

The Paradoxical Expression of *Maspin* in Ovarian Carcinoma¹

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ABSTRACT

Maspin is a noninhibitory member of the serpin family that is down-regulated in breast carcinoma but overexpressed in pancreatic carcinoma. There are no published data regarding the role of maspin in ovarian carcinoma, which is the focus of the present study. Ovarian cell lines (normal and cancer) and tumors (80 invasive, 14 benign, and 10 low malignant potential) were evaluated for maspin expression and localization. Normal ovarian surface epithelial cells had low levels of maspin. Two of four ovarian cancer cell lines (OVCAR3 and SKOV3) expressed maspin, whereas the cell line EG had weak expression, and 222 had no detectable maspin. Subcellular fractionation studies revealed that the two maspin-positive ovarian cancer cell lines contained maspin in both the nuclear and cytosolic compartments. Wild-type maspin was transfected into the aggressive ovarian cancer cell lines SKOV3 and 222. The *in vitro* invasive activity of the maspin-transfected cell lines was 44–68% lower than respective controls. The histopathology analysis revealed that among the ovarian tumors examined, 57 (71%) were ranked positive for maspin. Thirty (37%) of the invasive tumors overexpressed maspin. Invasive cancers were more likely to have predominantly cytoplasmic staining compared with benign and low-malignant-potential tumors. Maspin overexpression was significantly associated

with a high tumor grade ($P = 0.004$), the presence of ascites ($P = 0.02$), a lower likelihood of optimal surgical cytoreduction ($P = 0.04$), and a shorter duration of overall survival (median survival, 6.33 versus 2.67 years; $P = 0.003$). The Cox proportional hazards multivariate model revealed that maspin overexpression and high stage were independent predictors of survival. Thus, maspin was found to be overexpressed in a substantial proportion of ovarian tumors, which may serve as an adverse prognostic factor; however, its localization may provide new clues as to its activity and function. These paradoxical results may offer new insights regarding the role of maspin in ovarian cancer progression that may also impact diagnosis and treatment strategies.

INTRODUCTION

Maspin (mammary serpin) is a serine protease inhibitor member of the serpin family (1). The *maspin* gene was originally identified in normal mammary epithelium by subtractive hybridization on the basis of its expression at the mRNA level (1). It has been shown to have tumor suppressive activity attributable to the inhibition of breast cancer cell motility, invasion, and metastasis (2–4). Maspin encodes a 375-amino-acid protein (M_r of 42,000) with sequence homology to other inhibitory serpins (2, 5). The reactive site loop, situated near the COOH terminus, is one of the highly variable regions and is the domain that binds to the active site of the serine protease. The *maspin* gene is part of a serpin locus cluster at chromosome 18q21.3-q23. Several important transcription factor-binding sites are present within the 1-kb promoter region, namely Ets, Ap1, HRE, and p53 (6). Studies have revealed that maspin is largely an intracellular protein that is soluble in the cytoplasm and is also found associated with secretory vesicles.³ Maspin is located at the cell membrane interface with the extracellular matrix and does not act as a classical inhibitory serpin with antiprotease activity against trypsin-like proteases (7–9). Rather, small amounts of maspin are secreted but appear to remain associated with distinct structures at the cell surface.

Maspin appears to play a critical role in normal embryological development.⁴ The homozygous *maspin* knockout mice have been shown to produce an embryonic lethal.⁴ Interestingly, the existing knockout mice for other serpins and their protease targets are all viable.⁴ Female mice heterozygous for *maspin* are less likely to get pregnant, and, if they do, they deliver a smaller litter size compared with the wild-type mice.⁴ There are effects on normal ovarian function as well: ovulation efficiency of

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³ Pemberton, P. A. Maspin: functional insights from a structural perspective. *In*: M. J. C. Hendrix (ed.), *Maspin*. Internet address: www.landesbioscience.com.

⁴ Zhang, M. The role of maspin in tumor progression and normal development. *In*: M. J. C. Hendrix (ed.), *Maspin*. Internet address: www.landesbioscience.com.

maspin heterozygotes is greatly reduced compared with controls.

Although, at present, the molecular and biological mechanisms of the function(s) of *maspin* remains largely unknown, there is evidence that *maspin* interacts with the p53 tumor suppressor pathway and may function as an inhibitor of angiogenesis *in vitro* and *in vivo* (footnote⁴ and Ref. 10). Pemberton *et al.* (11) have demonstrated the presence of *maspin* in the epithelium of several normal human organs (such as prostate, thymus, testis, small intestine, and colon) and particularly in the myoepithelium of breast tissue, in which it is predominant and probably functions both intra- and extracellularly. However, *maspin* was not detected in the normal ovary in that study.

Maspin is expressed in normal human mammary and prostatic epithelial cells but is down-regulated during cancer progression (1, 12, 13). The loss of *maspin* gene expression with increasing malignancy is regulated at the transcriptional level (6). Recent studies have reported on the role of cytosine methylation and chromatin condensation in the down-regulation of *maspin* expression during neoplastic progression (14). However, other findings by Maass *et al.* (15) showed that *maspin* was overexpressed in pancreatic cancers. Specifically, 5 of 9 pancreatic cancer cell lines had *maspin* expression along with 23 of 24 tumor specimens. *Maspin* expression was not detected in normal pancreatic tissues, and patient outcome was not assessed in this study (15). To date, there have been no published reports evaluating the role of *maspin* in ovarian carcinomas, particularly with respect to clinical outcome. Thus, we undertook the present study with the following aims: (a) evaluate the clinical relevance of *maspin* expression in ovarian cancer, and; (b) evaluate the role of *maspin* in ovarian cancer invasion in experimental models.

