

Review Article

Biomarkers of chronic spontaneous urticaria

Shreya Datta¹, Abhishek De¹, Sushil Singh¹, Aarti Sarada², Sandipan Dhar³

¹Department of Dermatology, Calcutta National Medical College, ²Department of Dermatology, Wizderm Skin and Hair Specialty Clinic, ³Department of Dermatology, Institute of Child Health, Kolkata, West Bengal, India.

ABSTRACT

Chronic spontaneous urticaria (CSU) is a distressing skin condition that is characterized by the daily or nearly daily appearance of pruritus and wheals of more than 6-week duration. CSU is now believed to have two endotypes, namely, the more common auto-allergic type and the more recalcitrant autoimmune type. It is often difficult to treat the disorder and various treatment modalities are recommended for symptom control, including second-generation non-sedative antihistamines, cyclosporin, and omalizumab. To track the progression of the disease and the efficacy of treatment, certain biomarkers play a key role. Biomarkers identified for CSU include some major ones such as Interleukin (IL)-6, IL-17, and IL-31 and minor ones such as periostin and oncostatin-M. Not only do they may serve as important prognostic tools for proper diagnosis of the disease, but they have also been utilized in several clinical studies to track the progression of the disease, which underlines their importance in the clinical setting.

Keywords: Chronic spontaneous urticarial biomarkers, Biomarkers, Cytokines, Interleukins

INTRODUCTION

Chronic spontaneous urticaria (CSU) is a distressing skin condition that is characterized by the daily or nearly daily appearance of pruritus and wheals of more than 6-week duration.^[1]

Over the last decade, scientists have worked to better understand what causes CSU and how it progresses so that they may better utilize biomarkers to measure illness severity, track its course over time, and forecast how well treatments will work for individual patients. It is also crucial for the doctor providing treatment to have access to clinical biomarkers helpful for predicting the future progression of the illness and the most probable response to therapy when a new patient suffering from CSU is identified [Figure 1]. Clinical and laboratory indicators have been suggested for the evaluation of CSU severity and thus can be employed in the treatment plan to keep track. Although mast cells in the skin play a crucial role in the pathophysiology of CSU, little is known about the underlying mechanisms of their activation. Since systemic immunoglobulin G (IgG) autoantibodies directed to thyroid antigens and/or to immunoglobulin E (IgE) or to its IgE receptor (FcεRI) have been detected in a substantial subset of patients, autoimmunity seems to play a role in the etiology of CSU.^[2,3] Nonetheless, the fact that autoantibodies are undetectable in a sizable proportion of CSU patients indicates that additional processes are likely

involved in the development of the illness, paving the door for the discovery of biomarkers outside autoantibodies.^[4]

CLINICAL PRESENTATION OF URTICARIA

Presentation of CSU varies markedly in disease severity, presence or absence of angioedema, presence or absence of flare with inducing factors, quality of life impairment, course of the disease, and clinical response to treatment. CSU is now believed to have two endotypes, namely, the more common auto-allergic type and the more recalcitrant autoimmune type. More than one-third of CSU patients have IgG antibodies against the FcεRI alpha subunit of the high-affinity IgE receptor,^[5] whereas 5–10% demonstrate the generation of IgG toward IgE antibodies,^[6] furthermore, up to one-third of CSU patients have anti-thyroid autoantibodies^[7] [Figure 2]. CSU is presently diagnosed more clinically and there are no disease-specific biomarkers available to use in the diagnosis. Recent research by Schmetzer *et al.* found a substantial connection between the existence of anti-interleukin (IL)-24 IgE and CSU, and although the results are limited, they are encouraging.^[8] That research also shows that IL-24 is more expressed in the serum of CSU patients in comparison with healthy controls, indicating that it is an auto-antigen of IgE. Despite several studies documenting biomarker-based subgroup distinctions among CSU patients, only a few factors are potentially useful phenotypic or endotypic biomarkers. For example, low basophil numbers, high C-reactive protein (CRP), low

*Corresponding author: Dr. Abhishek De, Flat 3A, Arcadia1, Dream park, Sonarpur Station Road, Kolkata - 700103, West Bengal, India. dr_abhishek_de@yahoo.co.in

Received: 30 March 2023 Accepted: 11 June 2023 EPub Ahead of Print: 04 September 2023 Published: 27 October 2023 DOI: 10.25259/IJSA_14_2023

