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Original Article

Oxidative Stress-Associated Autophagy Correlates to the Disease Severity of de Quervain's Disease

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Abstract

Background: de Quervain's disease is a well-recognized tendon disorder affecting the wrist, yet its pathogenesis remains poorly understood. Some research indicates that the disease may stem from intrinsic degeneration, while others suggest an inflammatory component. Autophagy, often initiated by oxidative stress, plays a critical role in both degenerative and inflammatory conditions and could be a significant factor in de Quervain's disease. However, the role of autophagy in this disease has not been previously explored. This study aims to investigate the involvement of oxidative stress in de Quervain's disease.

Methods: Specimens from the first dorsal retinaculum were collected from 45 patients diagnosed with de Quervain's disease for analysis. These specimens were classified into mild, moderate, and severe groups based on disease severity.

Results: The analysis revealed that levels of IL-6, LC-3, beclin-1, and Malondialdehyde (MDA) in the retinaculum specimens correlated positively with the severity of de Quervain's disease. Furthermore, nitric oxide and lipid peroxidation levels were significantly elevated in the severe group compared to the moderate and mild groups.

Conclusion: The results suggest that autophagy-related to oxidative stress may be a key factor in the pathogenesis and progression of de Quervain's disease. Therefore, antioxidants could be potentially useful in managing and preventing the progression of de Quervain's disease.

Keywords: Autophagy, de Quervain's disease, degeneration, inflammation, oxidative stress

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Introduction

de Quervain's disease, a stenosing tenosynovitis affecting the first dorsal compartment of the wrist, is a frequent tendon disorder encountered in clinical practice.[1] A study suggests that de Quervain's disease may arise from an intrinsic degenerative mechanism rather than an inflammatory one.[2] Other studies indicate that non-specific chronic inflammation is associated with the degree of histological changes.[3] In this study, it is proposed that the mechanism regulating degeneration and inflammation is involved in the pathogenesis and development of de Quervain's disease.

Autophagy plays a critical role in both degeneration and inflammation. It is a programmed process that can ultimately lead to cell death. Under cellular stress conditions, such as oxidative stress, LC3 (light chain 3)-II and beclin-1 work together to form an autophagic vacuole, which is digested after docking and fusing with a lysosome.[4] Autophagy is involved in the pathogenesis of various human degenerative diseases, including neurodegenerative disorders,[5,6] retinal degeneration,[7] intervertebral disc degeneration,[8,9] and cartilage degeneration.[10,11] Additionally, the interaction between autophagy and the inflammatory response has been revealed. Recent studies indicate that activating the autophagic pathway results in an increase in ILR/TLR-dependent NF-kB pathway activation and subsequent pro-inflammatory mediator expression, such as interleukin (IL)-1 and IL-6.[12]

Oxidative stress is a key regulatory pathway in the initiation of autophagy. It represents a status of imbalance between oxidants, such as free radicals, and circulating antioxidants. Specific types of reactive oxygen species (ROS) and reactive nitrogen species (RNS) include hydrogen peroxide, superoxide, peroxynitrite, and nitric oxide (NO).[13,14] Nitric oxide reacts with superoxide to generate peroxynitrite, a highly cytotoxic free radical.[15] Furthermore, oxidative stress has been reported to increase autophagy,[16] accumulating LC3-II and inducing Drp1 (dynamin-related protein 1)-mediated mitochondrial fission, which further increases mitophagy.[17,18] It is plausible that oxidative stress and autophagy participate in the pathogenesis of de Quervain's disease, although this has not been investigated previously. This study aims to investigate the

role of oxidative stress and autophagy in the development of de Quervain's disease.

Methods

Ethics Statement

This study complied with the Declaration of Helsinki, and the Institutional Review Board of the E-Da Hospital approved the research protocol (approval no: EMRP-111-045, date: 2022/04/21). Patients diagnosed with de Quervain's disease were thoroughly briefed on the study's objectives and procedures, and they subsequently provided written consent to participate. The study population consisted of 45 individuals, including 5 men and 40 women, with an average age of 52 years, spanning from 22 to 83 years old. To maintain the integrity of the study, patients with a history of systemic inflammatory disorders, previous trauma, or prior surgical interventions on the dorsal compartment of the wrist were excluded. The study focused on patients who had been suffering from de Quervain's disease for over 3 months and had not achieved relief through conservative treatments, making them candidates for operative release.

Specimen Harvesting and Preparation

Specimens of the first dorsal retinaculum were collected from 45 patients with de Quervain's disease who were undergoing open release surgery. Local infiltration anesthesia with 3-4 mL of 2% lidocaine HCl was used, followed by a 2 cm transverse skin incision made 1 cm proximal to the radial styloid process, over the first dorsal compartment. Care was taken to identify and protect the sensory branches of the radial nerve and nearby blood vessels. The extensor retinaculum was then incised along its dorsal margin to expose the Abductor pollicis longus (APL) and extensor pollicis brevis (EPB) tendons. A longitudinal sample measuring 3 mm by 5 mm was excised from the dorsal portion of the extensor retinaculum, including the fibrous sheath and adjacent synovium covering the tendons. The incision was closed using 3.0 or 4.0 absorbable sutures, and a dressing was applied to the area.