MATERIALS AND METHODS

Cell Culture. The ovarian cancer cell lines used in this study were OVCAR3, SKOV3, EG, and 222. The derivation and sources of these cell lines have been reported previously (16). These cells were maintained and propagated *in vitro* by serial passage in RPMI 1640 supplemented with 15% fetal bovine serum and 0.1% gentamicin sulfate (Gemini Bioproducts; Calabasas, CA). The immortalized normal human ovarian surface epithelial cell line HIO 180 was a kind gift from Dr. Andrew Godwin at the Fox Chase Cancer Center, Philadelphia, PA. The immortalized normal breast epithelial cell line 1436N1 was a kind gift from Dr. Shijie Sheng at Wayne State University, Detroit, MI (16). These lines were maintained in Medium 199/MCDB 105 supplemented with 15% fetal bovine serum and 0.1% gentamicin sulfate. All of the cell lines are routinely screened for *Mycoplasma* species (GenProbe detection kit, Fisher, Itasca, IL). All of the experiments were performed with 70–80% confluent cultures.

Invasion Assay. The Membrane Invasion Culture system (MICS) chamber was used to measure the *in vitro* invasiveness of all of the cell lines used in this study (17, 18). Briefly, a polycarbonate membrane with 10 μ m pores (Osmonics; Livermore, CA) was uniformly coated with a defined basement membrane matrix consisting of human laminin/type IV collagen/gelatin and used as the intervening barrier to invasion. Both

upper and lower wells of the chamber were filled with serum-free RPMI containing 1 \times MITO+ serum supplement (Collaborative Biomedical; Bedford, MA). Single-cell tumor suspensions were seeded into the upper wells at a concentration of 1 \times 10⁵ cells/well. After a 24-h incubation in a humidified incubator at 37°C with 5% CO₂, cells that had invaded through the basement membrane were collected, stained, and counted by light microscopy (18). For chemoinvasion assays, conditioned medium from normal skin fibroblasts (kindly provided by Dr. Gregory Goldberg, Washington University, St. Louis, MO) was added to the lower wells. Invasiveness was calculated as the percentage of cells that had successfully invaded through the matrix-coated membrane to the lower wells compared with the total number of cells seeded into the upper wells and corrected for cell proliferation.

Formalin-fixed, Paraffin-embedded Samples for *Maspin* Immunohistochemical Staining. All of the samples were collected in compliance with requirements of the Institutional Review Board for the Protection of Human Subjects. Formalin-fixed, paraffin-embedded samples were sectioned at 4 μ m and stained with H&E for identification. Sections adjacent to the H&E-stained sections were used for immunohistochemical staining. All of the slides were deparaffinized using xylene, 100% ethanol, and 95% ethanol, followed by a thorough deionized water wash. A water bath antigen-recovery technique using citrate buffer (pH 6.0) was performed on all of the slides. The immunohistochemical staining for *maspin* was performed on the Dako Autostainer using the Vectastain Universal Elite ABC, Peroxidase kit (Vector Laboratories, Inc., Burlingame, CA) to detect mouse antihuman *maspin* (dilution 1:200; PharMingen, San Diego, CA). After deparaffinization and antigen recovery, slides were washed in TBST.⁵ Three blocking steps were applied: 0.03% hydrogen peroxide (Dako) for 15 min followed by a TBST wash, avidin and biotin blocks were applied for 15 min in each solution followed by a TBST wash after each step, and finally the Protein Block Serum-Free (Dako) was applied for 15 min. The primary antibody was applied to the slides and incubated for 60 min; slides were rinsed in TBST, followed by application of the vectastain secondary for 20 min. This procedure was followed by a TBST wash and then incubation with the ABC Reagent for 20 min. Color was produced by using DAB+ (brown) substrate (Dako) for 3 min. Slides were counterstained with Mayer's hematoxylin for 5–10 min.

All of the samples were reviewed by a board-certified pathologist (M. S. F.) who was blinded to the clinical outcome of these patients. *Maspin* expression was determined by assessing semiquantitatively the percentage of stained tumor cells and the staining intensity. The percentage of positive cells was rated as follows: 0 points, 0–5%; 2 points, 6–50%; 3 points, >50%. The staining intensity was rated as follows: 1 point, weak intensity; 2 points, moderate intensity; 3 points, strong intensity. Points for expression and percentage of positive cells were

⁵ The abbreviations used are: TBST, Tris-buffered saline and Tween 20; OMS, overall *maspin* score; RT-PCR, reverse transcription-PCR; LMP, low malignant potential; HRE, hormonal responsive element; GAPDH, glyceraldehyde-3-phosphate dehydrogenase.

added, and an OMS (0–3) was assigned. Tumors were categorized into four groups: negative (OMS = 0), $\leq 5\%$ cell stained, regardless of intensity; weak expression (OMS = 1), 2–3 points; moderate expression (OMS = 2), 4–5 points; and strong expression (OMS = 3), 6–7 points.

