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Original Article

Model for predicting metabolic activity in athletes based on biochemical blood test analysis

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ABSTRACT

Improving the efficiency of athletic performance and reducing the likelihood of overtraining are primarily determined goals that can be achieved by the correct organization of the training process. The nature of adaptation to physical stress is associated with the specificity, focus, and degree of biochemical and functional changes that occur during muscular work. In this study, we aimed to develop a diagnostic model for predicting metabolic processes in athletes based on standard biochemical blood analysis indicators. The study involved athletes from the track and field athletics team (men, $n = 42$, average age was [22.55 ± 3.68] years). Blood samples were collected in the morning at the beginning and end of the training week during the annual cycle. During the entire period, 3 625 laboratory parameter tests were conducted. Capillary blood sampling in athletes was conducted from the distal phalanx of the finger after overnight fasting, according to standard diagnostic procedures. To determine the predominance of anabolic or catabolic processes, equations were derived from a linear discriminant function. The discriminant function of predicting metabolic processes in athletes has a high information capacity (92.1%), as confirmed by the biochemical results of neuroendocrine system activity, which characterized the body's stage of adaptive regulatory mechanisms in response to stress factors. The classification matrix used to predict the metabolic processes based on the results of the discriminant function calculation demonstrates the statistical significance of the model ($p < 0.01$). Consequently, an informative mathematical model was developed, which enabled the reliable and timely prediction of the prevalence of one of the metabolic activity phases in the athlete's body. The use of the developed model will also allow us to assess the nature of adaptation to specific muscular work, identify an athlete's weaknesses, forecast the success of their performance, and timely adjust both the training process and the recovery program.

1. Introduction

Intense physical exercise training significantly impacts the metabolic processes in an athlete's body; therefore, changes occur in the biochemical parameters, which can be identified from the laboratory analysis of blood serum indicators.[1–4] One of the main responsibilities of a sports medicine doctor is to determine and provide timely information to the coach and athlete about the functional state of the body systems. Therefore, identifying predictors that describe the changes that emerge in the metabolic regulation mechanisms of the body between microcycles.

Previous articles have described various physiological markers that can serve as early identifiers or potential markers of overtraining and overwork in athletes. Creatine kinase (CK), lactate dehydrogenase (LDH), urea, uric acid, and myoglobin are the most distinguished among blood serum markers characterizing catabolism processes[5,6] in the case where there is no other pathology leading to changes in these indicators. Monitoring CK levels provides control over the state of the muscles. The peak concentration of CK occurs approximately 24 hours (h) after physical training and can remain elevated for up to seven days.[7] A chronically elevated CK level may indicate insufficient recovery. Other muscle components, such as myoglobin, may enter the bloodstream during muscle injury (peak 1–3 h post-workout), and urea nitrogen may indicate muscle breakdown processes.[8]

Moreover, regarding the amino acid profile, decreased glutamine levels and increased glutamate levels are often associated with an impaired immune system in overtrained athletes.[6] Elevated peripheral

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List of abbreviations

ALP	Alkaline phosphatase
CK	Creatine kinase
DFA	Discriminant function analysis
DHEA	Dehydroepiandrosterone
Gamma GT	gamma-glutamyl transpeptidase
HPA	Hypothalamic-pituitary-adrenal
LDF	Linear discriminant function
LDH	Lactate dehydrogenase
TRIMP	Training impulse
$\dot{V}O_2$ peak	peak oxygen uptake

blood concentrations of aspartate aminotransferase, alanine aminotransferase, LDH, and γ-glutamyl transferase are the precursors of liver metabolic disturbances in response to prolonged physical exercise training.[7,8] Increased alkaline phosphatase **(**ALP**)** values indicate the predominance of amino acid catabolism and fat hydrolysis for maintaining homeostasis during prolonged physical exercise training.[9–14]

Depending on the load, volume, and duration hormonal profiles change and cause specific training adaptations. Testosterone, cortisol, dehydroepiandrosterone (DHEA), growth hormone, insulin-like growth factor 1, sex hormone-binding globulin, and luteinizing hormone are some of the key hormones proven to be critical for athletes. Changes in basal hormone levels have been frequently reported in overtrained athletes. Catabolic hormones such as cortisol and catecholamines' tended to increase, whereas anabolic hormones such as testosterone and estradiol showed inconsistent results. Some argue that hormonal responses to muscle stimuli are more accurate indicators of overtraining and overload than basal hormone levels.[15–19]