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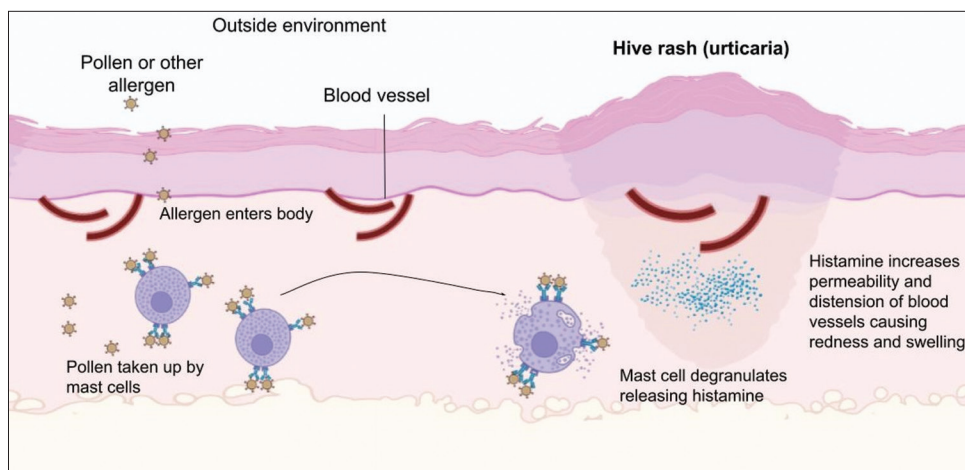


Figure 1: Pathophysiology of urticarial.

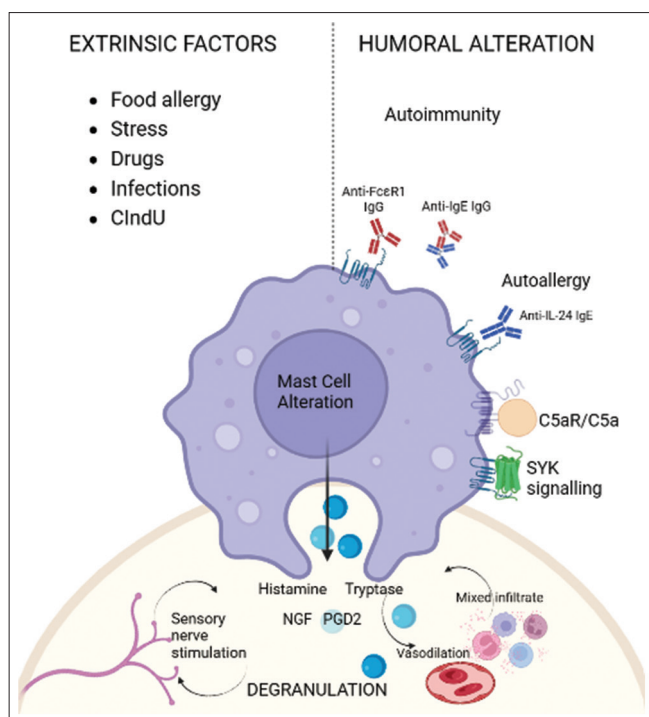


Figure 2: Mast cell activation.

IgE, and the presence of anti-thyroid peroxidase antibodies (TPO) may be associated with Type 2B autoimmune CSU, with a recalcitrant course.^[9]

SERUM BIOMARKERS IN URTICARIA

C-Reactive Protein (CRP)

CRP has been shown to rise in CSU patients, particularly those with positive autologous serum skin test (ASST), and to have a high association with other inflammatory indicators (such as erythrocyte sedimentation rate, blood leukocyte/neutrophil counts, and IL-6 serum levels) and with disease activity in a number of

clinical investigations.^[10,11] CRP has been suggested as a biomarker of response to medication, which is an interesting development in the dynamic landscape of personalized healthcare. Recent research suggests that a high CRP level may indicate an inadequate response to antihistamines but an adequate response to oral cyclosporin.^[12,13] CRP is a widely used biomarker for inflammatory and autoimmune disorders, although it is important to note that CRP levels in individuals with CSU are quantitatively lesser when compared to those identified in other conditions.