Subcellular Fractionation Studies. Cells were harvested and cell pellets used to prepare cytosolic and nuclear fractions. The cell pellet was suspended in buffer A [10 mM HEPES buffer (pH 7.9), containing 10 mM NaCl, 1 mM DTT, 10% glycerol, 15 mM MgCl₂, 0.2 mM EDTA, 0.1% NP40, protease inhibitor cocktail, and 1 mM phenylmethylsulfonyl fluoride] and subjected to three cycles of freeze-thaw and centrifuged at $4500 \times g$ for 10 min. The supernatant (cytosolic fraction) was removed, the pellet washed twice with buffer A, resuspended in buffer B (buffer A containing 500 mM NaCl) and left on ice for 30 min with occasional vortexing. The mixture was centrifuged at $25,000 \times g$ for 20 min to yield the nuclear fraction. The protein content of each fraction was determined using a bicinchoninic acid protein assay reagent kit (Pierce Corporation, Rockford, IL).

Maspin Transfection. Cells were plated at 5×10^5 cells/well on 6-well dishes. The cell lines 222 and SKOV3 were transfected with 2 μ g of wild-type *maspin* cDNA in pcDNA3.1 vector (Invitrogen Corporation, Carlsbad, CA) using LipofectAMINE 2000 Reagent (Invitrogen), following the manufacturer's protocol. Forty-eight h after the transfection, G418-containing medium was added and changed every 48–72 h thereafter. Sham constructs were created by transfecting pcDNA3.1 alone into both cell lines.

Western Blot Analysis. Cells were lysed with 1 \times RIPA buffer (50 mM Tris, 150 mM NaCl, 1% Triton X-100, and 0.5% deoxycholate) containing 25 μ g/ml leupeptin (Sigma Chemical Co., St. Louis, MO), 10 μ g/ml aprotinin (Sigma Chemical Co.), 1 mM sodium orthovanadate, and 2 mM EDTA. Cells were removed from the dishes by cell scraping. The samples were then subjected to three cycles of freeze-thaw and centrifuged at 12,500 rpm for 30 min. The protein concentration of the samples was determined using a bicinchoninic acid Protein Assay Reagent kit, and whole cell lysates were analyzed by 10% SDS-PAGE and stained with Coomassie BBR-250 (Sigma Chemical Co.) to ensure equal loading (data not shown). Samples were transferred to nitrocellulose (Schleicher and Schuell, Keene, NH). Blots were blocked with 5% nonfat milk for 1 h at room temperature. Blots were incubated with the monoclonal maspin antibody (1:500 dilution; PharMingen) for 1 h at room temperature with agitation, followed by incubation with a horseradish peroxidase-conjugated antimouse secondary antibody (1:5000; The Jackson Laboratory, Bar Harbor, ME). Blots were developed using an enhanced chemiluminescence detection kit (ECL; Amersham Pharmacia Biotech, Piscataway, NJ). For subcellular fractionation analyses, monoclonal actin (1:1500, Chemicon International, Temecula, CA) and monoclonal lamin B1 (1:500; Zymed, San Francisco, CA) antibodies were used.

RT-PCR Analysis. Total RNA was extracted from cells using a monophasic solution of phenol and guanidine isothiocyanate (Trizol reagent; Invitrogen). Total RNA (1 μ g) was reverse transcribed using an oligo(dT) primer and M-MLV reverse transcriptase (Life Technologies, Inc., Rockville, MD) in a final reaction volume of 20 μ l (60 min at 42°C). The

reaction was stopped by heating at 95°C for 5 min. The resulting cDNA was amplified by PCR in GeneAmp 10 \times PCR buffer (Perkin-Elmer, Branchburg, NJ) with 20 pmol of gene-specific 3' and 5' primers, 2 units of Taq DNA polymerase in a total volume of 50 μ l. Reactions were carried out for 30 cycles at 94°C for 1 min, 60°C for 2.5 min, and 72°C for 1 min in an Infinity Robocycler (Stratagene, La Jolla, CA). The following primers were used for maspin detection: forward, 5'-CCACAG-GCTTGGAGAAGATTGA-3'; reverse, 5'-GGTCAGCATTCA-ATTTCATCCTTGT-3'.

After RT-PCR, the reaction products were separated by electrophoresis on a 1% agarose gel. Gels were stained with ethidium bromide to visualize the PCR product size. To control for variance in loading and in PCR, samples were compared with GAPDH PCR products.

Northern Blot Analysis. The RNA extracted as above was separated by gel electrophoresis in 1% agarose containing 2.2 M formaldehyde. The gels were capillary blotted onto GeneScreen Plus nylon membranes (NEN/DuPont, Boston, MA), baked, and UV cross-linked. The membranes were then probed with radiolabeled cDNA probe. These blots were then reprobed with an actin cDNA to ensure equal loading.