The lack of accurate diagnostic markers of metabolic activity in athletes is evident in the conflicting results of recent studies in this area. Notably, the analysis of biomarkers is associated with many problems: individual biomarkers are not indicative of conditions such as overtraining and overload in sports; the sensitivity of individual biomarkers to detect the risk of overtraining or injury is limited; and reference ranges for athletes and specific sports are not clearly defined.[20] An ideal biological marker should be easy to measure, minimally invasive, and affordable.

This study aimed to develop a diagnostic model for predicting metabolic processes in athletes based on indicators of standard biochemical blood analyses.

2. Materials and methods

2.1. Ethics statement

All participants were informed of the risks and discomforts associated with the investigation and had signed a written consent to participate. The study was approved by the Board for Ethical Questions in the A. I. Burnazyan State Research Center of the Federal Medical-Biological Agency of Russia (Protocol No 12 from 02.03.2021), according to the principles expressed in the Declaration of Helsinki.

2.2. Study participants

The inclusion criteria for the study were: male sex, age ranging from 18 to 25 years, non-smokers, and no intake of medications or dietary supplements during the study period. Based on the inclusion criteria**,** 42 male athletics team members voluntarily participated in the first part of the clinical and laboratory study. The average age of the athletes was (22.55 ± 3.68) years.

The hormonal profiles of the female athletes differed from those of the male athletes; therefore, they were not included in this study. According to the in-depth medical examination results, athletes were non-smokers included in this study. The examination included fluorography, ultrasound examination of the abdomen and pelvic organs, echocardiography, electrocardiography, stress testing “to failure,” total urine analysis, and biochemical and total clinical blood tests. Additionally, examinations were conducted by the following doctors: ophthalmologist, otolaryngologist, surgeon, cardiologist, neurologist, dentist, and endocrinologist. During the clinical and laboratory research period, athletes did not take pharmacological drugs and dietary supplements, which would affect the metabolic processes in their bodies.

All study participants were team members. The training consisted of the following main elements: warm-up, running technique drills, strength training, cardio training, water training, and general physical preparation (according to the field of expertise and approved plan of the national team).

All athletes participating in the study fell asleep and woke up at the same time every day, which contributed to synchronizing the circadian rhythms and ensured the optimal functional state of the participants. The average duration of sleep varied from 7 to 9 h per day.

To ensure optimal hormonal balance, athletes followed a proper diet regimen that considered the balance of macronutrients and micronutrients, as well as the meal schedule and timing intervals between food intake, aiming to maintain blood glucose levels at an optimal level and prevent hormonal fluctuations. Throughout the entire observation period, athletes maintained an optimal level of hydration.

The intensity of physical exercise training was moderate to high for 1.5 h, twice a day, six days a week. At the beginning of the exercise, the continuous training protocol was 60% of the $\dot{V}O_2$ peak for 45 minutes (min). Subsequently, the intensity of the load was increased to 80% of the $\dot{V}O_2$ peak test determined during the in-depth medical examination. Physical exertion was assessed by measuring heart rate every 5 min during training with the Polar H10 device (Polar Electro, Kempele, Finland).

2.3. Study design

This study was conducted in the A. I. Burnazyan State Research Center of the Federal Medical-Biological Agency of Russia between October 2021 and August 2022 for one training year. All athletes trained twice a day for 90 min, six times a week (one day of rest per week). The training load was calculated using the modified training impulse (TRIMP) method: the product of training time in minutes and training intensity (HR zone). The TRIMP index at the pre-competitive and competitive stages was 360, and that at the other stages was 270 for all athletes.

The athletes were divided into two groups based on the results of the hypothalamic-pituitary-adrenal (HPA) analysis. The first group ($n = 22$; [23.62 ± 6.8] years old) included athletes whose cortisol and DHEA levels were within the reference values. The second group ($n = 20$; [25.3 ± 6.01] years old) included athletes whose cortisol concentrations were outside the reference limits and whose DHEA levels were within or below the normal range.[21–23] Reference ranges for young and elderly individuals are defined according to the regulatory documentation of good laboratory practice within the network of international clinics “Laboratory DNCOM".[24] The general study design and patient distribution are shown in Fig. 1.