Complement system

The activation of the complement system is critical to the etiology and progression of CSU because its components may activate mast cells. Few studies have found that C3 and C4 levels are much higher in CSU patients than in healthy individuals and that their concentrations strongly correlate with CRP in chronic urticaria (CU) patients, but not in healthy ones. However, only a subset of patients with severe illness (up to 5–10%) show evidence of a rise in C3 and C4 levels, reducing their significance as indicators of disease activity.^[14] Some authors suggested that an increased liver production of C3 and C4 may occur in response to pro-inflammatory cytokines such as IL-1, IL-6, or tumor necrosis factor.^[15] In addition, the anaphylatoxin C3a is expressed on a wide variety of cells involved in urticarial inflammatory processes, such as mast cells, neutrophils, basophils, monocytes, and eosinophils.^[16] It also appears that C5a, C3a-like, is necessary for IgG-dependent activation of mast cells in CU.^[17] These findings suggest that the complement system plays a role in the pathogenesis of CSU, either directly, by causing mast cell degranulation, or indirectly, by intensifying the autoimmune response.

Interleukins

Since IL-6 plays a crucial role in generating inflammatory responses, it shows promise as a biomarker in CSU. In

individuals with CSU, greater concentrations of IL-6 were found with CRP; the concentration of IL-6 seems to differentiate between more severe and milder form of the illness, as well as between the active and quiescent stages of urticaria.^[11,18,19] IL-6 can be therefore considered as a potent stimulator, serving as an inducer of the most acute-phase proteins, including CRP, and controlling the extent of the local and systemic inflammatory responses. Hence, this cytokine has been proposed as a biomarker of disease activity. Pathogenesis of CSU has been also linked to other IL-1 family cytokines like IL-18. Although there is some evidence that IL-18 levels are elevated in the blood of people with CSU by attracting and stimulating eosinophils in inflamed tissue and setting up a feedback loop that promotes the production of IL-8, its involvement in the disease process still remains unclear.^[20-22] It has been postulated that the IL-23/IL-17 axis and tumor necrosis factor alpha (TNF- α) have a similar pathogenic function in CSU as IL-1 family cytokines. Several autoimmune disorders rely heavily on IL-17A-producing CD4 T cells (Th17). The capacity to generate IL-17F, IL-21, IL-22, IL-6, and TNF- α , as well as their dependence on the pro-inflammatory cytokine IL-23, has allowed for their identification.^[23] Mast cells along with additional inflammatory cells in the skin are known to generate TNF- α , lending credence to its participation in the etiology of urticarial lesions as IL-17 promotes mast cell proliferation by triggering stem cell factors in keratinocytes.^[24] There is a substantial correlation between the levels of IL-17, IL-23, and TNF- α in CSU patients and the disease activity score, suggesting that these cytokines may serve as biomarkers for disease progression.^[25] Important in the production of chronic inflammation of the skin, IL-31 is mainly generated by primed Th2 lymphocytes, skin-homing CD45RO CLA+T cells, and mast cells. Serum IL-31 levels were shown to be higher in CSU patients; however, this was unrelated to illness severity.^[26]

Adipokines

Adipokines are pro-inflammatory or anti-inflammatory cytokines and other proteins (e.g., leptin, adiponectin, resistin, IL-6, and TNF- α) that are secreted by the adipose tissue. A discrepancy between pro- and anti-inflammatory adipokines has been hypothesized as a source of inflammatory mediators in the development and clinical context of CSU. Lipocalin-2 (LCN2) levels were shown to rise in CSU patients, but adiponectin levels fell.^[27] Additional investigations revealed an intriguing correlation between LCN2 concentrations and disease activity, showing that individuals who had elevated LCN2 values were more likely to benefit from AH treatment. These findings together suggest that adipokines' pro- and anti-inflammatory components may be valuable as biomarkers for monitoring disease activity and the efficacy of various treatments in the clinic.

Vascular endothelial growth factor (VEGF)

VEGF, the most powerful pro-angiogenic mediator, had been implicated to the findings that patient suffering from CSU has new blood vessels.^[28,29] Confocal imaging with the lectin Ulex europaeus agglutinin 1 verified the enhanced vascularity and showed that the lesional tissue contained greater numbers of CD31-positive endothelial cells compared to the surrounding normal skin.^[30] CSU patients have been shown to have elevated levels of VEGF.^[30] Not only can inflammatory cells such as mast cells, eosinophils, and basophils produce VEGF, but they may also be the intended recipients of VEGF.^[31]

Endostatin (ES) and thrombospondin-1 (TSP-1)

Endogenous anti-angiogenic intermediaries, including ES and TSP-1, are mostly responsible for controlling the physiological function of VEGF. ES and TSP-1 concentrations in the serum of CSU patients are found to be elevated, but it was unrelated to the severity.^[32] Therefore, these anti-angiogenic mediators may play a role in the etiology of CSU by performing different roles in the inflammatory process. TSP-1 contributes to cutaneous vasodilation and subsequent escape of plasma by destabilizing connections between endothelial cells. The proteolytic fraction of ES has an effect on endothelial cells through nitric oxide production, making it a vasoactive facilitator.^[33,34] Consequently, vessel leakage in the skin of patients, which leads to the onset of CSU's clinical symptoms including wheals and flare development, may be influenced by both ES and TSP-1. In spite of these mediators being elevated in CSU patients' blood, but they are not an useful biomarkers since they have no association with disease progression or severity.