Clinicopathological Variable Analysis. All of the patients underwent surgical exploration and cytoreduction as the initial treatment. The treating gynecologic oncologist determined the adjuvant therapy. Diagnosis was verified by a pathology review at the institutional gynecologic oncology tumor board. All of the patients were staged according to the International Federation of Gynecology and Obstetrics (FIGO) surgical staging system. A gynecologic pathologist reviewed the pathology for all patients.

Statistical Analysis. Either the χ^2 test or Fisher's exact test was used as appropriate to determine differences between variables using SPSS (SPSS Inc., Chicago, IL). Kaplan-Meier survival plots were generated and comparisons between survival curves were made with the log-rank statistic. The Cox proportional hazards model was used for multivariate analysis. A *P* of <0.05 was considered statistically significant.

RESULTS

Maspin Expression in Ovarian Cell Lines. Maspin expression in selected ovarian cell lines was assessed by RT-PCR, Western blot, Northern blot, and immunohistochemistry (Fig. 1A–E). The cell line 1436N1 is a normal breast epithelial cell line and was used as a positive control. The cell line HIO-180 is known to be poorly invasive (17) and demonstrated minimal maspin expression by Western blot and immunohistochemistry; and no expression was noted by RT-PCR and Northern blot (Fig. 1). Immunohistochemistry revealed that the maspin was mostly nuclear in location (Fig. 1C). Among the cancer cell lines, OVCAR3, SKOV3, and EG are known to be moderately invasive and cell line 222 is highly invasive in an *in vitro* invasion assay (17). The cell lines OVCAR3 and SKOV3 both expressed maspin, detected by Western blot, RT-PCR, and immunohistochemistry (Fig. 1, A, C, and E). Northern blot analysis revealed that maspin was expressed in OVCAR3, and a weaker band was seen for SKOV3 (Fig. 1E). Subcellular fractionation studies revealed that maspin was present in both the