Athletes with predominant anabolic regulatory processes were included in the first group HPA activity within the reference limits: cortisol levels of 1.4–10.1 ng/mL and DHEA levels of 0.69–2.6 ng/mL). Those with predominant catabolic bioregulatory mechanisms were included in the second group HPA activity above the functional activity limits: cortisol levels higher than 10.1 ng/mL or lower than 1.4 ng/mL and DHEA levels of 0.69–2.6 ng/mL or lower than 0.69 ng/mL[1,19]

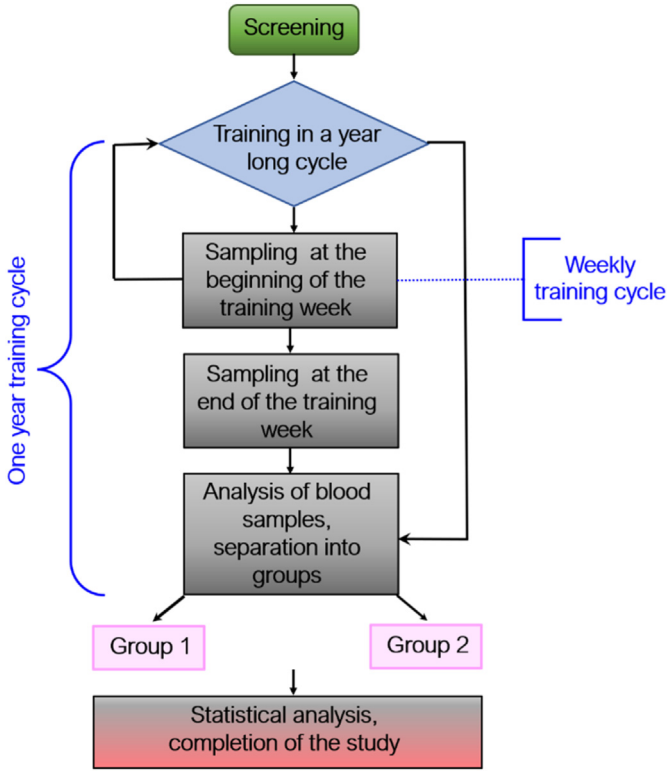

Fig. 1. Study design and distribution of participants.

Table 1
Biochemical parameters of venous blood and their reference values.

Parameter	Reference values	Unit of measure
Total protein	66 – 87	g/l
Albumin	39.7 – 49.4	g/l
Creatinine	62 – 106	μmol/l
Urea	2.76 – 8.07	mmol/l
Uric acid	202 – 416	mmol/l
Triglycerides	0.4 – 1.7	mmol/l
Total cholesterol	3.9 – 5.2	mmol/l
High-density lipoprotein cholesterol	0.9 – 1.45	mmol/l
Low-density lipoprotein cholesterol	0.26 – 2.6	mmol/l
Total bilirubin	5 – 21	μmol/l
Direct bilirubin	0 – 5.1	μmol/l
Alanine aminotransferase	5 – 41	U/l
Aspartate aminotransferase	5 – 40	U/l
Creatine kinase	7 – 190	U/l
Creatine kinase - MB	3 – 25	U/l
Lactate dehydrogenase	135 – 225	U/l
Gamma GT	10 – 60	U/l
Alkaline	35 – 130	U/l
Lactate	0.5 – 2.2	mmol/l
Amylase	28 – 100	U/l
Total Calcium	2.1 – 2.6	mmol/l
Phosphorus	0.81 – 1.45	mmol/l
Magnesium	0.66 – 1.07	mmol/l
Iron	5.83 – 34.5	μmol/l
Acid phosphatase	0.5 – 6.6	U/l
Somatotropic hormone	0.03 – 2.47	ng/ml
Total testosterone	8.64 – 29	nmol/l
Cortisol	171 – 536	nmol/l
Thyrotropic hormone	0.27 – 4.2	μME/ml
Free thyroxine	12 – 22	pmol/l
Myoglobin	23 – 72	μg/L

Gamma GT - gamma-glutamyl transpeptidase.