Hematoxylin and Eosin and Immunohistochemistry Staining

To evaluate collagen structure and identify target molecules, Hematoxylin and Eosin (H&E) and Immunohistochemistry staining were employed. Samples were first fixed in formalin, then embedded in paraffin, and sliced into 4 µm-thick sections for H&E staining. For IHC staining, the samples were permeabilized using 0.01 M phosphate-buffered saline (PBS). Following this, they were blocked by incubating for 1 hour with a mixture of 5% normal goat serum, 0.1% bovine serum albumin, and 0.2% Triton-X 100 in 0.01 M PBS before the primary antibody was applied. Monoclonal antibodies targeting IL-6 (1:400), LC-3 (1:400), beclin-1 (1:400), MDA (1:400), and PGx (1:100) (Zymogenetics, Seattle, WA, USA) were utilized. Secondary antibodies, biotinylated anti-mouse, or anti-rabbit, depending on the primary antibody's source, were then applied. Immunoreactivity was detected using the Mouse/Rabbit PolyDetector HRP/DAB System (Bio SB, Santa Barbara, CA), and sections were subsequently counterstained with hematoxylin.

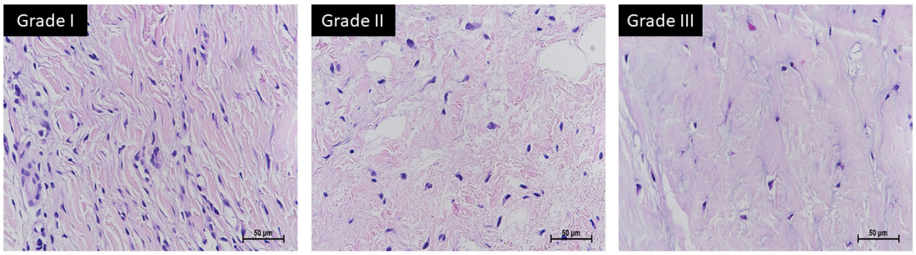

Figure 1. Criteria for grouping in the study: Severity was evaluated based on collagen fiber and extracellular matrix characteristics. The grading system was as follows: Grade 1: Slight degradation of the collagen structure with minimal waviness and slight splitting between contiguous fiber bundles. Grade 2: Moderate degradation with some separation between bundles, increased waviness, loss of parallel arrangement, and moderate fragmentation. Grade 3: Severe degradation with a complete loss of fiber orientation and extensive fiber fragmentation. The groups—mild, moderate, and severe—were defined according to the percentage of samples categorized as Grade 1 and 2.

Grading System and Grouping Criteria

The stained slides were scanned and converted into digital images. Two independent pathologists evaluated the samples individually, and their assessments were compared to establish a consensus grade. The extent of degradation was measured by examining the state of the collagen fibers and the extracellular matrix (ECM) (FIgure 1):

Grade 1: Slight degradation with minor waviness and minimal separation between fiber bundles.

Grade 2: Moderate degradation with some separation between bundles, increased waviness, loss of parallel alignment, and moderate fragmentation.

Grade 3: Severe degradation with a complete loss of fiber orientation and extensive fragmentation.

Samples were categorized into 3 groups according to these grades:

Mild: 0% < Area (Grade 2 + Grade 3) < 25%.

Moderate: 25% < Area (Grade 2 + Grade 3) < 50%.

Severe: 50% < Area (Grade 2 + Grade 3) < 100%.

Statistical Analysis

All measurements were expressed as mean ± SD. The analysis of the various graded regions was conducted using GraphPad Prism 5.0 (GraphPad Software, Inc., La Jolla, CA). Data were assessed using one-way analysis of variance (ANOVA), followed by Student's t-test for comparison. A *P*-value of less than .05 was deemed statistically significant.

Results

The expression of pro-inflammatory mediators in tissue samples from patients with de Quervain's disease was analyzed. To explore the role of inflammation in the disease's development, IL-6 levels were measured. Immunohistochemical (IHC) staining indicated that the percentage of IL-6 positive cells increased with disease severity, with significantly higher IL-6 expression observed in the severe group compared to the mild and moderate groups (Figure 2).

Additionally, the expression of autophagy-related proteins was evaluated. To understand the involvement of autophagy in de Quervain's disease, LC-3 and Beclin-1 expressions were assessed. The IHC analysis revealed that LC-3 expression was significantly higher in the moderate and severe groups compared to the mild group (Figure 3). Moreover, Beclin-1 expression was markedly higher in the severe group compared to the mild and moderate groups (Figure 4).