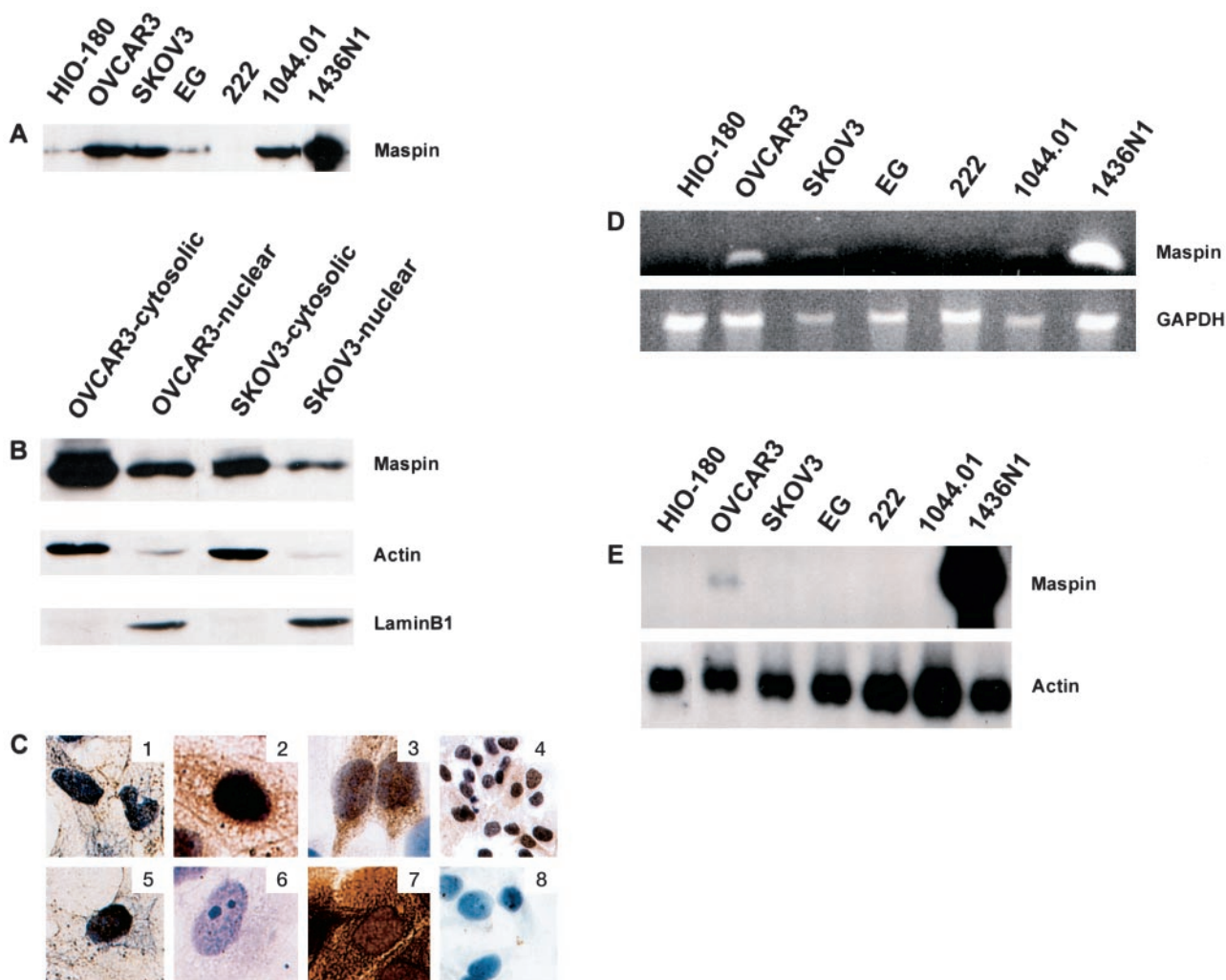


Fig. 1 Maspin analysis in normal ovarian surface epithelial cells (*HIO-180*), ovarian cancer cell lines (*OVCAR3*, *SKOV3*, *EG*, and *222*), and a high-stage tumor (*1044.01*). The cell line *1436N1* is a normal breast epithelial cell line and was used as a positive control. Maspin was analyzed by: (A) Western blot of whole cell lysates; (B) Western blot of subcellular fractions; (C, 1–8) immunohistochemical peroxidase staining for maspin in: (1) *HIO-180*, (2) *OVCAR3*, (3–4) *SKOV3*, (5) *EG*, (6) *222*, (7) *1436N1*, and (8) negative control; (D) RT-PCR; and (E) Northern blot. C, 1–3 and 5–8, $\times 630$; C, 4, $\times 400$.

nuclear and cytosolic fractions of *OVCAR3* and *SKOV3* (Fig. 1B). However, both immunohistochemistry and subcellular fractionation studies showed that most of the maspin was cytoplasmic in location. Monoclonal antibodies for actin and laminB1 were used as markers of cytosolic and nuclear fractions respectively (Fig. 1B). Full-length sequencing of the *maspin* gene was performed in *OVCAR3* and *SKOV3* to evaluate for a potential mutation. The following variations in sequence were noted: *OVCAR3* [CTA \rightarrow GTA (Leu \rightarrow Val), nucleotide 408]; *SKOV3* [GTG \rightarrow GCG (Val \rightarrow Ala), nucleotide 969]; TTA \rightarrow TTG (Leu \rightarrow Leu), nucleotide 1030]. The cell line *EG* had weak maspin expression, detected by Western blot and immunohistochemistry, but no mRNA expression was detected by RT-PCR or Northern blot analysis. The cell line *222* had no detectable maspin by any of the modalities used. The tumor *1044.01* was obtained from a patient with stage III ovarian cancer and ex-

pressed maspin by Western blot, RT-PCR (Fig. 1, A and D), and immunohistochemistry (data not shown).

Wild-Type Maspin Suppresses Invasion in Ovarian Carcinoma. Wild-type maspin cDNA was transfected into *222* and *SKOV3* ovarian cancer cells (Fig. 2). Immunofluorescence and immunohistochemical peroxidase staining demonstrated that most of the transfected maspin localized to the nucleus (Fig. 2). The baseline invasion rates of these ovarian cancer cell lines, measuring invasive ability through a basement membrane matrix *in vitro*, have been reported previously (17). *SKOV3* is moderately invasive (6.3%), and the cell line *222* is highly invasive (11.8%). After maspin transfection, two stably transfected clones (*222-MC2* and *222-MC3*) were tested for *in vitro* invasive ability. Wild-type maspin decreased stimulated invasion rates by 67% (from 12.04% to 4%) in *222-MC2* and by 44% in *222-MC3* (Fig. 3). The cell line *SKOV3* was success-