2.4. Sampling and laboratory indicators

Blood samples were collected after a rest day and before rest day in the morning during the annual sports cycle.

During the entire period, 3 625 laboratory parameter tests were conducted, 54 samples were rejected for technical reasons, and data from 3 571 samples were used for the statistical analysis. Capillary blood sampling in athletes was conducted from the distal phalanx of the finger after overnight fasting, according to standard diagnostic procedures. A capillary blood collection system was used, with three capillaries of 200 μL each for biochemical and hematological analyses with the following anticoagulants lithium heparin and ethylenediaminetetraacetic acid. The first drop of blood was discarded into a special biocontainer and the remaining biomaterial was centrifuged at 3 500 rpm, no later than 2 h after collection and then analyzed with a Cobas 6000 modular platform (Roche Diagnostics, Germany). Table 1 describes the serum biomarkers.

The functional state of HPA was characterized by determining the concentration of cortisol and DHEA in saliva using high-performance liquid chromatography-mass spectrometry. Samples for analysis were collected in the morning at the beginning and end of the training week[21,22,25,26] collection tube the mark.

The oral cavity was rinsed with water for 20 min before saliva collection. The athletes were instructed to refrain from eating for 2 h before biomaterial collection, manipulating or traumatizing the oral mucosa (with toothbrushes or floss), and physically and emotionally overexerting themselves 3 h before the biomaterial collection.

After the biomaterial was collected, the tube was tightly sealed. Samples were stored in a freezer at −20 °C until each sampling stage was completed. Subsequently, the saliva samples were sent to the clinical diagnostic laboratory of the A.I. Burnazyan Federal Biomedical Center.

DHEA and cortisol concentrations in saliva were determined in using high-performance liquid chromatography-mass spectrometry.[27,28] The results were expressed in units recommended by the manufacturer's instructions (ng/mL for DHEA and cortisol).

2.5. Statistical analysis

The 31 indicators (Table 1) were selected for discriminant analysis. These parameters were identified based on the knowledge that athletes' anabolic processes are associated with normal or elevated DHEA levels, and the predominance of catabolic regulatory mechanisms is associated with high cortisol levels in the blood of the subject. Testosterone and cortisol indicators were logarithmically transformed. Other biochemical indicators were not changed.

In the first step, discriminant function analysis (DFA), cortisol and testosterone were used as predictor variables for a simple linear model only to divide athletes into groups with the predominance of anabolic or catabolic regulatory mechanisms. Using the variables cortisol and testosterone, Fisher's stepwise linear DFAs were determined to separate the groups. The DFA resulted in new values (scores), for the analytical univariate variable in each subject, and the gradient of these variables maximizes the difference between groups. The mathematical DFA model is a linear combination of the included variables (creatinine, uric acid, urea, testosterone, alkaline phosphatase, albumin, total calcium and total protein). The probability density distribution in the DFA model is based on the group size that was applied in the classification in all observations as either anabolic or catabolic regulatory process in athletes. The DFA classification model was further evaluated as correct or incorrect based on initial HPA activity. Equality of group (catabolic and anabolic) mean values of the included variables in each model was tested using Wilk's Lambda distribution and associated F-criterion and probability, the results of which are presented in Table 1. The coefficients of the linear discriminant function (LDF) were included in the model because they were significant for each prognostic variable in the derivation of the univariate discriminant function.

Significant predictors were added to construct consistent DFA models with greater predictive value, potentially allowing better distinction between groups with predominant metabolic regulatory mechanisms. Group averages and LDF coefficients were then retested for equality of

group averages and LDF coefficients to compare successive DFA models and assess their relative strength using a classification table of predictors (Table 2). Sensitivity was defined as a correct classification of HPA activity with a predominance of catabolic regulatory mechanisms (i.e. sensitivity = true positive catholic process/(true positive catholic process + false negative catholic process).

Specificity was defined as the correct classification of HPA activity, with predominance of anabolic regulatory mechanisms (i.e., specificity = true positive anabolic process in the body of the subjects/(true positive anabolic process + false positive anabolic process).

The obtained data were processed using the special software application package STATISTICA v 13.1 (Stat Soft, Inc., 2016). When processing biochemical data, statistical significance was set at $p < 0.05$. To classify and model the metabolic regulation mechanisms in athletes, based on the biomarker indicators, we processed and analyzed the collected data, statistically grouped the results with the description of features, and conducted correlation analysis using the Spearman rank correlation coefficient.