Matrix metalloproteinase-9 (MMP-9)

A few members of MMPs are also found to be elevated in the blood of CSU patients.^[35] MMP-9 is upregulated in the peripheral bloodstreams of both adult and pediatric CSU patients, and its influence on the remodeling of tissues is hypothesized to contribute to CSU pathogenesis.^[36,37] Inflammatory cells such as macrophages, neutrophils, T cells, and mast cells generate MMP-9.^[38,39] There are conflicting reports on the correlation between MMP-9 levels in plasma and disease progression.^[37,40] Thus, further research is needed before MMP-9 may be considered as a biomarker in the activity and development of CSU.^[41]

Leukocyte adhesion molecules

Enhanced production of leukocyte adhesion molecules including intercellular adhesion molecule (ICAM-1), vascular cell adhesion molecule 1 (VCAM-1), and E-selectin is an effect of VEGF during the angiogenesis process.^[42] Elevated levels of soluble ICAM-1 and VCAM-1 in the blood and skin biopsies of CSU patients seem to represent a pro-inflammatory endothelial phenotype, which is commonly employed as an indicator of impaired endothelial

function.^[43,44] Increased expression of VCAM-1 and ICAM-1 contributes to the pathophysiology of wheal development by increasing vascular permeability. Patients with CSU have elevated levels of soluble vascular endothelial (sVE)-cadherin, a soluble form of VE-cadherin found between endothelial cells. The severity of CSU is correlated with sVE-cadherin levels, indicating its potential for prognosis. Histamine production contributes to increased sVE-cadherin, which can be mitigated by AH medications.^[45]

D-dimer

Patients with CSU exhibit elevated levels of factor VIIa, prothrombin fragment 1+2, and D-dimer. This is significant due to the potential role of thrombin in increasing blood vessel permeability and stimulating mast cell degranulation. The concentrations of prothrombin fragment 1+2 and D-dimer are also associated with the prevalence and severity of CSU. However, further research is needed to establish the specificity of increased D-dimer levels in CSU. D-dimer has been proposed as a measure of AH resistance, response to omalizumab treatment, and monitoring of clinical response to cyclosporin.^[46-54]

Mean platelet volume (MPV)

Due to its correlation with inflammation, MPV has been investigated as a diagnostic measure of active disease and its progression in CSU.^[55,56] Patients with a positive ASST had a statistically significant relationship between the CSU severity score and MPV, but those with a negative ASST did not.^[57] MPV may be a measure of the activity of the disease and may have a part in the inflammatory processes causing CSU. Unfortunately, subsequent research did not replicate these encouraging findings.^[58] Serum CRP concentration was found to be positively correlated with platelet count.^[58]

Vitamin D

Woo *et al.* examined vitamin D levels as a potential indicator of disease severity in CSU. Their study revealed lower Vitamin D levels in CSU patients compared to healthy controls, with CSU patients exhibiting the lowest levels. A negative correlation was found between CSU activity score and disease progression. Vitamin D supplementation was recommended for improved CSU prognosis, but its use as a biomarker for the condition requires further investigation.^[59-61]

Serotonin (5-hydroxytryptamine, 5-HT)

The skin 5-HT transporter levels in CU patients with anxiety were substantially greater compared to healthy controls, and it was positively linked to the severity of anxiety, suggesting that the 5-HT transporter might be considered a particular biomarker and an unusual pharmaceutical target.^[62-64]

Platelet-activating factor (PAF)

Patients with CSU and those with low H1 receptor sensitivity had significantly greater blood PAF levels compared to

controls.^[65,66] Rupatadine, a dual antagonist of H1-histamine, and PAF receptor, is used in the management of CSU.^[67,68]

Oncostatin M (OSM)