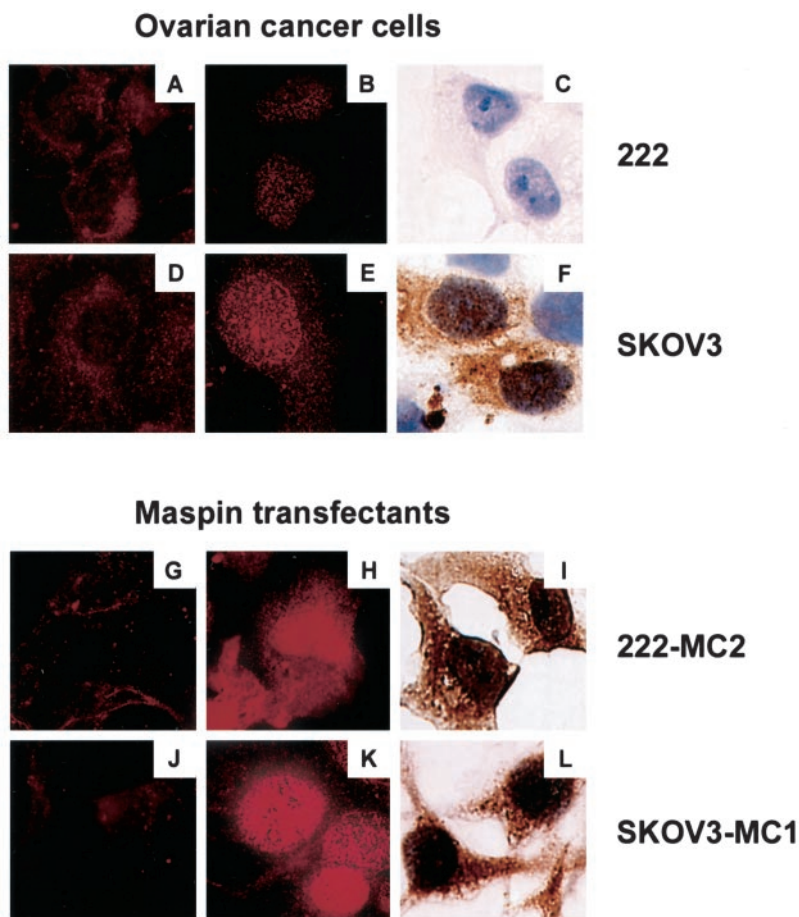


Fig. 2 Immunofluorescence and immunohistochemical peroxidase staining for *maspin* in the ovarian cancer cell lines 222 (A–C) and SKOV3 (D–F), and the maspin transfectants 222-MC2 (G–I) and SKOV3-MC1 (J–L). A, D, G, and J are negative controls. $\times 630$.

fully transfected with wild-type maspin, and three stable clones (SKOV3-MC1, -MC2, and -MC3) were further tested. The average invasive activity of the maspin-transfected clones was decreased by 62–68% when compared with SKOV3. There was no significant difference in invasion of either cell line with sham transfection (Fig. 3B). To prove that the effect on invasion was indeed caused by wild-type maspin expression, a monoclonal antibody (2 $\mu\text{g/ml}$) was used to inhibit maspin activity. As shown in Fig. 4, the antibody had no significant effect on the invasive activity of the 222 cell line. However, when the cell line 222-MC2 was exposed to the antibody, the invasive ability was restored to baseline levels. In contrast, even although SKOV3 and OVCAR3 cells expressed maspin, the monoclonal antibody had no significant effect on their invasive ability *in vitro*.

Maspin Expression in Human Ovarian Samples.

Maspin expression was assessed using immunohistochemistry in 14 benign epithelial ovarian tumors, 10 ovarian tumors of LMP, and 80 invasive epithelial ovarian cancers. Representative staining results in these samples are shown in Fig. 5. Maspin expression was seen in four benign epithelial ovarian tumors and was mostly nuclear in localization (Fig. 5A). All of the LMP tumors had maspin staining. More specifically, eight (80%) of LMP tumors had mostly nuclear staining (Fig. 5B), and only two

tumors had cytoplasmic staining primarily. Among the invasive ovarian cancers, 57 (71%) were considered positive, based on the OMS of ≥ 1 , and 23 (29%) were considered negative. Thirty (37%) of the invasive tumors overexpressed maspin (OMS = 3). Among the 57 invasive ovarian cancers with OMS ≥ 1 , only 15 (26%) had $\geq 50\%$ nuclear staining ($P = 0.001$ compared with benign and LMP tumors).

Clinicopathological Features of Invasive Ovarian Cancers.

The demographic features of the patients in this study are listed in Table 1. The mean age of patients in this cohort was 59.6 years. Eighty-one % of all of the patients had advanced stage (III or IV) disease and 43% had high-grade (III) disease. Sixty-eight % of all of the patients underwent optimal surgical cytoreduction (less than 1 cm of residual disease at the end of surgery). The correlation of maspin overexpression and various clinical variables are listed in Table 2. There was no association of maspin overexpression with histological subtype (serous *versus* other), stage, likelihood of nodal positivity, or menopausal status. Maspin overexpression was associated with high tumor grade and presence of ascites. Thirty-eight (76%) of 50 patients with tumor OMS ≤ 2 achieved optimal cytoreduction, compared with only 53% of those with maspin overexpression ($P = 0.04$). As expected, survival was adversely affected by high-stage, high-grade, and residual disease >1 cm (all *Ps*

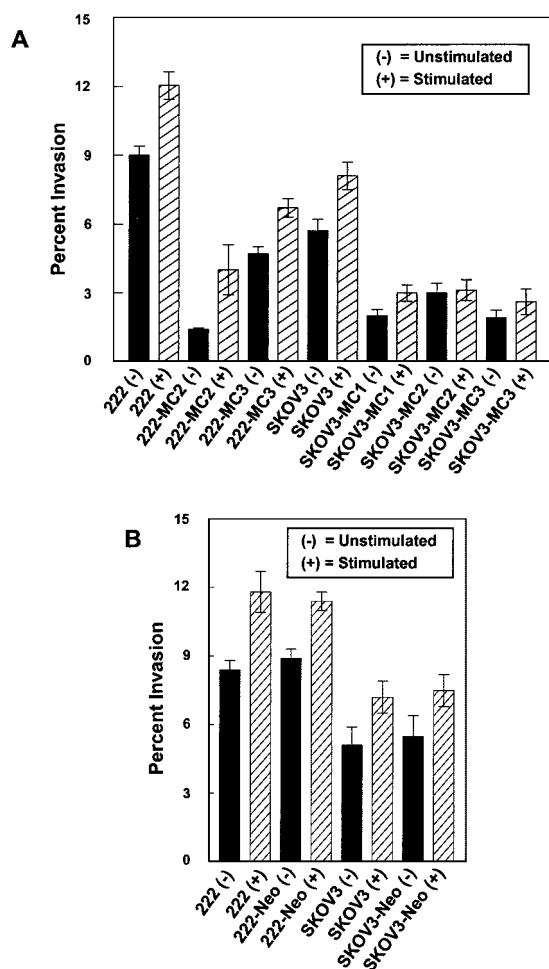


Fig. 3 Invasion profile of ovarian cancer cell lines (222 and SKOV3) compared with (A) maspin transfectants (222-MC2, 222-MC3, SKOV3-MC1, SKOV3-MC2, and SKOV3-MC3); and (B) sham transfectants (222-Neo and SKOV3-Neo), based on their ability to invade a basement membrane matrix *in vitro*, in the presence (▨) or absence (■) of a chemoattractant. Error bars, SE.