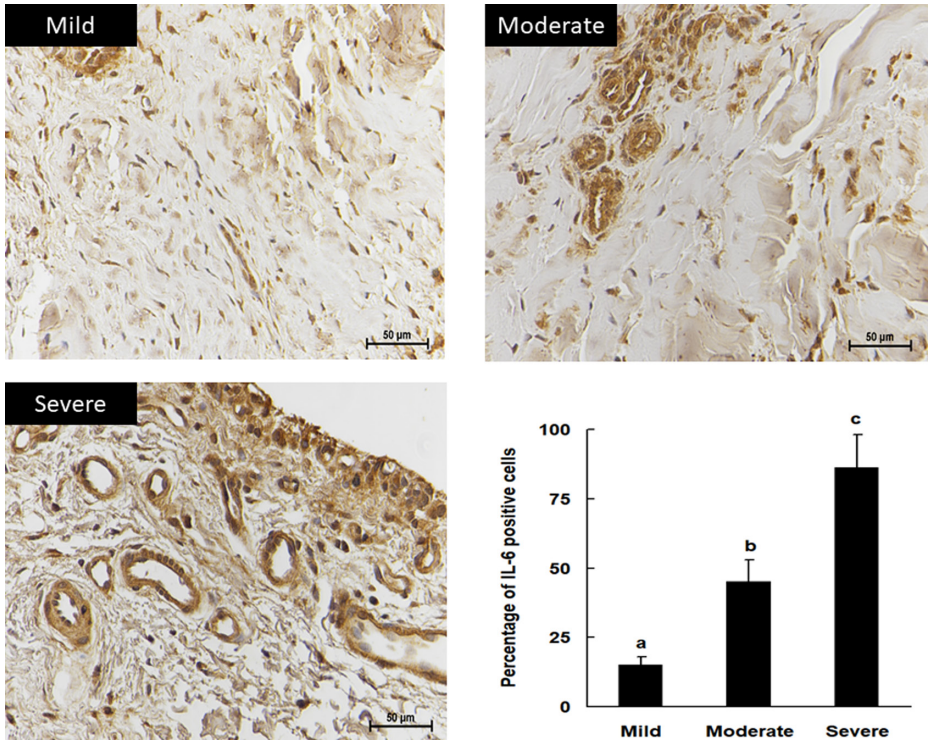

Figure 2. Immunohistochemistry (IHC) staining of IL-6 in tissue samples from de Quervain's disease patients. IL-6 protein appears brown (magnification ×40). Data are expressed as means ± SD and analyzed by one-way ANOVA followed by Student's *t*-test. Statistically significant differences ($P < .05$) are marked with different letters, indicating significant variations between the severe group and the moderate and mild groups.

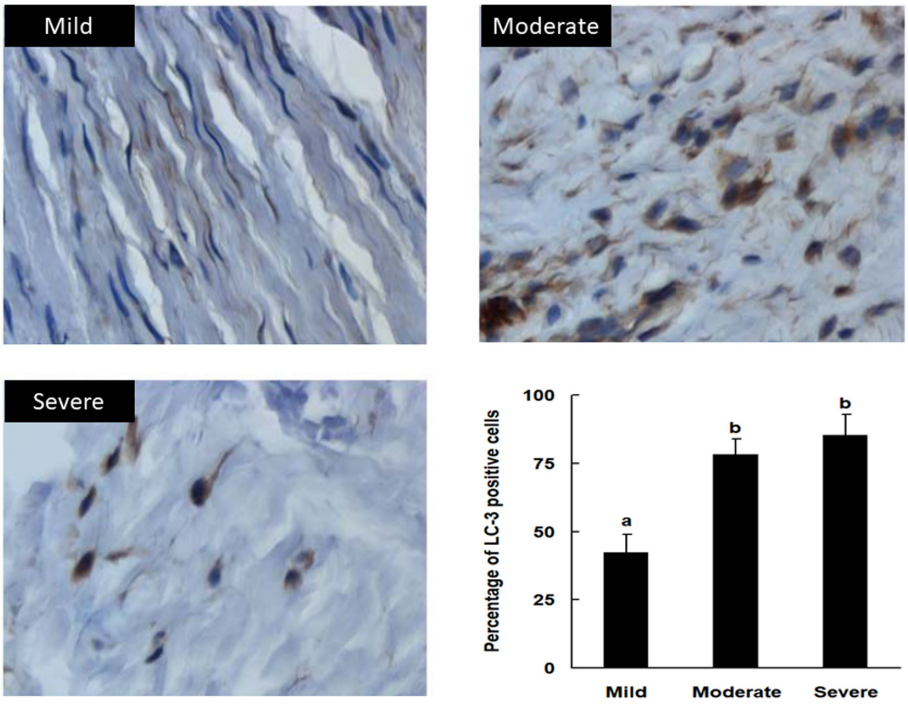

Figure 3. Immunohistochemistry staining of LC-3 in tissue samples from de Quervain's disease patients. LC-3 protein is stained brown (magnification ×40). Data are presented as means ± SD and analyzed by one-way ANOVA followed by Student's *t*-test. Different letters denote statistically significant differences ($P < .05$) between the severe and moderate groups compared to the mild group. Identical letters indicate no significant difference between the moderate and severe groups.

To explore the role of oxidative stress in de Quervain's disease, MDA levels (a marker of lipid peroxidation) and GPx expression (a significant antioxidant) were measured in tissue samples from patients. A higher percentage of MDA-positive cells was observed in tissues with greater disease severity (Figure 5), while GPx expression was notably lower in the severe group compared to the mild group (Figure 6).

Additionally, lipid peroxidation levels were assessed in wet tissue samples to further confirm oxidative stress involvement. MDA production was significantly higher in the severe group compared to the mild and moderate groups, indicating increased oxidative stress in more severe cases of de Quervain's disease (Figure 7).

To investigate the role of nitric oxide in oxidative stress associated with de Quervain's disease, nitrite levels were evaluated in wet tissue samples. Nitrite production was significantly higher in the severe group compared to both the mild and moderate groups (Figure 8).