OSM, a cytokine belonging to the IL-6 family, plays a crucial role in inflammatory reactions and metabolic disorders. T-lymphocytes in the skin release OSM. The physiological effects of OSM are mediated by its receptor gene, OSM receptor (OSMR), which binds to gp130. A study on CSU revealed that OSMR is overexpressed in CSU patients, leading to increased expression of genes involved in the Janus Kinase/Signal Transducers and Activators of Transcription 3 (JAK/STAT3) signaling pathway. Inhibiting OSMR resulted in reduced eosinophils, inflammatory cytokines, and gene expression related to the JAK/STAT3 pathway. OSMR expression was primarily observed in the superficial and middle dermis, as well as surrounding blood vessels.^[69-71]

Periostin

It was shown that the periostin levels correspond with the severity of CSU. Serum periostin levels were lower in CSU patients than in healthy controls. In addition, individuals with CSU who were classified as having a severe to very severe case of CSU had considerably lower serum periostin levels in comparison to those who had mild to moderate disease. It is of utmost necessity for more research into fibroblast activity in CSU, because it is generally known that fibroblasts are key producers of periostin.^[72]

Serum amyloid A (SAA)

SAA is an acute-phase protein produced in the liver by monocytes and macrophages.^[73] Higher SAA levels were seen in CSU patients, suggesting a correlation between SAA levels and the development of urticaria.^[74]

LIGHT (homologous to lymphotoxins, exhibiting inducible expression, and competing with herpes simplex virus [HSV] glycoprotein D)

Moderate-to-severe CSU is associated with higher plasma concentrations of soluble LIGHT, a pro-inflammatory protein belonging to the TNF superfamily. LIGHT has been linked to autoimmune diseases and T lymphocyte activation. Exposure to LIGHT can trigger the release of IL-8 and other inflammatory cytokines. The presence of soluble LIGHT suggests its malfunctioning in CSU, impacting the immune system's response. Severe CSU symptoms correlate with higher levels of soluble LIGHT, potentially indicating its involvement in other inflammatory conditions. LIGHT may contribute to the development of severe manifestations in CSU.^[75,76]

CELLULAR BIOMARKERS IN URTICARIA

Basophils and basophil activation markers

Grattan demonstrated that a decrease in the overall quantity of basophil in the peripheral blood was associated with the

activity of CSU. Basophils are attracted to skin lesion sites, which may explain why this group found an unfavorable linear connection between basophil counts and Urticaria activity score (UAS) in untreated CSU patients.^[77-80] Ye *et al.* found a correlation between CD203c-expressing basophils and clinical indicators of intensity in 82 patients with urticaria. Severe urticaria patients exhibited higher levels of CD203c-expressing basophils compared to those with milder symptoms and healthy controls.^[81] CD203c on the basophil membrane confirms cellular stimulation and can serve as a marker for severe CSU, guiding treatment approaches. Histamine production through FcεRI activation has been used as a biomarker to indicate basophil involvement in CSU development.^[82-85]

Mast cell-related biomarkers and mediators

Heparin, stored in mast cell granules, affects vessel permeability and muscle contraction. It is rapidly released on cellular stimulation.^[86] Heparin is associated with mast cell collections in urticaria pigmentosa lesions and can cause hemorrhagic complications in severe mast cell proliferation diseases. However, most patients of CSU maintain normal coagulation times.^[87,88]

Tryptase is highly expressed in basophils and retained in human mast cells. The active tetrameric form of mature β-tryptase is exclusively secreted by active mast cells. In contrast, the low levels of the monomeric form of tryptase, produced by resting mast cells, represent baseline serum levels (ranging from 1 ng/mL to 11 ng/mL). The increase in serum tryptase levels indicates mast cell degranulation and can be used potentially as a biomarker of CSU.^[89-91]

BIOMARKERS PREDICTING TREATMENT RESPONSE OR RELAPSE

Antihistamines

Second-generation non-sedating antihistamines are the primary treatment for CSU. Clinical trials have demonstrated that higher doses of antihistamines are more effective and well-tolerated compared to standard doses or combined use of different antihistamines.^[92,93]

However, a significant number of CSU patients show inadequate improvement despite up dosing of AHs. Factors predicting positive treatment response are not well understood. Refractory CSU has been linked to coexistent morbidities such as atopic asthma, rhinitis and rhinosinusitis, thyroid disease, and hypertension.^[94]