The discriminant analysis provided an opportunity for classification through data generalization, processing, and analysis. Consequently, the intergroup variance was determined, and a step-wise selection was conducted by including significant variables, exclusion unreliable variables, performing hypothesis estimation, and dividing the degree of influence of qualitative indicators with a gradation into two levels.[29] The derived linear-discriminant function enabled the prediction of the probability of the predominance of catabolic regulatory mechanisms in athletes.

3. Results

A discriminant analysis of standard biochemical blood parameters was conducted to identify the predictors of the metabolic pathway. We identified eight significantly influencing indices to develop a mathematical model that classifies metabolic processes into anabolic or catabolic phases. These indices were creatinine ($p < 0.001$), uric acid ($p < 0.001$), urea ($p < 0.001$), testosterone ($p < 0.001$), ALP ($p = 0.001$), albumin ($p = 0.006$), total calcium ($p = 0.005$), and total protein ($p = 0.037$). These results are summarized in Table 2, where a Wilkes lambda value (λ) = 0.044 (F [82.065] = 319.76; $p < 0.001$), it indicates good discrimination, as the λ value is close to 0.

As shown in Table 2, the smaller the partial λ-Wilkes value, the greater the contribution to the diagnostic model. Based on these results, we concluded that creatinine, uric acid, and urea were the main variables contributing to the discrimination between the phases characterizing the metabolic process. The tolerance index (tolerance) measures the redundancy of a variable in the model, which high values confirm the significance for most criteria and ALP, to a lesser extent. However, this biochemical index reflects the current phase of the metabolic process, which confirms the necessity for its inclusion in the diagnostic model. The remoteness of independent variables and variance differences, which affect the assessment of the metabolic process, was confirmed using the

Table 2
Evaluation of the informativity of signs in diagnosing metabolic processes included in the linear-discriminant function.

Indicators	λ – Wilkes	Partial λ – Wilkes	F – exceptions	p- level	Toler
Creatinine	0.57	0.77	602.183	< 0.001	0.76
Uric acid	0.60	0.74	718.324	< 0.001	0.96
Urea	0.48	0.92	174.034	< 0.001	0.95
Testosterone	0.45	0.99	18.687	< 0.001	0.89
Alkaline phosphatase	0.44	0.99	10.857	0.001	0.74
Albumin	0.44	0.99	7.352	0.006	0.99
Total calcium	0.44	0.99	7.654	0.005	0.89
Total protein	0.44	0.997	4.348	0.037	0.89

Table 3
Biochemical parameters included in the model for determining metabolic processes and linear discriminant function coefficients.

Signs	Conditional designation	Coefficients	
		LDF1	LDF2
Creatinine	X1	0.936	0.801
Uric acid	X2	0.072	0.047
Urea	X3	4.018	3.281
Testosterone	X4	0.029	0.169
Alkaline phosphatase	X5	0.081	0.077
Albumin	X6	0.001	0.001
Total Calcium	X7	127.092	125.615
Total protein	X8	1.794	1.823
Constant		−305.144	−278.649

LDF – Linear discriminant function.

Table 4
Decisive rules for the differential diagnosis of metabolic processes in athletes based on the maximum linear discriminant function value.

LDF1	the highest probability of predominance **of catabolic** processes (LDF1 > LDF2)
LDF1 = −305.1 + 0.9 × X1 + 0.07 × X2 + 4.02 × X3 + 0.03 × X4 + 0.08 × X5 + 0.001 × X6 + 127.1 × X7 + 1.8 × X8	
LDF2	the highest probability of predominance **of anabolic** processes (LDF2 > LDF1)
LDF2 = −278.7 + 0.8 × X1 + 0.05 × X2 + 3.3 × X3 + 0.17 × X4 + 0.08 × X5 + 0.001 × X6 + 125.6 × X7 + 1.8 × X8	

LDF – Linear discriminant function.

λ-Wilkes criterion values ($p < 0.001$) and F-factor $p < 0.001$). As a result of the step-wise discriminant selection of the most significant ($p < 0.05$) features with a level of reliability of at least 95%, the problem of developing the final discriminant function was solved. The coefficients for the linear classification functions with grading levels of the features are discussed in Table 3.