<0.05, data not shown). In univariate analysis, maspin overexpression was associated with significantly worse survival (median survival, 6.33 versus 2.67 years; $P = 0.003$; Fig. 6). However, the presence of $\geq 50\%$ nuclear maspin was associated with improved survival ($P = 0.003$). In multivariate analysis using the Cox proportional hazards model that involved age, stage, grade, volume of residual disease, maspin overexpression, and maspin subcellular localization, only high-stage ($P < 0.02$) and OMS of 3 ($P < 0.02$) were significant predictors of poor survival.

DISCUSSION

Maspin was originally described as a tumor suppressor gene important in cell motility and invasion (1). High maspin expression has been noted in normal human mammary and prostate epithelial cells but is decreased in the cancer cells from these respective organs, and is lost in metastatic cells (12, 13).

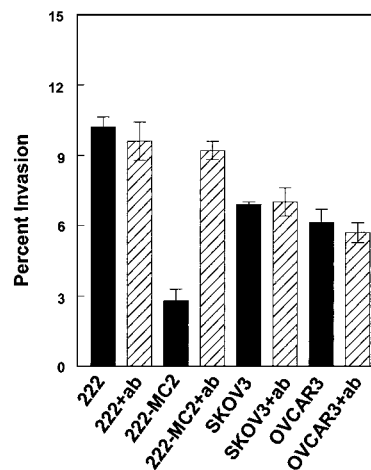


Fig. 4 Invasion profile of ovarian cancer cell lines, based on their ability to invade a basement membrane matrix *in vitro* with or without an inhibitory monoclonal antibody to maspin (ab). Error bars, SE.

Previously published data regarding maspin expression in normal ovarian tissue showed no expression in normal ovaries (11). However, maspin very likely plays a significant role in ovarian function, e.g., the ovarian ovulation efficiency of maspin heterozygote mice is greatly reduced compared with controls.⁴ The homozygous maspin knockout mice are known to be embryonic lethal. With respect to cancer progression, maspin inactivation that results in a lack of expression in prostate and breast tumors has been thought to play a role in tumor invasion and motility. Studies indicate that the loss of maspin expression during tumor progression results from both the absence of transactivation through the Ets element and the presence of transcription repression through the negative HRE recognized by the androgen receptor (19).

Interestingly, recent findings in pancreatic cancer are in sharp contrast to those reported in breast and prostate tumors. Specifically, Maass *et al.* (15) reported that maspin was detected in five of nine pancreatic cancer cell lines but was not detected in normal pancreatic tissue. In addition, maspin was expressed in 23 of 24 tumor specimens, but clinical correlates were not presented. Most of the tumor samples had strong cytoplasmic staining, but subcellular localization of maspin was not described in the preneoplastic pancreatic lesions. Similar to the pancreatic model, maspin was minimally expressed to absent in normal and benign ovarian samples in our present study. It is possible that the subcellular localization of maspin may play a critical role in its biological function. Alterations in subcellular localization and function of genes have been reported with other genes including β -catenin (20–22), cyclin E (23), 12-lipoxygenase (24), the cyclin-dependent kinase inhibitor p27(Kip1) (25), and cyclin D1 (26). Aust *et al.* (22) have demonstrated that, compared with normal colonic epithelium, colorectal cancers showed an overall shift from membranous to cytoplasmic expression of β -catenin and E-cadherin. Sgambato *et al.* (25) showed that, compared with normal colonic epithelium, the amount of p27(Kip1) in the cytoplasmic fraction was significantly higher in colon tumor samples. In our study, most of the

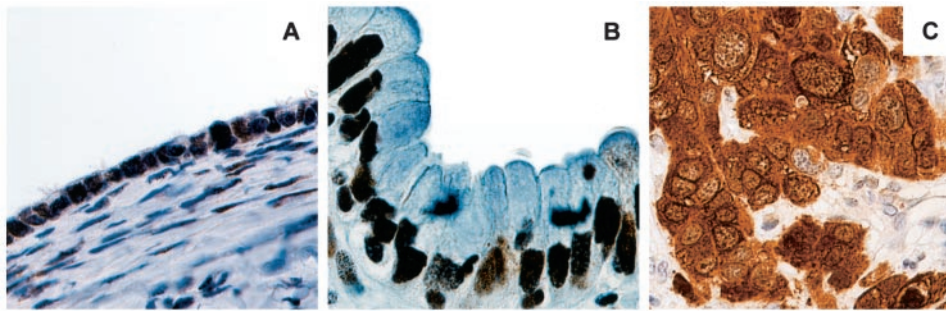


Fig. 5 Representative immunohistochemical peroxidase staining for maspin in: (A) normal ovary, (B) LMP ovarian tumor, and (C) stage IV, grade III ovarian cancer obtained from a patient. $\times 630$.

