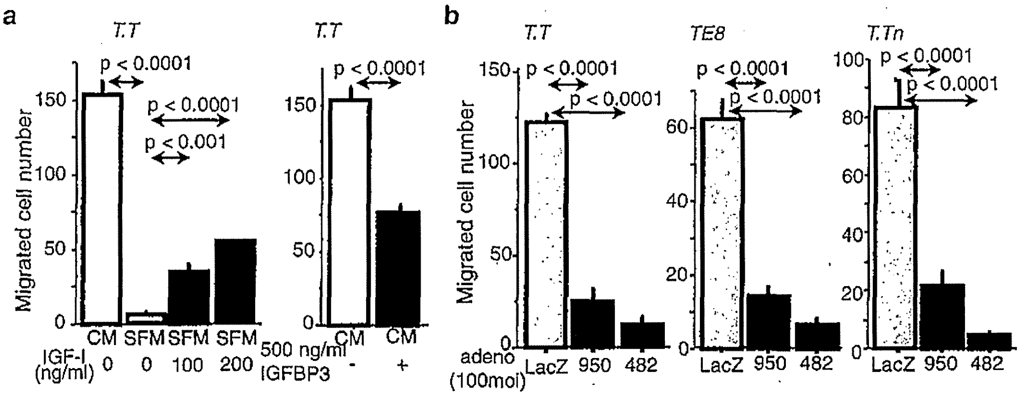


**Fig. 6** The effect of IGF axis on migration of ESCC assessed by wounding assays. a TT cells were cultured with or without FBS ± IGF-I for 24 h and were cultured with/without IGFBP3. b Migration assay was performed for adenoviruses-infected cells