Discussion

In this study, it was demonstrated that levels of oxidative stress and autophagy are related to the severity of de Quervain's disease. It was found that high levels of autophagy and oxidative stress were present in more severe cases. Additionally, autophagy-related molecules were highly expressed in these areas. Therefore, it was suggested that increased oxidative stress-associated autophagy may be involved in the pathogenesis and progression of de Quervain's disease.

Autophagy has been proposed to play a crucial role in regulating the inflammatory process[19,20] It was anticipated that autophagy may influence the expression of inflammatory mediators observed in patients with de Quervain's disease. Activating the autophagic pathway leads to the activation of NF-kB, a nuclear transcription factor.[12] Activated NF-kB enters the cell nucleus and transcribes inflammation-related proteins, such as IL-6.[21] Inhibiting autophagy reduces the expression of pro-inflammatory cytokines and the inflammatory response in various experimental settings.[12] In this study, IL-6, as well as LC-3 and beclin-1 expression, were higher in the severe group compared to the mild and moderate groups. It is likely that increased autophagy is associated with higher levels of inflammation in patients with de Quervain's disease. Previous studies indicate that autophagy plays a regulatory role in various degenerative diseases.[22] Therefore, it

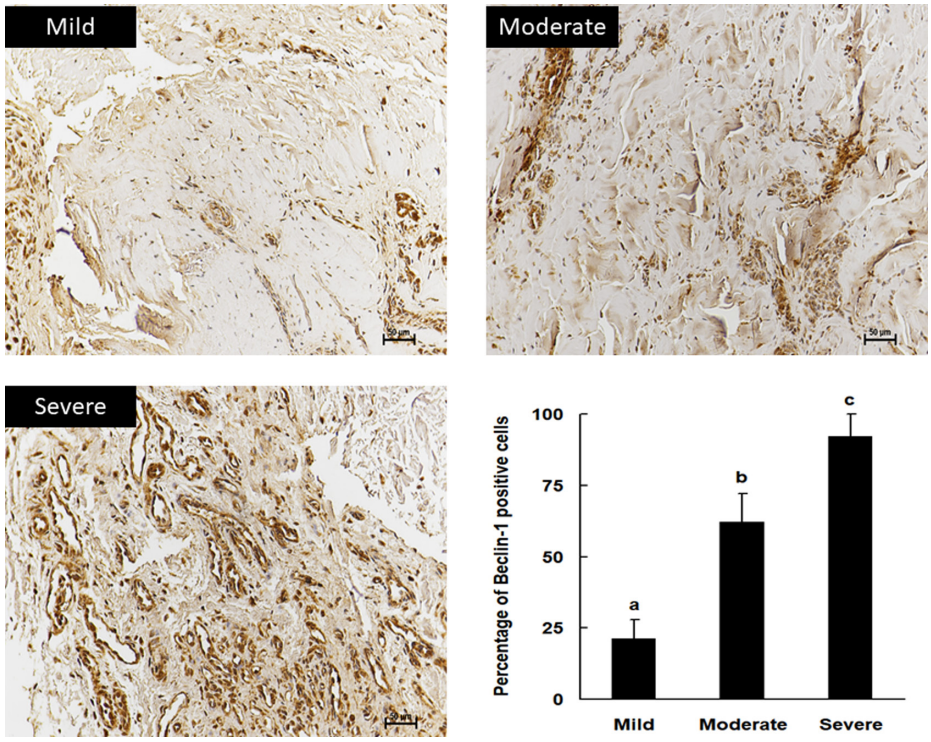

Figure 4. Immunohistochemistry staining of Beclin-1 in tissue from patients with de Quervain's disease. Beclin-1 protein appears brown (magnification ×40). Data are shown as means ± SD and analyzed with one-way ANOVA followed by Student's *t*-test. Different letters indicate statistically significant differences ($P < .05$) in the severe group compared to the moderate and mild groups.

was suggested that autophagy, inflammation, and degeneration may be critical mechanisms involved in the pathogenesis of de Quervain's disease.

