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Altered expression balance of matrix metalloproteinases and their inhibitors in human carotid plaque disruption: Results of quantitative tissue analysis using real-time RT-PCR method

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Abstract

Background: The balance between degradation and synthesis of extracellular matrix determines its content in atherosclerotic tissue. To examine the role of expression balance of matrix metalloproteinases (MMPs) to their inhibitors, tissue inhibitors of metalloproteinases (TIMPs) and tissue factor pathway inhibitor-2 (TFPI-2) in the development and disruption of atherosclerotic plaque, these gene expressions in human carotid plaque were quantitatively determined by real-time reverse transcription (RT)-polymerase chain reaction (PCR) method.
Methods: Total RNA for cDNA synthesis was extracted from tissues in 24 patients with carotid endarterectomy. The amounts of cDNAs for MMP-1, -2, -3 and -9, TFPI-2 and TIMP-1, -2 and -3 were determined by real-time RT-PCR method, and normalized with glutaraldehyde 3-dehydrogenase.
Results: In plaques, the expression MMP-1 (1.53 ± 0.25, mean ± S.E.M.), MMP-3 (1.99 ± 0.59) and MMP-9 (2.00 ± 0.51) was augmented compared to those in the adjacent control regions (0.60 ± 0.16, 0.46 ± 0.18 and 0.58 ± 0.21, respectively, $p < 0.05$). The expression of TFPI-2 was lower in plaques (0.32 ± 0.08) than in controls (0.94 ± 0.23, $p < 0.01$). Although the expression of TIMP-1 was higher in plaques (1.28 ± 0.23) than in controls (0.81 ± 0.10, $p < 0.05$), the indices of MMP-1/TIMP-1, MMP-3/TIMP-3 and MMP-9/TIMP-1 were still significantly higher in plaques. Interestingly, MMP-9 and the resulting MMP-9/TIMP-1 balance in plaques with disruption were significantly higher (3.36 ± 1.52 and 1.66 ± 0.12, $n = 11$) than those in non-disrupted plaques (1.11 ± 0.52 and 0.76 ± 0.12, $n = 13$, $p < 0.05$).
Conclusion: With the decreased expression of TFPI-2, upregulation of MMPs in atherosclerotic plaque was disproportional to that of TIMPs, suggesting that imbalanced degradation and synthesis of extracellular matrix persists in advanced lesions, particularly in plaques with disruption.

Keywords: Atherosclerosis; Extracellular matrix; Matrix metalloproteinases; Tissue inhibitor of metalloproteinases; Tissue factor pathway inhibitor-2; Plaque disruption

1. Introduction

Disruption of atherosclerotic plaque during its development can expose the thrombogenic core to luminal blood flow, frequently resulting in ischemic cardiac events and stroke

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[1,2]. During this process, structural changes in extracellular matrix (ECM) were shown to play a crucial role in plaque development and disruption [3]. The structural integrity of plaques seems to depend on a balance between synthesis and degradation of the ECM which is mainly regulated by proteinases such as matrix metalloproteinases (MMPs) including interstitial collagenase or MMP-1, gelatinase A or MMP-2, stromelysin 1 or MMP-3, gelatinase B or MMP-9 [4,5].

The activities of MMPs are controlled on multiple levels: transcription and translation of their inactive precursors (zymogens), post-translational activation of zymogens by proteolysis and interactions with tissue inhibitors of metalloproteinases (TIMPs) [6] and/or tissue factor pathway inhibitor-2 (TFPI-2) [7]. Indeed, TIMPs-1, -2, -3 and TFPI-2 are expressed in atherosclerotic lesions [7–9], and these inhibitors bind to and inactivate most of the MMPs [7,10]. Thus, the expression balance of MMP to TIMP and TFPI-2 is considered to regulate the net degeneration of ECM, thus contributing to maintaining plaque stability [7,11,12]. However, few systematic data exist regarding quantitative evaluation of the expression of MMPs and their inhibitors in human atherosclerotic plaques, probably because of technical difficulties in simultaneous determination of multiple gene expression in small tissue samples obtained in clinical settings. In the present study, we used real-time reverse transcription (RT)-polymerase chain reaction (PCR) and analyzed gene expression levels of MMPs, TIMPs and TFPI-2 in human carotid plaque and an adjacent control region. We also compared expression and function of MMPs between histologically disrupted and non-disrupted plaques.

2. Subjects and methods

2.1. Subjects

The protocol of this study was approved by the institutional committee for ethical review. Written informed consent was obtained from all 24 patients who underwent carotid endarterectomy for severe stenosis of the extracranial carotid artery (all male with mean age of 68 ± 2 years). All patients presented clinical symptoms of cerebral ischemic attack related to carotid stenosis. Seven patients had a history of recent ischemic attack within 1 month prior to endarterectomy. The prevalence of risk factors for atherosclerosis was as follows: hypertension (systolic pressure >160 mmHg) in 20, hyperlipidemia (total cholesterol >220 mg/dl) in 22, smoking in 15 and diabetes mellitus (fasting blood glucose >110 mg/dl) in 10 patients. High sensitive (hs) CRP level (normal range <3 mg/l) just before surgery was 2.45 ± 0.43 mg/l (Table 1).

2.2. Tissue sampling

Samples of the plaque region were obtained immediately after endarterectomy. Endarterectomy was extended in a caudal direction to include a sample of minimally affected common carotid artery proximal to the plaque but in continuity with the plaque to act as a paired control. Under these conditions, the stenotic segment and adjacent areas were dissected undisruptedly as a single specimen, preserving circumferential integrity as much as possible. Also special care was taken not to damage luminal surface and plaque interior. After removing a part of the tissue for histological examination, all samples were immediately frozen in liquid nitrogen and stored at −80 °C until extraction of mRNA.

Procedures for RNA preparation and cDNA synthesis were already described elsewhere in detail [13]. Briefly, the samples were homogenized in 1.0 ml ISOGEN™ reagent (Nippon Gene, Tokyo, Japan), thoroughly mixed with 0.2 ml chloroform and centrifuged at 15,000 × *g* for 15 min at 4 °C. The aqueous supernatant was transferred into a micro test tube, mixed with 0.6 ml isopropanol and centrifuged at 15,000 × *g* for 15 min at 4 °C. The precipitated total RNA was rinsed with 70% ethanol, air-dried and then resuspended in RNase-free water. Then, all the total RNA was treated with DNase Free™ reagent (Ambion, Austin, TX) for 60 min, and then reverse-transcribed with Superscript II™ (Invitrogen, Carlsbad, CA) at 37 °C for 60 min using random primers (TaKaRa, Tokyo, Japan). The integrity of each cDNA mixture was checked by amplification of glutaraldehyde 3-phosphate dehydrogenase (GAPDH) with *ExTaq* (TaKaRa), using the primer set 5′-ACCACAGTCCATGCCATCAC-3′/5′-TCCACCACCCTGTTGCTGTA-3′.

Table 1
Patient Characteristics

	All patients (*n* = 24)	With disruption (*n* = 11)	Without disruption (*n* = 13)	*p*-Value
Age	68 ± 2	66 ± 3	69 ± 2	NS
Male sex	24	11	13	NS
Hypertension	20	8	12	NS
Diabetes	10	5	5	NS
HbA1c (%)	6.5 ± 0.4	7.0 ± 0.8	6.2 ± 0.4	NS
Hyperlipidemia	22	9	13	NS
LDL (mg/dl)	132 ± 6	140 ± 10	128 ± 7	NS
Smoking	15	5	10	NS
hs-CRP (mg/l)	2.45 ± 0.43	2.68 ± 0.49	2.12 ± 0.81	NS