Table 1 Demographic features of invasive ovarian cancer patients

Variable	n
Age, yr	59.6 (34–83)
Stage	
I	10
II	5
III	51
IV	14
Menopausal	
Yes	61
No	19
Histology	
Serous	52
Other	28
Grade	
Low (I or II)	46
High (III)	34
Ascites	
Yes	60
No	20
Cytoreduction	
Optimal	54
Suboptimal	26
Node status	
Positive	10
Negative	22
Not done	48
Status	
Alive without disease	21
Alive with disease	12
Dead of disease	43
Dead of other causes	4

LMP tumors of the ovary expressed maspin, although it was mostly nuclear in localization. Analogous to invasive pancreatic tumors, the majority of invasive ovarian cancers also expressed cytoplasmic maspin staining. Thus, it is tempting to speculate that the maspin expressed in these tumors may be inactive. Indeed, our data with the SKOV3 cell line would support this finding: invasion was not affected by an inhibitory antibody. However, definitive proof for this hypothesis will require a functional assay of maspin activity, which is presently unavailable.

The *maspin* gene is part of a *serpin* locus at chromosome 18q21.3-q23. Several important transcription factor-binding sites are present within the 1-kb promoter region, namely Ets, AP1, HRE, and p53 (6). It contains seven exons (exon 1 is noncoding) and 6 introns. Interestingly, the region on 18q con-

Table 2 Correlation of clinicopathological variables with maspin overexpression in invasive ovarian cancer patients

Variable	Maspin overexpression		P
	Yes (n = 30)	No (n = 50)	
Stage			
Low	4	11	0.34
High	26	39	
Histology			.23
Serous	22	30	
Other	8	20	
Grade			0.004
Low (I or II)	11	35	
High (III)	19	15	
Ascites			0.02
No	3	17	
Yes	27	33	
Cytoreduction			0.04
Optimal	16	38	
Suboptimal	14	12	
Node status			0.16
Positive	3	7	
Negative	5	17	
Not done	22	26	
Menopausal			0.25
Yes	5	14	
No	25	36	

taining *maspin* is one of the most common areas of loss of heterozygosity in ovarian carcinoma (27). However, no significant mutations within the *maspin* coding sequence have been reported to date. Lack of any significant mutations in *maspin* is consistent with its being a class-I tumor suppressor molecule because such molecules are not expected to harbor any mutations within the coding sequences.³ Although, at present, the molecular and biological mechanisms of the maspin function remain unknown, there is evidence that maspin interacts with the p53 tumor suppressor pathway and may function as an inhibitor of angiogenesis *in vitro* and *in vivo* (10, 12). Also, maspin appears to be regulated by wild-type p53. Zou *et al.* (28) reported that there was robust induction of maspin in prostate and breast cancer cells after wild-type p53 expression. p53 was found to activate the maspin promoter by binding directly to the p53 consensus binding site present in the maspin promoter. It is not known whether such reliance on wild-type p53 occurs in other tumor systems. Most ovarian cancers are known to harbor p53 gene mutations (29, 30). Therefore, we are actively inves-

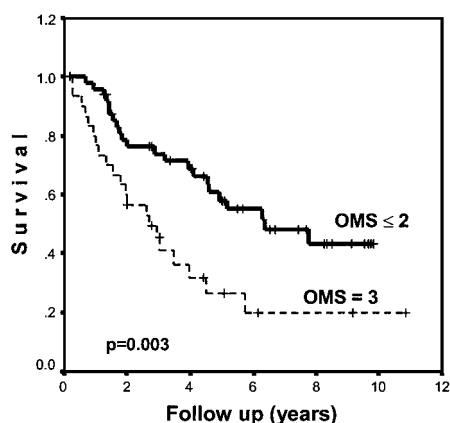


Fig. 6 Kaplan-Meier survival of ovarian cancer patients based on *maspin* staining intensity using the log-rank statistic.

titating the role of p53 in *maspin* expression in ovarian carcinoma to address this possible relationship.

Ovarian cancer continues to result in a high mortality rate among gynecological malignancies. This is reflective of the advanced stage at presentation in most patients. There are no reliable preoperative tests that consistently distinguish pelvic masses into benign or malignant. Because cytoplasmic *maspin* was detected in most ovarian cancer patients and it is minimally expressed in benign adnexal masses, it may serve as a useful marker for the detection of ovarian cancer. Paradoxically, nuclear localization of *maspin* (which may represent the active form of this molecule) was associated with improved survival, which may represent an additional utility.

In summary, *maspin* was found to be minimally expressed in adult normal ovarian epithelium. This study provided the first evidence that *maspin* is expressed by a substantial proportion of ovarian cancers. We have also provided *in vitro* evidence that wild-type *maspin* can inhibit ovarian cancer invasion. The precise role of *maspin* in ovarian cancer remains to be demonstrated. However, it is clear that the nuclear localization of *maspin* is associated with increased survival, whereas the cytoplasmic localization is associated with poor outcome in ovarian carcinoma, thus rendering it an attractive therapeutic target.

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