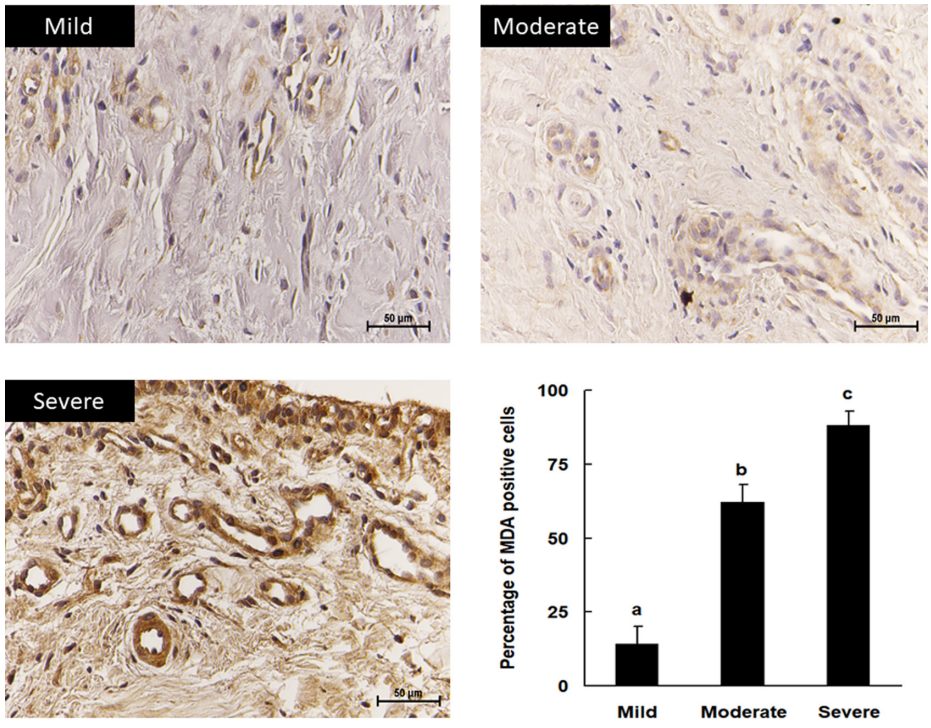

Figure 5. Immunohistochemistry staining of MDA in tissue samples from patients with de Quervain's disease. MDA is stained brown (magnification ×40). Data are presented as means ± SD and analyzed using one-way ANOVA followed by Student's t-test. Different letters indicate statistically significant differences ($P < .05$) between the severe group and the moderate and mild groups.

Besides these mechanisms, oxidative stress may be a significant underlying cause of de Quervain's disease. Oxidative stress is closely related to mitochondrial dysfunction, as mitochondria are both sources and targets of reactive oxygen species.[23] Autophagy is commonly induced by oxidative stress in cells.[24,25] Increasing oxidative stress enhances the activation of the autophagic pathway, while inhibiting oxidative stress significantly reduces autophagy.[26] Nitric oxide, one of the RNS, reacts with superoxide to generate peroxynitrite, which can initiate further protein oxidation and nitration.[27,28] Previous studies indicate that NO increases LC3-II accumulation, mitochondrial fission, and mitophagy.[29] Furthermore, higher levels of lipid peroxidation and lower levels of glutathione peroxidase (GPx) were found in the severe group compared to the mild or moderate groups. In this study, higher levels of lipid peroxidation (LPO) and NO were also found in tissues removed from patients with de Quervain's disease. Thus, it was suggested that oxidative stress may be another important mechanism contributing to the severity of de Quervain's disease.

Treatments for de Quervain's disease are limited due to its unknown etiology. While current investigations focus on inflammatory mediators that may predispose individuals to this condition,[30-32] other recently identified risk factors include exposure to somatotropin and genetic predisposition.[33] Patients should receive customized instructions based on their specific clinical conditions, covering aspects like activity, function, and pain management. These instructions should be complemented by appropriate interventions, which may include nonsteroidal anti-inflammatory drugs (NSAIDs), splinting, corticosteroid injections, and, if needed, surgical options.[34] The choice of intervention should be guided by the severity and duration of the disease, as well as previous treatments.[34] Although new treatment options for de Quervain's disease, such as hyaluronic acid injections, extracorporeal shockwave therapy, acupuncture, ultrasonographic therapy, and laser therapy, are becoming available, evidence supporting their effectiveness remains limited.[35] Therefore, deciding on the most suitable management approach can be challenging due to the range of available treatments and their potential combinations. In light of the findings, future treatment strategies for de Quervain's disease should consider the interplay between oxidative stress, autophagy, and inflammation. While current anti-inflammatory therapies such as NSAIDs and corticosteroids target downstream inflammatory