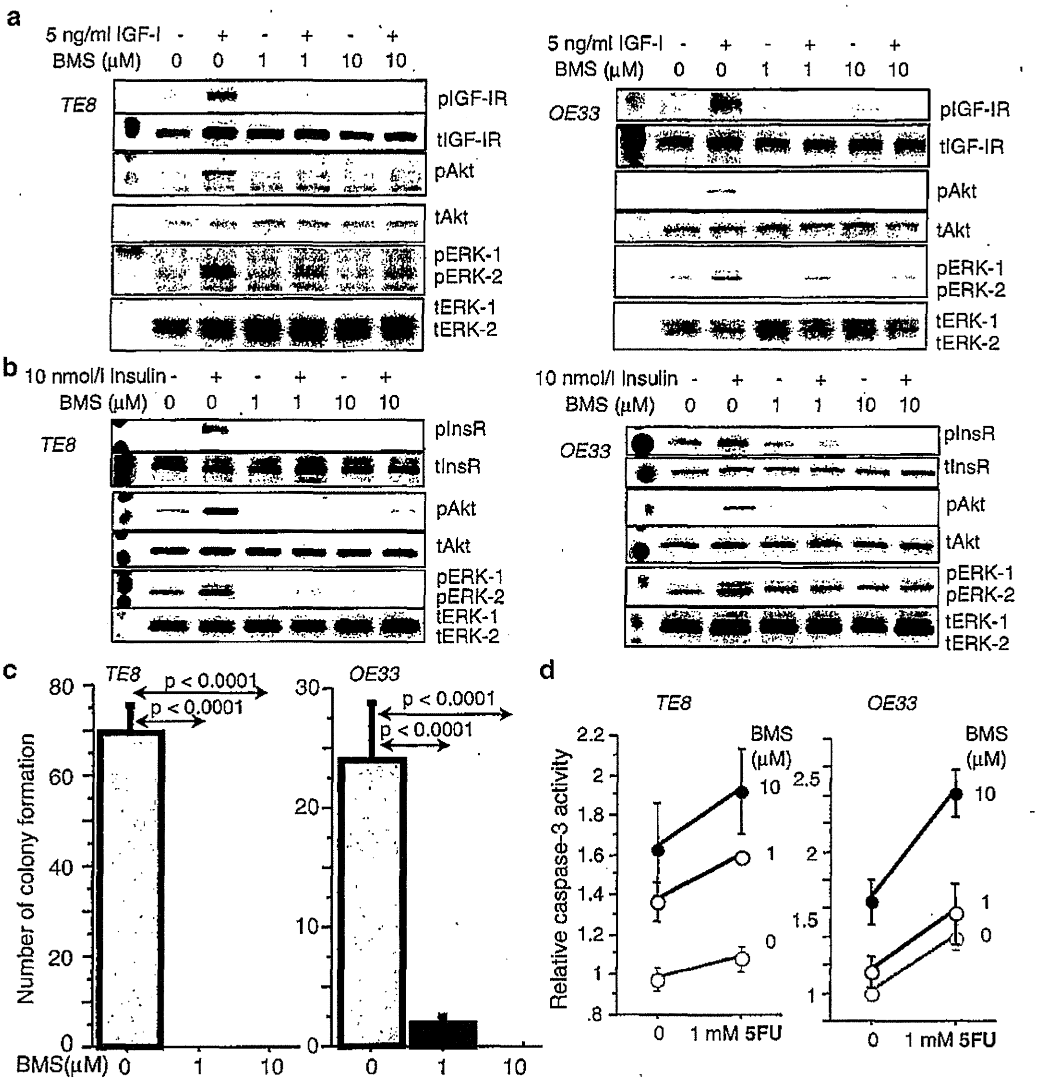


Fig. 7 The effect of BMS-536924 on both ESCC, TE8 and EAC, OE33. **a** After the cell was cultured with several amounts of BMS-536924, cells were stimulated for 5 min with IGF-I. Then Western blotting was performed. **b** After BMS-536924 treatment, the cells were stimulated for 5 min with insulin. **c** Colony formation assay revealed that this inhibitor reduced the number of colonies. **d** Caspase-3 assay revealed 5-FU-induced apoptosis

[22]. IGF-IR expression could also be useful as a novel prognostic marker for EAC [42]. Thus, IGF-IR might be a therapeutic target for many esophageal carcinomas.

In our previous study, we demonstrated that the IGF-IR axis is not only frequently overexpressed in ESCC and is associated with poor outcome but that it is also an exciting potential target for therapeutic intervention in this specific disease [21]. One of the possible mechanisms of IGF-IR overexpression in ESCC is that the miR-375 is downregulated by promoter methylation as miR-375 has a strong tumor-suppressive effect through inhibiting the expression of IGF-IR [43].

In this study, ad-IGF-IR/dn suppressed in vitro tumorigenicity, survival, and migration of both ESCC and EAC cells and also enhanced chemotherapy-induced apoptosis. In several cell lines representative of the two esophageal cancer subtypes (that express different patterns of IGF-IR and IGF ligand expression), the effects of ad-IGF-IR/dns were very similar, suggesting that IGF-IR targeting might have therapeutic potency for a variety of patients with esophageal carcinomas. This is also supported by the results from the multiple different inhibitors used in this study: IGF-IR/dns, shIGF-IR, and BMS-536924 all showed tumor-suppressive effects for esophageal carcinomas.

We showed here that IGF-IR blockade enhanced the effect of chemotherapy for esophageal carcinoma. It has been reported that IGF axis is responsible for chemoresistance. IGF-I inhibits 5-FU-induced apoptosis through increasing survivin levels, which prevents Smac/DIABLO release and blocks the activation of caspases [44].

As IGF-IR is closely related to the InsR [5], it is important to avoid adverse effects related to co-inhibition of the InsR and perhaps ideally that any strategy designed to block IGF-IR would have a high degree of specificity for IGF-IR compared to InsR. We show here that ad-IGF-IR/dn does not suppress insulin-induced Akt-phosphorylation, indicating a high degree of receptor selectivity. Thus, our ad-IGF-IR/dn strategy has the distinct potential advantage of blocking both IGF ligand signals, being independent of IGFBPs, interrupting signaling between IGF-IR and Akt-1, and not affecting insulin receptor signaling.

On the other hand, InsR could also work as accelerator of proliferation in cancer cells. Thus, the dual targeting TKI might have some advantages to block cancer progression. However, it was reported that insulin enhances anticancer functions of 5-FU when it is treated before 5-FU for the appropriate time in esophageal and colonic cancer cell lines [45]. As there is discrepancy in the effects of insulin on esophageal cancers, further analysis will be needed.

Several humanized mAbs and TKIs for IGF-IR have been generated, some of which are now in clinical studies [26–28]. This study provides support for testing of these therapies in esophageal cancer. Although some phase III studies for IGF-IR mAbs (but not TKIs) were withdrawn, others including a dual targeting TKI for IGF-IR/InsR, BMS-754807, continue in clinical trials [46].

It is reported that the insensitivity of TE1 to an IGF-IR TKI NVP-AEW541 occurred through maintained ras/ERK activity. Moreover, the transduction of mutant ras reduced the sensitivity of TE-1 cells to NVP-AEW541 [47]. However, these results are different from our reported data that NVP-AEW541 inhibited the cancer progression of four gastrointestinal cancer cell lines, including TE-1 [48]. It would be interesting to analyze the reasons for the differences between these studies.

In addition, we have reported an IGF-IR mAb, figitumumab (CP-751,871), that could suppress gastrointestinal cancers expressing k-ras mutations, including TE-1 [49]. Further studies are needed to assess the effect and mechanism of IGF-IR blockade in k-ras mutated cancers.