Patients with antihistamine resistant CSU exhibit higher levels of complement C5a in the serum, longer duration of wheals, and increased positivity in ASST.^[95] Furthermore, patients with CU who test positive for ASST or the basophil activation test (BAT) are less likely to benefit from antihistamine therapy.^[96,97] Asero *et al.* recommended that high plasma D-dimer concentrations be used as a biomarker for CSU that has

developed resistance to antihistamines. Patients with higher D-dimer levels are more likely to be unresponsive to cetirizine.^[98] CSU patients show imbalances in pro- and anti-inflammatory adipokines, with lower levels of adiponectin and higher levels of TNF-α, IL-6, and IL-10 in their serum. Higher blood IL-6 levels are observed in refractory CSU patients. LCN2 correlates with UAS7 and was suggested to be as a biomarker to predict clinical outcomes after antihistamine therapy.^[99]

Omalizumab

The basophil histamine release assay (BHRA) is used to detect autoantibodies against cell-bound IgE or empty FcεRI. Studies showed BHRA-positive individuals typically exhibit a delayed response to omalizumab, with an average response duration of 29 days, whereas BHRA-negative patients respond within 2 days. The ASST was also used to examine this concept. A positive ASST response may be a predictor of a sluggish reaction.^[100,101] Slow response to omalizumab treatment is predicted by a positive BHRA, suggesting that omalizumab's effect is mediated via the downregulation of FcεRI production in such individuals. IgG antibodies to unoccupied IgE receptors have been hypothesized to stimulate mast cell mediator release, resulting in a delayed response to omalizumab.

Only basophils, mast cells, and CD34 progenitor cells in the peripheral circulation express the ectoenzyme CD203c (ectonucleotide pyrophosphatase/phosphodiesterase). The specificity and sensitivity of CD203c make it a promising basophil activity indicator.^[102,103]

An absence of basophil CD203c-upregulating function in the serum of CSU patients corresponds to an excellent outcome after receiving omalizumab.^[103-105] Eighteen of the 41 participants had upregulating activity for CD203c. Only nine of the 18 individuals with CD203c-upregulating activity responded well to omalizumab in terms of symptomatic recovery. Conversely, omalizumab was clinically effective for 20 out of 23 (87%) patients who did not exhibit CD203c-upregulating function ($P = 0.02$, Fisher's exact test). Age, gender, or the existences of thyroid autoantibodies were not shown to be related to effectiveness. Overall, 71% of CSU patients indicated that omalizumab had benefited them, which is a little higher than the success rate reported in the previous trials.^[106-108] The existence of autoantibodies against IgE and/or FcεRIα was shown to indicate a reduced chance of a good response, and the basophil CD203c-upregulating activity might indicate this.

Patients with CSU have been shown to have considerably greater blood IL-31 levels compared to healthy controls.^[109] A recent study found that omalizumab dramatically lowered IL-31 levels in individuals with CSU, but a placebo had no such effect. However, IL-31 was not associated with urticaria activity score, wheal score, or itch score.^[110] Researchers concluded that further study is needed to determine how

IL-31 contributes to CSU's pathogenesis and the severity of its symptoms.

Cyclosporin A

Cyclosporin A is the second medication that has demonstrated potential for individuals with CSU resistant to therapy.^[111-113] Patients with CSU who have a positive BAT had more favorable responses to cyclosporin therapy.^[111] Another research provided more evidence for this observation, reporting that the results of a positive BHRA suggested a greater chance of response in individuals treated with cyclosporin.^[114] A positive response to cyclosporin therapy is also predicted by a shorter duration of illness and greater initial severity.^[115]

There is a strong inverse connection between baseline D-dimer levels and cyclosporin responsiveness.^[54] Therefore, baseline D-dimer can prove to be a helpful index of disease progression in most individuals with CSU and may be used to track the therapeutic effect of cyclosporin.^[116]