The following LDF equations were used (Table 4) to determine the metabolic process phase and predict the activation of adaptive regulatory mechanisms. The obtained biochemical values (creatinine, uric acid, urea, testosterone, ALP, albumin, total calcium, and total protein) were substituted for each athlete.

To determine the predominance of anabolic or catabolic processes in athletes, the equations in Table 4 were solved and the highest value of LDF values corresponded with the relevant metabolic process phase. The discriminant function of the prediction of metabolic processes in the body of athletes has a high information capacity (92.1%), which was confirmed by the biochemical results of the activity of the neuroendocrine system, which characterized the stage of adaptive regulatory mechanisms in the body of athletes in response to stress factors. The classification matrix for predicting metabolic processes based on the results of the discriminant function calculation demonstrates the statistical significance of the model ($p < 0.01$). The sensitivity of the decision rules for determining the predominance of anabolic or catabolic regulatory mechanisms is listed in Table 5.

The predictions of the prevalence of catabolic and anabolic processes in the body of athletes using the proposed model were in agreement with

Table 5
Classification matrix for the prognosis of metabolic processes in the body of athletes with the highest achievements in their respective sports ($n = 42$).

Metabolic processes	Sensitivity	Classification of the condition according to the LDF value		Total cases
		LDF 1	LDF 2	
Catabolic phase	88.3%	1 176	156	1 332
Anabolic phase	94.7%	119	2 120	2 239
Total	92.1%	1 295	2 276	3 571

LDF – Linear discriminant function.

the results in 88.3% and 94.7% of the cases, respectively. The classification sensitivity of the model provides a predicted agreement in 92.1% of cases compared with the study results. Accordingly, LDF2 athletes had the most optimal biochemical parameters.

4. Discussion

In our previous study,[1] analysis of the biochemical indicators dynamics enabled the observation of significant differences in the indicators, allowing for characterizing anabolic or catabolic processes in athletes. Identifying of the prevailing metabolic mechanisms that are regulated in the body during the annual macro cycle in high-performance sports does not require a comprehensive examination. However, it can be monitored using common serum biomarker analysis, questionnaires assessing fatigue levels and clinical observations (such as fatigue or over fatigue). Changes in the body of athletes due to catabolism are accompanied by an increase in the products of amino acid breakdown, lipid per oxidation, and nucleic acid breakdown. In some cases, intense and prolonged physical exercise training is associated with changes in the rate of metabolic regulation in the body and biochemical shifts in the catabolic direction, there by confirming the alteration of metabolic processes in muscle tissues and internal organs.[30–33]

Regarding blood lactate, its levels may depend on the athlete's training status and numerous metabolic variables. However, blood lactate testing is considered an ineffective approach for assessing overload and overtraining.[8] In addition, in power sports, against the background of the load, an increase in lactate is not observed.[32] Other factors that are equally important when discussing changes in blood lactate concentration are glycogen concentration and the possible decrease in its storage in the muscles and liver due to increased training. A common trend in endurance and strength endurance athletes overtrained, is a decrease in maximum lactate concentration, while submaximal values remain unchanged or decrease slightly.[20]

Circulating CK levels increase with eccentric and unaccustomed exercise and persist for several days to weeks. CK levels in combination with resting urea levels accurately reflect muscle and/or metabolic stress, but they are ineffective in recognizing overload or overtraining.[20,31] A recent study showed no statistical difference in CK changes between normal and overtrained athletes.[32] This study also showed that circulating catecholamine levels did not change significantly among participants.

Plasma glutamine concentration has been proposed as a possible indicator of excessive training stress.[33] However, not all studies found a drop in glutamine during periods of increased training and overtraining, and altered plasma glutamine concentrations are not a causal factor in immunosuppression.