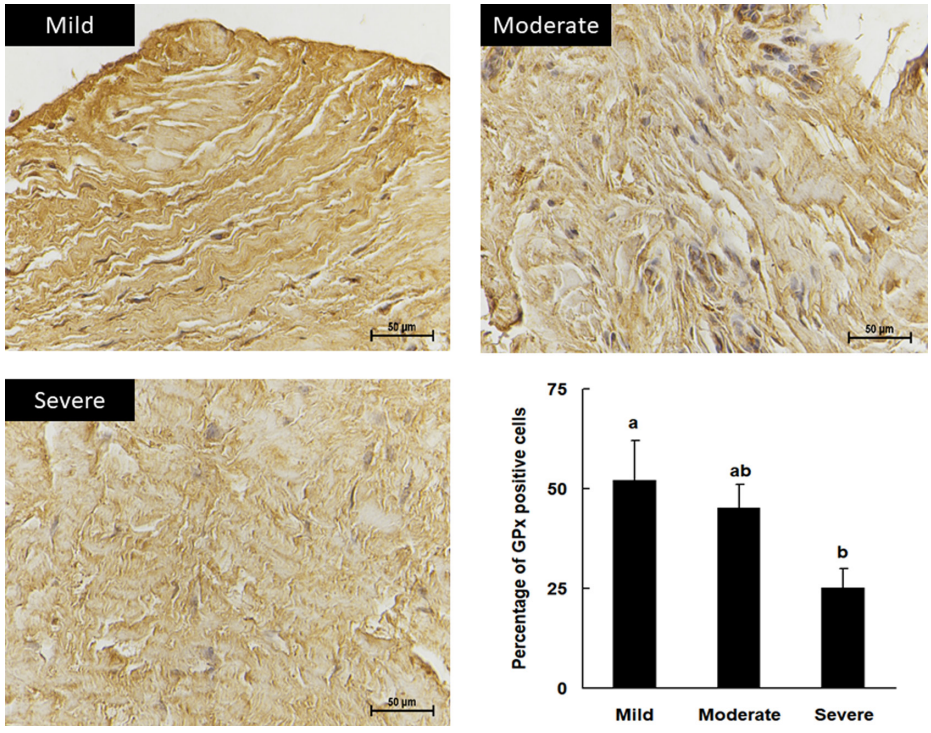

Figure 6. IHC staining of GPx in tissue from patients with de Quervain's disease. GPx protein is stained brown (magnification ×40). Data are presented as means ± SD and analyzed by one-way ANOVA followed by Student's *t*-test. Different letters indicate statistically significant differences ($P < .05$) between the severe group and the mild group. The same letters signify no significant differences between the mild and moderate groups, or between the moderate and severe groups.

mediators, they may not adequately address the upstream drivers of cellular stress and degeneration. As oxidative stress is a potent inducer of both autophagy and inflammatory signaling via pathways such as NF-κB,[36-38] combining anti-inflammatory agents with antioxidants or other ROS-scavenging compounds could provide a more comprehensive therapeutic approach. Moreover, targeting specific oxidative or autophagic pathways may help prevent the chronic progression of tissue degeneration and inflammation observed in more severe cases.

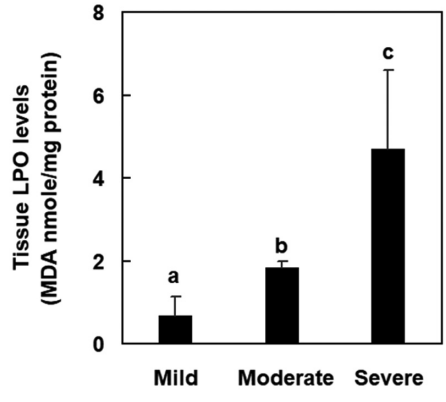

Figure 7. Levels of MDA production in tissue from patients with de Quervain's disease. Data are presented as means ± SD and analyzed using one-way ANOVA followed by Student's *t*-test. Different letters indicate statistically significant differences ($P < .05$) in MDA production between the severe group and both the moderate and mild groups.

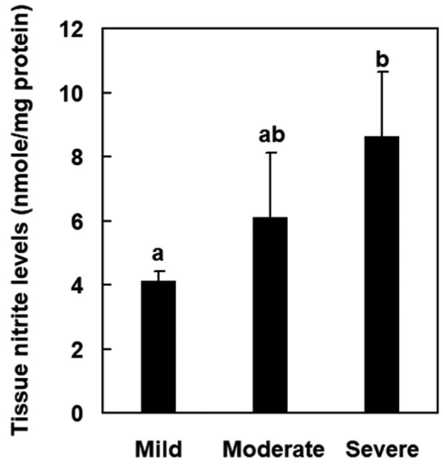

Figure 8. Levels of nitrite production in tissue from patients with de Quervain's disease. Data are shown as means ± SD and analyzed using one-way ANOVA followed by Student's *t*-test. Different letters represent statistically significant differences ($P < .05$) in nitrite production between the severe group and the mild group. Identical letters indicate no significant differences between the mild and moderate groups, or between the moderate and severe groups.

An intriguing genome-wide association study using publicly available data from the Research Program in Genes, Environment, and Health (RPGEH)—which included 4129 cases and 98 374 controls—found that rs35360670 on chromosome 8 is significantly associated with de Quervain's tenosynovitis.[39] Located about 15 kb upstream of the MTSS1 gene's transcription start site, rs35360670 is noteworthy. MTSS1 encodes metastasis suppressor protein 1, which plays a role in actin scaffolding and is often reduced in various cancers.[40] MTSS1 is also known to inhibit cancer cell growth,[41,42] suggesting a possible connection to the association with somatotropin exposure as a risk factor for de Quervain's disease.[33] It was speculated that a deficiency in certain growth suppressor genes might lead to excessive cell growth in the dorsal retinaculum, similar to the abnormal synovial fibroblast proliferation observed in rheumatoid arthritis, which contributes to synovial inflammation and tissue damage.[43] Single-cell sequencing of specific cell types in de Quervain's tenosynovitis could provide valuable insights into the disease's molecular mechanisms and potential new therapeutic approaches.

A potential correlation between oxidative stress and autophagy and the severity of de Quervain's disease was found, indicating that these cellular processes may influence the progression or severity of the condition. These results suggest that antioxidants could be beneficial by alleviating symptoms or slowing disease progression through mitigating oxidative stress and downstream autophagy. Consequently, incorporating antioxidant therapy alongside traditional anti-inflammatory treatments may offer a more effective, mechanism-based strategy to improve patient outcomes. Future studies should explore the therapeutic efficacy of antioxidant and autophagy-modulating agents, ideally through preclinical or clinical trials. In addition, single-cell sequencing and molecular profiling of affected tissues may uncover specific cell populations or signaling pathways involved in disease progression, opening new avenues for targeted interventions.

Data Availability Statement: The data that support the findings of this study are available on request from the corresponding author.

