UDC: 616-002.3/-08-039.71 + 616.379-008.64

DIAGNOSTIC CRITERIA AND A PROGNOSTIC MODEL FOR THE COURSE OF SOFT TISSUE NECROBIOTIC INFECTIONS IN DIABETES PATIENTS BASED ON ARTIFICIAL INTELLIGENCE

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Abstract. Expanding the model using artificial intelligence technologies has transformed the scale into a dynamic system adaptable to the characteristics of each patient and based on a wide array of accumulated data.
Keywords: necrotizing soft tissue infections, prognosis, diabetes mellitus, artificial intelligence

Relevance. According to the Surgical Infection Society of North America (SISNA), 30-day mortality from severe forms of NSTI against the background of severe comorbid diseases reaches approximately 18-22%, and the annual mortality exceeds 30%, which emphasizes the severity of the pathology and the significant burden on healthcare systems (1,3,5,7). Diabetes mellitus is the most common endocrine disease in the world, competing for third place after cardiovascular diseases and oncological diseases (20). Its prevalence among the adult population reaches 7-9% of the entire population of the Earth (19). According to the World Health Organization, there are 347 million patients with diabetes mellitus in the world (2,6,8,10). While 17.9 million patients are diagnosed with diabetes mellitus (DM), 5.7 million worldwide are unaware of their diagnosis, in more than 50% of cases DM is diagnosed late (4,9,10,11,12,.13). The most typical surgical complications in patients with diabetes are purulent-inflammatory diseases of soft tissues. Changes in cellular and humoral immunity significantly affect the course of the wound healing process, prolonging both its phases: the healing process is delayed for weeks and even months (5,14,15,16). The solution to these problems is becoming increasingly important socio-economically (1,17,18). According to the literature, patients with type 2 diabetes mellitus exhibit high levels of proinflammatory cytokines in the blood serum, which affects the functional state of fibroblasts and keratinocytes, as well as the dynamics and duration of the inflammatory process (1). However, the regulation of the wound healing process mediated by intercellular interactions, including the participation of connexins and growth factor receptors, remains poorly understood.

The search for prognostic criteria, optimization of the extent of surgical intervention, and the integration of modern methods of local intervention can significantly improve treatment outcomes, reduce the incidence of amputations and mortality, and ensure a more rational use of healthcare resources.

Study objective: to develop diagnostic criteria and a prognostic model for the course of the necrobiotic process of soft tissues in patients with diabetes mellitus based on artificial intelligence.

Materials and methods. The clinical material consisted of 128 patients with diabetes mellitus who underwent treatment and examination for severe forms of NSTI at a multidisciplinary medical center in the Bukhara region from 2016 to 2025. In accordance with the goals and objectives of the study, all patients were divided into two groups: the control group included 63 patients treated in 2016-2020,

when the tactics for necrotizing lesions were built according to the traditional scheme; The main group included 65 patients observed between 2021 and 2025, using the comprehensive LDA we developed.

Results and discussion. The "PIN-SD" scale (Prognostic Index of Necrobiosis in Diabetes Mellitus) we developed combines key cytological and rapid microbiological indicators that reflect the intensity of the necrobiotic process in patients with diabetes and severe forms of NIMT. Each of the 7 indicators has 3 severity levels and is scored from 0 to 2 points, allowing us to identify both early deviations corresponding to the initial phases of necrobiosis and signs of deep destruction that pose a significant risk of progression to purulent-necrotic disease. The resulting indicator reflects the overall degree of disruption of the cellular and microbial balance and serves as the basis for predicting potential developmental dynamics. The scale is designed so that the minimum score is zero, which corresponds to a favorable cytological and microbiological picture and the absence of signs of active destruction. The maximum value of 14 points reflects the extreme severity of changes, at which the tissue structure becomes unstable and the microbial profile is mixed and aggressive. Intermediate values are distributed evenly and create a moderate-risk range, which is most often encountered in clinical practice and requires careful dynamic monitoring. For ease of clinical interpretation, three levels of the total score are provided. Values ≤3 points are associated with a low probability of process progression. The range from 4 to 10 points reflects a moderate level of risk. In this range, a borderline state develops, in which local defense mechanisms remain active, but microbial pressure and cellular destruction have already noticeably increased. Values ≥11 points are considered high and indicate a significant shift of all pathogenic elements toward profound destruction.