PROGNOSTIC BIOMARKERS FOR LONG-TERM OUTCOMES

Various clinical indicators of the degree of severity, responsiveness to therapy, and relapse rates have been shown to be beneficial in CSU research. Patients <19 year old had a far greater rate of improvement than adults, and there is some evidence that suggests a negative correlation between age and illness severity.^[117,118] The CU-Q2oL is a disease-specific quality of life instrument, and it seems that older individuals with CSU fare worse on this scale than younger ones. Patients under the age of 40 showed the most impairment in terms of functionality and pruritus, while those above the age of 40 showed the greatest impairment in terms of sleep and eating.^[118] Epidemiological investigations have shown that women between the ages of 20 and 59 make up the majority of those diagnosed with CSU and that being a woman seems to be a predictor of an extended period of remission and a worse quality of life.^[119,120] Despite the fact that research is lacking, sex hormones may have a role as catalysts in a minority of individuals.^[121] The majority of the women in the study did not develop CU until after puberty. Other pregnant women reported their symptoms being worse, and others found that using hormonal birth control made their CU worse.^[121] Patients with CSU also had lower amounts of dehydroepiandrosterone sulfate in their blood compared to those who were asymptomatic or in remission.^[121,122] A further indicator of illness severity is the length of affliction.^[119] Patients experiencing urticaria for less than a year have been shown to benefit more from therapy than those with longer-lasting symptoms.^[118] Angioedema and anti-thyroid antibody positivity were also linked to longer illness duration.^[123] Patients with CSU who also exhibit simultaneous angioedema have a more severe course and a later remission point than those without.^[123]

BIOMARKERS IN URTICARIA SUBTYPES AND COMORBIDITIES

Specific biomarkers in physical urticarias

Several studies have identified promising biomarkers associated with different types of physical urticarias. For instance, in cold urticaria, the presence of cryoglobulins and cold-induced histamine release has been observed, providing insights into the disease process.^[124] Similarly, heat urticaria is associated with elevated levels of heat-shock proteins and cytokines, indicating the involvement of immune and inflammatory pathways.^[125] In pressure urticaria, mast cell activation markers and eosinophil cationic protein have shown relevance, highlighting the role of mast cells and eosinophils in the condition.^[126] These specific biomarkers not only aid in accurate diagnosis but also hold the potential for targeted therapeutic interventions.

Autoimmune urticaria

Autoimmune urticaria, a subset of chronic urticaria, is characterized by dysregulated immune responses leading to recurrent and persistent hives. Extensive research has shed light on the autoimmune mechanisms underlying this condition and identified a range of biomarkers associated with autoimmune urticaria. Autoantibodies targeting specific components of the skin, such as IgE receptors (e.g., anti-FcεRI) and complement proteins (e.g., anti-C1q), have been detected in patients with autoimmune urticaria.^[127,128] These autoantibodies serve as crucial biomarkers, indicative of immune dysregulation, and provide insights into the pathogenesis of the disease. In addition to autoantibodies, elevated levels of inflammatory mediators have also been implicated as biomarkers of autoimmune urticaria. For instance, increased histamine release and elevated levels of cytokines (e.g., IL-6, IL-17) and chemokines (e.g., CCL5, CXCL8) have been observed in the affected individuals.^[129] These biomarkers reflect the inflammatory processes and immune activation associated with autoimmune urticaria. The identification and validation of these biomarkers not only contribute to the accurate diagnosis of autoimmune urticaria but also hold promise for the development of targeted therapies aimed at modulating the autoimmune response [Table 1].

FUTURE PERSPECTIVES AND CHALLENGES

Recent years have witnessed a surge in research on the possibilities of identifying novel biomarkers helpful for predicting treatment response and monitoring CSU activity and treatment effectiveness.

Heat shock proteins (Hsps) have recently gained attention for their role in inflammation and the immune system. In patients with CSU, higher levels of Hsp70 and anti-Hsp70 antibodies have been found in the bloodstream. The

Table 1: Prospective biomarkers and their role in the disease prediction.

Biomarkers	Prognosis and severity predictive ability
Clinical markers	
Age	Young patients have a better prognosis.
Sex	Females patients have a poorer prognosis and more severe symptoms.
Duration of the disease	Disease duration more than 1 year is linked to a poorer outcome.
Presence of Angioedema	Presence of angioedema is associated with a poorer prognosis.
Aggravation on NSAID consumption	When NSAID consumption leads to aggravation, a poor prognosis is often demonstrated.
Molecular markers	
IL-6	Elevated levels are associated with poor outcome. ^[11,18,19]
IL-18	Elevated levels are associated with poor outcome. ^[20]
MMP-9	Elevated levels are associated with poor outcome. ^[36,37]
CRP	Elevated levels are associated with poor outcome. ^[12,13]
D-dimer	Elevated levels are associated with poor outcome. ^[49-52]
F1+2	Elevated levels are associated with poor outcome. ^[46,47]
Vitamin D	Lower levels are associated with poor outcome. ^[61]
MPV	Higher values are associated with poorer outcome. ^[57]
Basophil counts	Lower counts have been associated with disease progression. ^[77]
CD203c basophils	Increased numbers have been associated with worsening of symptoms. ^[81]