Ethics Committee Approval: The study was conducted in accordance with the Declaration of Helsinki, and approved by the Institutional Review Board of E-Da hospital (approval no.: EMRP-111-045, date: 2022/04/21).

Informed Consent: Written informed consent was obtained from the patients who agreed to take part in the study.

Peer-review: Externally peer-reviewed.

Author Contributions: Concept – Y.X.C., T.X.J., C.H.W.; Design – Y.X.C., C.H.W.; Supervision – Y.X.C., T.X.J., C.H.W.; Resources – Y.X.C., T.X.J., C.H.W.; Materials – Y.X.C., C.H.M., I.M., C.H.W.; Data Collection and/or Processing – Y.X.C., T.X.J., C.H.M.; Analysis and/or Interpretation – Y.X.C., T.X.J., C.H.M.; Literature Search – Y.X.C., C.H.M., I.M., C.H.W.; Writing Manuscript – Y.X.C., T.X.J., C.H.W.; Critical Review – Y.X.C., T.X.J., C.H.W.

Declaration of Interests: The authors have no conflict of interest to declare.

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References

1. Ranney D, Wells R, Moore A. Upper limb musculoskeletal disorders in highly repetitive industries: precise anatomical physical findings. *Ergonomics*. 1995;38(7):1408-1423. [CrossRef]
2. Clarke MT, Lyall HA, Grant JW, Matthewson MH. The histopathology of de Quervain's disease. *J Hand Surg Br*. 1998;23(6):732-734. [CrossRef]
3. Keon-Cohen B. De Quervain's disease. *J Bone Joint Surg Br*. 1951;33-B(1):96-99. [CrossRef]
4. Gao Q. Oxidative stress and autophagy. *Adv Exp Med Biol*. 2019;1206:179-198. [CrossRef]
5. Frake RA, Ricketts T, Menzies FM, Rubinsztein DC. Autophagy and neurodegeneration. *J Clin Invest*. 2015;125(1):65-74. [CrossRef]
6. Metaxakis A, Ploumi C, Tavernarakis N. Autophagy in age-associated neurodegeneration. *Cells*. 2018;7(5):37. [CrossRef]
7. Kaarniranta K, Tokarz P, Koskela A, Paterno J, Blasiak J. Autophagy regulates death of retinal pigment epithelium cells in age-related macular degeneration. *Cell Biol Toxicol*. 2017;33(2):113-128. [CrossRef]
8. Zhang SJ, Yang W, Wang C, et al. Autophagy: a double-edged sword in intervertebral disk degeneration. *Clin Chim Acta*. 2016;457:27-35. [CrossRef]
9. Yurube T, Ito M, Kakiuchi Y, Kuroda R, Kakutani K. Autophagy and mTOR signaling during intervertebral disc aging and degeneration. *JOR Spine*. 2020;3(1):e1082. [CrossRef]
10. Li YS, Zhang FJ, Zeng C, et al. Autophagy in osteoarthritis. *Joint Bone Spine*. 2016;83(2):143-148. [CrossRef]
11. Jeon H, Im GI. Autophagy in osteoarthritis. *Connect Tissue Res*. 2017;58(6):497-508. [CrossRef]
12. Liang H, Yang X, Liu C, Sun Z, Wang X. Effect of NF-kB signaling pathway on the expression of MIF, TNF-α, IL-6 in the regulation of intervertebral disc degeneration. *J Musculoskelet Neuronal Interact*. 2018;18(4):551-556.
13. Bhat AH, Dar KB, Anees S, et al. Oxidative stress, mitochondrial dysfunction and neurodegenerative diseases; a mechanistic insight. *Biomed Pharmacother*. 2015;74:101-110. [CrossRef]
14. Islam MT. Oxidative stress and mitochondrial dysfunction-linked neurodegenerative disorders. *Neurol Res*. 2017;39(1):73-82. [CrossRef]
15. Radi R. Oxygen radicals, nitric oxide, and peroxynitrite: redox pathways in molecular medicine. *Proc Natl Acad Sci U S A*. 2018;115(23):5839-5848. [CrossRef]
16. Rodney GG, Pal R, Abo-Zahrah R. Redox regulation of autophagy in skeletal muscle. *Free Radic Biol Med*. 2016;98:103-112. [CrossRef]
17. Janjetovic K, Misirkic M, Vucicevic L, Harhaji L, Trajkovic V. Synergistic antiglioma action of hyperthermia and nitric oxide. *Eur J Pharmacol*. 2008;583(1):1-10. [CrossRef]
18. Barsoum MJ, Yuan H, Gerencser AA, et al. Nitric oxide-induced mitochondrial fission is regulated by dynamin-related GTPases in neurons. *EMBO J*. 2006;25(16):3900-3911. [CrossRef]
19. Matsuzawa-Ishimoto Y, Hwang S, Cadwell K. Autophagy and inflammation. *Annu Rev Immunol*. 2018;36:73-101. [CrossRef]
20. Racanelli AC, Kikkers SA, Choi AMK, Cloonan SM. Autophagy and inflammation in chronic respiratory disease. *Autophagy*. 2018;14(2):221-232. [CrossRef]