Some authors have suggested that plasma concentrations of nitrogenous waste products (such as urea, 3-methylhistidine, and uric acid), may indicate muscle protein breakdown and, therefore, may be a marker of overtraining due to a presumed association with a catabolic state or natural process of the organism. This is presumably caused by chronically elevated glucocorticoid levels. However, prolonged acute exercise is associated with a transient increase in plasma uric acid and urea concentrations, and the latter is also markedly affected by recent dietary protein intake.[31]

For a long time, the ratio of testosterone and cortisol in resting plasma was considered to be an indicator of overtraining. However, this ratio decreases with respect to training intensity and duration. Moreover, this ratio only indicates the actual physiological stress of training and cannot be used to diagnose overtraining and fatigue.[20]

Problems regarding the analysis of athlete hormonal profiles include the influence of food intake. Nutrient composition and/or sampling before and after meals can significantly change the basal concentration of some hormones (cortisol, DHEA and total testosterone), or their concentration in response to physical activity (cortisol and growth hormone). In female athletes, the hormonal response will depend on the menstrual cycle phase; hence, there are daily and seasonal fluctuations in hormones. The conflicting research results are also related to other factors. In several instances, the time of sampling, meals and time after the end of training are not considered. Moreover, the measurement methods and/or limits of detection of the analytical equipment used may vary from study to study.

When predicting the predominance of anabolic or catabolic processes in athlete's, current analysis and subsequent analyses of the changes in the four-year macro cycle are paramount tasks in sports medicine. A new approach for the objective control of catabolic and anabolic processes can help effectively manage the training activities of athletes while achieving the highest fitness goals.

The reason for the shift in regulation is that the functional state of the body significantly differs in metabolic requirements due to differences in the energy processes that occur untill the moment of full recovery. The intensity (load volume within required time) of physical exercise training determines the severity of catabolic and anabolic mechanisms.

The mathematical model used to determine the phases of metabolic regulation in athletes provided a statistically significant ($p < 0.01$) prediction based on eight standard biochemical indices (creatinine, uric acid, urea, testosterone, ALP, albumin, total calcium, and total protein).

A metabolic regulation phases diagnostic model was further used to rapidly predict possible changes in adaptation mechanisms in response to unfavorable environmental factors as well as their dynamic control during intensive training and direct competition. This diagnostic procedure is a screening method aimed at identifying athletes with a high probability of catabolic over anabolic mechanisms of body regulation.

The study results allowed us to hypothesize that the metabolic processes in the body depend on the activity of the hypothalamic-pituitary-adrenal system. In this regard the development of a mathematical model that predicts the predominance of one of the phases of metabolic activity in athletes was developed.[1]

The developed model is only a primary diagnostic tool that enables the assessment of metabolic processes in athletes at an early stage and the initiation of nutritional and metabolic support at the point of maximum effectiveness.

5. Conclusions

Dynamic analysis of serum biochemical indicators (creatinine, uric acid, urea, testosterone, ALP, albumin, total calcium, and total protein) in athletes revealed significant balance shifts in metabolic processes in the body. These indicators provided an opportunity to form linear classification functions to determine the anabolic or catabolic phase of regulation in athletes based on the mathematical and statistical processing of biochemical results using discriminant analysis. As a result, an informative mathematical model was developed, which allowed us to reliably and timeously predict the prevalence of one of the phases of metabolic activity in athletes.

5.1. Limitations

In our study, only male athletes were the sample population. In the future, conducting a study that includes female athletes and athletes from other disciplines are advisable. Moreover, the small sample size was a limitation. Further studies with an increased sample size ($n \geq 50$) will be needed to determine metabolic process biological markers accurately. Furthermore, long-term studies are needed because the present study did not allow for outcome-based studies that considered model modifications, including training, nutrition, and social aspects. Further rigorous search for new metabolic biomarkers is required.

Ethical approval statement

All participants were informed of the risks and discomforts associated with the investigation and had signed a written consent to participate.

The study was approved by the Board for Ethical Questions in the A. I. Burnazyan State Research Center of the Federal Medical-Biological Agency of Russia (Protocol No 12 from 02.03.2021), according to the principles expressed in the Declaration of Helsinki.

Data statement

The datasets generated during and/or analyzed during the current study are available from Vasiliy I. Pustovoyt (vipust@yandex.ru) on reasonable request.

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CRediT authorship contribution statement

Victoria A. Zaborova: Software. **Evgenii I. Balakin:** Methodology, Investigation. **Ksenia A. Yurku:** Visualization. **Olga E. Aprishko:** Investigation. **Vasiliy I. Pustovoyt:** Data curation, Conceptualization.

Conflict of interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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