Combining cytological, microbiological, and clinical characteristics into a single framework opened the possibility of using them not only for manual risk assessment but also for building an intelligent model capable of comparing individual cases with the accumulated data set. This approach became a logical extension of work on the scale and led to the development of the PIN-SD-AI program, which integrates these criteria into an automated process for generating a prognosis and selecting optimal patient management strategies.

The PIN-SD-AI technology is based on the step-by-step integration of various data reflecting the condition of soft tissues in severe forms of NIMT in patients with diabetes. The program is designed so that the physician can consistently enter the initial information, avoiding unnecessary time spent on complex calculations and comparisons. After entering the initial data, the physician proceeds to enter the express indicators obtained during the initial examination of the wound. The physician enters the values of four cytological indices that most fully reflect the cellular changes in the affected area. Express bacterioscopy smear parameters are entered simultaneously. The physician specifies the microbial density, the ratio of Gram-negative to Gram-positive flora, and the proportion of polymicrobial complexes. The expanded set includes parameters typically available only through in-depth laboratory analysis. Integration of such data allows the algorithm to compare the current wound with previously observed patterns and identify more subtle differences between patients. At the same time, the basic version of the program remains applicable even when using only express methods. Once the data is entered, the program creates an integrated patient profile, creating a necrobiotic process phenotype that integrates cellular, microbiological, and clinical components. This comparison mechanism provides the basis for prognostication, as the AI analyzes not individual parameters, but the structure of relationships between them.

The central element of the program is the AI analytical module, which compares the entered patient data with a wide range of previously registered cases. The model is trained on combinations of parameters characterizing different types of necrobiosis progression, allowing it to identify similarities between the current situation and clinical cases in the database. Based on these comparisons, a prediction is made regarding the likelihood of the process progressing to a more severe phase. The module assesses the risk of progression in the coming hours and days, taking into account the overall "PIN-SD" score, a combination of rapid indicators, cellular response characteristics, and the microbial landscape.

After processing the information, the program generates a final report, accessible to the physician directly in the interface. The initial display is the total score on the PIN-SD scale and the patient's classification into one of three risk groups. Depending on the phenotype and risk level, the prognostic algorithm may indicate the need for surgical intervention, extended necrosectomy, or preparation for possible amputation if the lesion is widespread and necrobiosis is progressing rapidly. The final step of the program is storing patient data and monitoring results. This architecture makes PIN-SD-AI more than just a scoring tool, but a fully-fledged assistant that integrates a visual image of the wound, rapid methods, and elements of in-depth research into a single prognostic framework. Such a program can compensate for the shortcomings of subjective assessment and provide the physician with a quantitatively substantiated prediction of the further course of the necrobiotic process. The results of the study demonstrate that the combination of cytological indices and rapid microbiological indicators enables the development of a reliable set of criteria that reflect the key mechanisms of necrobiotic development in NIMT in patients with diabetes. Based on these criteria, the "PIN-DM" scale was developed, which combines the most significant elements of cellular and microbial imbalance and demonstrates high accuracy in predicting the likelihood of severe disease progression. Further expansion of the model using AI technologies enabled the scale to be transformed into a dynamic system adaptable to the characteristics of each patient and based on a wide array of accumulated data. The resulting structure ensures robust differentiation between disease progression variants and forms the basis for the development of comprehensive clinical diagnostic and treatment algorithms.

CONCLUSIONS

1. The combination of cytological indices and rapid microbiological indicators enables the development of a reliable set of criteria that reflect the key mechanisms of necrobiotic development in NIMT in patients with diabetes.
2. Expanding the model using AI technologies enabled the scale to be transformed into a dynamic system adaptable to the characteristics of each patient and based on a wide array of accumulated data. The resulting structure ensures stable differentiation of disease course variants and creates the basis for the development of comprehensive clinical treatment and diagnostic algorithms.

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