

DOI 10.36074/logos-13.03.2026.057

CLINICAL AND PROGNOSTIC ASSESSMENT OF THE RISK OF DIABETIC RETINOPATHY PROGRESSION IN PATIENTS WITH TYPE 2 DIABETES MELLITUS BASED ON THE CD54 BIOMARKER

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Relevance of the Study and Objective

Type 2 diabetes mellitus remains one of the most prevalent chronic non-communicable diseases worldwide and is characterized by a steady increase in incidence [1]. Of particular clinical significance are its microvascular complications, among which diabetic retinopathy (DR) occupies a leading position as one of the major causes of permanent vision impairment in the working-age population [2].

The risk of development and progression of DR is directly associated with the duration of the disease and the level of glycemic control [3]. Chronic hyperglycemia initiates a cascade of pathological changes, including oxidative stress, endothelial dysfunction, activation of pro-inflammatory cytokines, and cell adhesion molecules [4]. As a result, retinal microangiopathy develops, leading to ischemic and proliferative alterations.

One of the key components of the inflammatory–adhesive mechanism is the intercellular adhesion molecule ICAM-1 (CD54), which mediates leukocyte adhesion to the vascular wall and their transmigration through the endothelium [6]. Overexpression of CD54 contributes to leukostasis, impaired microcirculation, and progression of vascular changes in the retina. The staging of diabetic retinopathy is

determined according to the international clinical classification, which distinguishes non-proliferative, pre-proliferative, and proliferative forms [5].

Despite the established role of inflammatory mechanisms in the pathogenesis of diabetic retinopathy (DR), the use of adhesion biomarkers as components of a disease progression prediction system remains insufficiently studied. A number of studies have demonstrated an association between CD54 concentration and the clinical manifestations of retinopathy [7–9], supporting the rationale for developing a comprehensive prognostic model.

The aim of the study - was to perform a clinical and statistical assessment of the prognostic significance of CD54 and to develop a predictive model for the progression of diabetic retinopathy in patients with type 2 diabetes mellitus, taking into account clinical and metabolic parameters.

Materials, Methods, and Results

The study included 82 patients with diabetic retinopathy (DR) and type 2 diabetes mellitus (148 eyes). The mean age of the examined patients was 64.41 ± 1.18 years, and the mean duration of diabetes was 15.54 ± 0.83 years. The average level of glycated hemoglobin (HbA1c) was $9.17 \pm 0.22\%$, indicating inadequate metabolic control in the majority of patients.

The diagnosis of DR was established according to the WHO classification [5]. Depending on the severity of retinal changes, patients were divided into three groups: non-proliferative, pre-proliferative, and proliferative forms of DR.

The ophthalmological examination included assessment of visual acuity, intraocular pressure measurement, slit-lamp biomicroscopy, contact ophthalmoscopy using a Goldmann lens, and optical coherence tomography (OCT). The laboratory component of the study involved the determination of serum CD54 levels using an enzyme-linked immunosorbent assay (ELISA). Glycated hemoglobin (HbA1c) levels were measured using high-performance liquid chromatography (HPLC). Given the established involvement of cell adhesion molecules in the development of microvascular disorders in DR [6], CD54 was included in the multifactorial statistical analysis.

Data processing was performed using methods of descriptive and inferential statistics, as well as regression and discriminant analyses. Stepwise inclusion of variables made it possible to identify the most informative predictors of pathological process progression.

Results. The study demonstrated that CD54 levels varied depending on the stage of retinopathy and the degree of metabolic compensation. In patients with HbA1c levels above 7.5%, progression to more advanced forms of DR was associated with a tendency toward decreased CD54 concentrations. This finding may reflect



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the complex dynamics of interaction between inflammatory and metabolic factors during the progression of retinal damage.

The analysis of the structure of prognostic factors demonstrated that at the early stage of diabetic retinopathy (DR), the leading determinants were CD54 concentration, HbA1c level, and indicators of the functional state of the visual system. For the proliferative form, the duration of diabetes and the characteristics of glucose-lowering therapy were identified as the most significant factors. The intermediate stage was characterized by a relatively balanced contribution of laboratory and clinical parameters. Based on the obtained results, a discriminant-type mathematical model was developed, enabling the classification of patients according to their risk of DR progression. The classification accuracy ranged from 65.8% to 76.8%, indicating the practical applicability of the proposed approach.

The findings are consistent with previous studies regarding the involvement of CD54 in the pathogenesis of diabetic retinopathy [7–9]; however, this study is the first to integrate this biomarker into a comprehensive prognostic model.

Conclusions. 1. Cell adhesion molecules, particularly ICAM-1 (CD54), play an important role in the development of retinal microvascular damage. 2. The present study demonstrated that serum CD54 levels vary depending on the stage of diabetic retinopathy and the degree of compensation of type 2 diabetes mellitus. In the early stages of the disease, the combination of CD54 concentration, HbA1c level, and functional visual parameters represents the most significant risk factors. In the proliferative stage, the duration of diabetes and the characteristics of glucose-lowering therapy become more influential determinants. 3. The proposed discriminant model allows prediction of the probability of retinopathy progression with a satisfactory level of accuracy (65.8–76.8%). Unlike studies evaluating the isolated effect of CD54, the present work implements a comprehensive approach by integrating both clinical and laboratory parameters into a unified risk assessment system.

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