21. Edelman DA, Jiang Y, Tyburski JG, Wilson RF, Steffes CP. Cytokine production in lipopolysaccharide-exposed rat lung pericytes. *J Trauma*. 2007;62(1):89-93. [CrossRef]
22. Maiese K. Moving to the rhythm with clock (circadian) genes, autophagy, mTOR, and SIRT1 in degenerative disease and cancer. *Curr Neurovasc Res*. 2017;14(3):299-304. [CrossRef]
23. Lee J, Giordano S, Zhang J. Autophagy, mitochondria and oxidative stress: cross-talk and redox signalling. *Biochem J*. 2012;441(2):523-540. [CrossRef]
24. Vikram A, Anish R, Kumar A, Tripathi DN, Kaundal RK. Oxidative stress and autophagy in metabolism and longevity. *Oxid Med Cell Longev*. 2017;2017:3451528. [CrossRef]
25. Galati S, Boni C, Gerra MC, Lazzaretti M, Buschini A. Autophagy: a Player in response to Oxidative Stress and DNA Damage. *Oxid Med Cell Longev*. 2019;2019:5692958. [CrossRef]
26. Sureshbabu A, Ryter SW, Choi ME. Oxidative stress and autophagy: crucial modulators of kidney injury. *Redox Biol*. 2015;4:208-214. [CrossRef]
27. Beckman JS. Protein tyrosine nitration and peroxynitrite. *FASEB J*. 2002;16(9):1144. [CrossRef]
28. Pacher P, Beckman JS, Liaudet L. Nitric oxide and peroxynitrite in health and disease. *Physiol Rev*. 2007;87(1):315-424. [CrossRef]
29. Barsoum MJ, Yuan H, Gerencser AA, et al. Nitric oxide-induced mitochondrial fission is regulated by dynamin-related GTPases in neurons. *EMBO J*. 2006;25(16):3900-3911. [CrossRef]
30. Shen P-C, Wang P-H, Wu P-T, Wu K-C, Hsieh J-L, Jou I-M. The estrogen receptor-β expression in de Quervain's disease. *Int J Mol Sci*. 2015;16(11):26452-26462. [CrossRef]
31. Kuo Y-L, Hsu C-C, Kuo L-C, et al. Inflammation is present in de Quervain disease—correlation study between biochemical and histopathological evaluation. *Ann Plast Surg*. 2015;74(Suppl 2):S146-S151. [CrossRef]
32. Kuo Y-L, Jou I-M, Wang P-H, Yang T-H, Shen C-J, Hsu C-C. Correlation between IL-20 and de Quervain's disease severity. *Ann Plast Surg*. 2019;82(1S Suppl 1):S6-S12. [CrossRef]
33. Yurdakul OV, Aytüre L, Yalçinkaya EY. Persistent de Quervain tenosynovitis induced by somatotropin treatment. *J Pediatr Endocrinol Metab*. 2017;30(11):1223-1226. [CrossRef]
34. Huisstede BM, Coert JH, Fridén J, Hoogvliet P, European HANDGUIDE Group. Consensus on a multidisciplinary treatment guideline for de Quervain disease: results from the European HANDGUIDE study. *Phys Ther*. 2014;94(8):1095-1110. [CrossRef]
35. Challoumas D, Ramasubbu R, Rooney E, Seymour-Jackson E, Putti A, Millar NL. Management of de Quervain tenosynovitis: a systematic review and network meta-analysis. *JAMA Netw Open*. 2023;6(10):e2337001. [CrossRef]
36. Yin J, Duan J, Cui Z, Ren W, Li T, Yin Y. Hydrogen peroxide-induced oxidative stress activates NF-κB and Nrf2/Keap1 signals and triggers autophagy in piglets. *RSC Adv*. 2015;5(20):15479-15486. [CrossRef]
37. Song C, Mitter SK, Qi X, et al. Oxidative stress-mediated NFκB phosphorylation upregulates p62/SQSTM1 and promotes retinal pigmented epithelial cell survival through increased autophagy. *PLoS One*. 2017;12(2):e0171940. [CrossRef]
38. Lingappan K. NF-κB in oxidative stress. *Curr Opin Toxicol*. 2018;7:81-86. [CrossRef]
39. Kim SK, Ahmed MA, Avins AL, Ioannidis JPA. A genetic marker associated with de Quervain's tenosynovitis. *Int J Sports Med*. 2017;38(12):942-948. [CrossRef]
40. Xie F, Ye L, Ta M, Zhang L, Jiang WG. MTSS1: a multifunctional protein and its role in cancer invasion and metastasis. *Front Biosci (Schol Ed)*. 2011;3(2):621-631. [CrossRef]
41. Wang H, Zhao Y, Cao L, Zhang J, Wang Y, Xu M. Metastasis suppressor protein 1 regulated by PTEN suppresses invasion, migration, and EMT of gastric carcinoma by inactivating PI3K/AKT signaling. *J Cell Biochem*. 2019;120(3):3447-3454. [CrossRef]
42. Du P, Ye L, Ruge F, Yang Y, Jiang WG. Metastasis suppressor-1, MTSS1, acts as a putative tumour suppressor in human bladder cancer. *Anticancer Res*. 2011;31(10):3205-3212.
43. Komatsu N, Takayanagi H. Mechanisms of joint destruction in rheumatoid arthritis - immune cell-fibroblast-bone interactions. *Nat Rev Rheumatol*. 2022;18(7):415-429. [CrossRef]