NSAID: Nonsteroidal anti-inflammatory drug, IL: Interleukin, MMP-9: Matrix metalloproteinase-9, CRP: C-reactive protein, MPV: Mean platelet volume

exact cause and clinical relevance of this finding in CSU are still unclear. Hsp70 can have both pro-inflammatory and protective effects, while anti-Hsp70 antibodies may stimulate pro-inflammatory processes. Increased plasma concentrations of Hsp70 and anti-Hsp70 antibodies have been observed in CSU patients, regardless of disease severity. Further research is needed to understand the role of Hsp70 and anti-Hsp70 antibodies in CSU and their potential as biomarkers.^[130,131]

Environmental stressors in CSU may alter enzyme activity and trigger the generation of pro-inflammatory cytokines, indicating an imbalance in antioxidant defense systems. Nettis *et al.* found that advanced oxidation protein products (AOPPs) are significantly higher in CSU patients, while advanced glycation end products are not elevated, suggesting AOPPs as potential oxidative stress biomarkers.^[132]

Epigenetic research in skin diseases like urticaria has shed light on gene regulation processes. Micro-ribonucleic acids (miRNAs) play a crucial role in silencing genes by binding to specific locations on messenger RNA. In CSU, five miRNAs (2355-3p, 4264, 2355-5p, 29c-5p, and 361-3p) were found at significantly higher levels. These miRNAs may serve as biomarkers for chronic autoimmune urticaria, as they target genes involved in various cellular processes, including inflammation and leukocyte response.^[133]

In addition, reverse transcription-quantitative polymerase chain reaction was used to verify the expression of upregulated or downregulated miRNA in CSU patients. During the active phase of the illness, miR-125a-5p and CCL17 expression rates were found to be considerably elevated in the serum of these people. Still, they were dramatically reduced during the remission period.^[134]

A biomarker for illnesses such as cancer and skin disorders is a single-nucleotide polymorphism, or SNP, which is a variation in a deoxyribonucleic acid sequence that occurs as a result of a change in only one nucleotide at the genomic level.^[135] Many genes have been identified to have polymorphisms that are strongly correlated with urticaria and may be used as markers to predict disease severity or the impact of pharmacological therapy.

Mast cell degranulation involves a surge of calcium mediated by the ORAI1 gene. Polymorphisms in ORAI1 (rs12320939 and rs3741596) correlate with CU sensitivity and response to non-sedative H1 receptor antagonists, suggesting their potential for personalized treatment. Polymorphisms in FCER1A are associated with responses to non-sedative H1 receptor antagonists and aspirin-intolerant CU. The HNMT gene polymorphism (939A>G) predicts increased histamine release and aspirin-intolerant chronic urticaria. Polymorphisms in CRP (rs3093059) and C5AR1 (-1,330T/G) are linked to poor responses to specific AH.^[136-142]

Gremlin1, involved in tissue differentiation and organ development, promotes inflammation in CSU by activating the transforming growth factor beta pathway. Gremlin1 induces the production of pro-inflammatory factors and can be targeted for personalized therapy in CSU.^[143]

CONCLUSION

While researchers are diligently studying various biomarkers, the quest for a single molecule that can truly aid clinicians in the process of diagnosis and treatment decision-making for conditions like CSU remains ongoing. The significance of thoroughly describing and understanding this complex pathological process is amplified by the expanding array of

therapeutic options entering clinical practice. It becomes increasingly clear that a collaborative, multicentric effort is essential to amass the voluminous data necessary to unravel the intricate pathogenesis of CSU and validate valuable biomarkers for accurate diagnosis and prediction of treatment response. This collaborative endeavor holds the key to unlocking the mysteries of CSU, enabling healthcare professionals to offer more effective and personalized care to the patients of CSU.

Declaration of patient consent

Patient's consent not required as patient's identity is not disclosed or compromised.

Financial support and sponsorship

Nil.

Conflicts of interest

Dr. Abhishek De, Dr. Aarti Sarda, Dr. Sandipan Dhar are on the editorial board of the Journal.

Use of artificial intelligence (AI)-assisted technology for manuscript preparation

The authors confirm that there was no use of artificial intelligence (AI)-assisted technology for assisting in the writing or editing of the manuscript and no images were manipulated using AI.

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How to cite this article: Datta S, De A, Singh S, Sarda A, Dhar S. Biomarkers of chronic spontaneous urticarial. *Indian J Skin Allergy* 2023;2:60-70.