In this study, we showed that a dual IGF-IR/InsR TKI is effective for both types of human esophageal carcinomas. Several advantages of dual targeting strategies for esophageal carcinoma have been reported. TAE226, a dual tyrosine kinase inhibitor for FAK and IGF-IR, could suppress Barrett's EAC [50]. The combination of Her2 mAb, trastuzumab, and IGF-IR mAb, α-IR3, was more effective in inhibiting in vitro proliferation of EAC than treatment with either agent alone [42]. Thus, combined targeting of the IGF-IR axis with these other tumor drivers may show significant therapeutic promise.

IGF-IR might therefore be important in the progression of esophageal carcinomas, and IGF-IR target therapies might be candidate options for patients with both types of esophageal cancers.

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**Conflicts of interest** None

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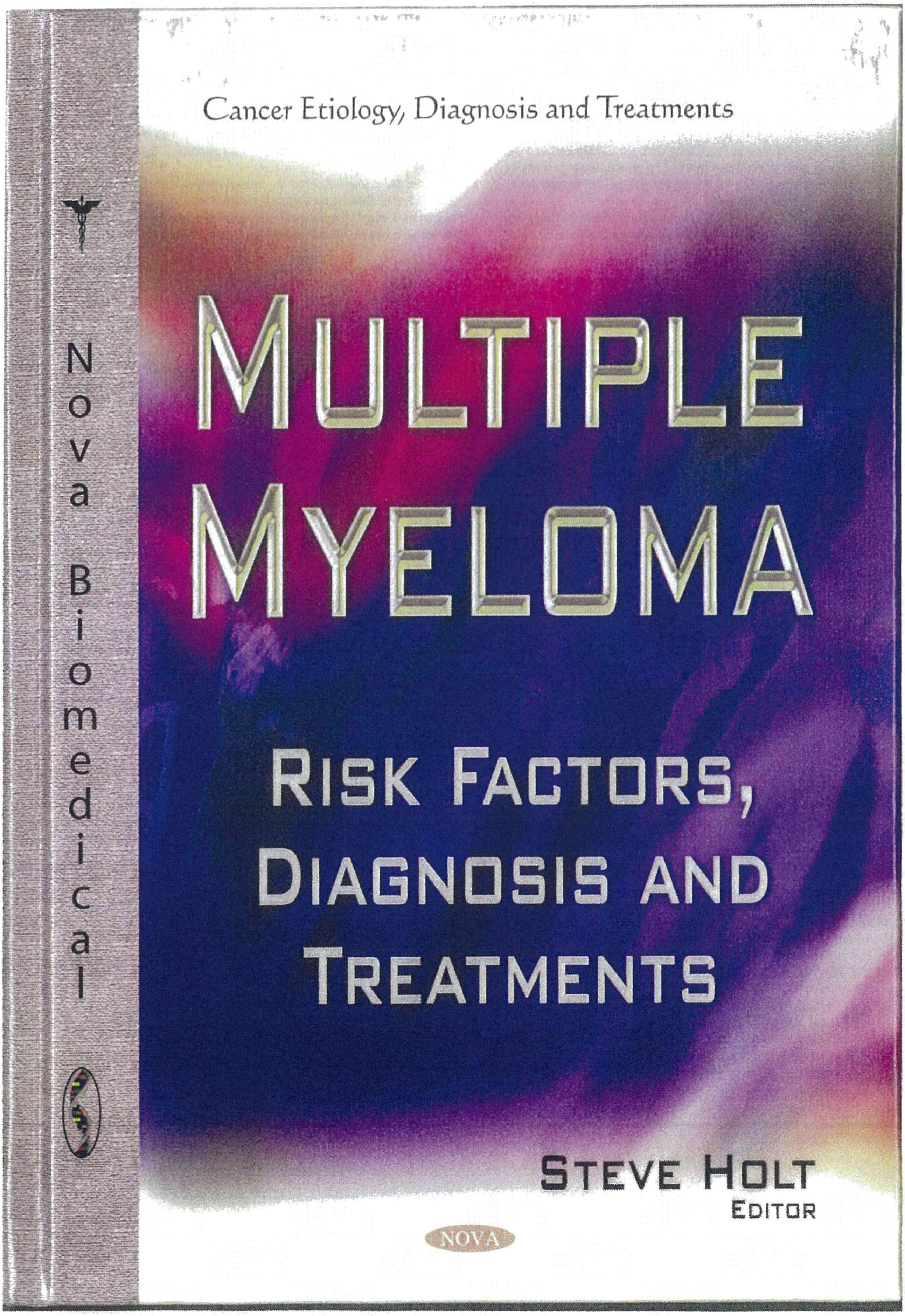

Cancer Etiology, Diagnosis and Treatments

# MULTIPLE MYELOMA

## RISK FACTORS, DIAGNOSIS AND TREATMENTS

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