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Article

Analysis and research on athlete biorhythm and sports injury

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Abstract: There is a certain correlation between sports injury and biorhythm status. Finding out the specific stage of the biorhythm can help athletes reduce injuries during training. This paper analyzes the athlete's biorhythm state through computational principles and biomolecular perspectives, and verifies the reliability of the relationship between the biorhythm state and sports injury. This article takes 132 samples of injured athletes from a university with complete sample records from the Google data analysis platform as the research object. According to the biological rhythm estimation method, the Google data analysis platform is used to calculate and analyze the relationship between the injury period and the biological rhythm of these samples. Then, the biorhythm state of the athlete is evaluated from the calculation principle of biorhythm and the level of biomolecules, and compared with the athlete's injury situation, so as to guide the athlete's sports training rhythm. The research results show that the relationship between the biological rhythm and sports injury obtained according to the biological rhythm calculation method has a large error. From the perspective of biomolecules, the rhythm regulator PPAR1 is regulated by unknown factors, and CLOCK is regulated by ribosylation. When the ratio of AMP/ATP is higher than 30%, liver kinase B phosphorylates AMP-activated protein kinase. At this time, the biological rhythm is in the climax period. At this time, people feel comfortable and energetic, and the incidence of sports injuries during training is low.

Keywords: biorhythm status; sports injury; circadian rhythm; physical strength rhythm

1. Introduction

Athletes' biological rhythms are divided into periodic phases over time, and athletes have different risks of sports injuries in different phases. Analyzing the relationship between the biological rhythm state and sports injury from the perspective of calculation principles and biomolecules can provide training guidance for athletes and reduce the risk of injury. The research on circadian rhythm of biomolecules at home and abroad mostly uses mice as experimental objects. These studies focus on understanding the biological state of these organisms. However, in the analysis of the relationship between biological rhythms and sports injuries, little research has been done on the calculation principles and the state of biomolecules. Sports injuries are inevitable. Sports injuries have a greater impact on the body, and it will not recover in a short time. During the recovery period, the inconvenience of exercise will have a greater impact on life. If you are a student of sports or have sports injuries, you cannot exercise for a short period of time. If the wound is handled well, there may be no sequelae. In sports, sports injuries and sports diseases such as shock, absence, bleeding, cardiac arrest, and respiratory arrest are often seen. Some sports injuries are not life-threatening but can be very harmful to your health, so be very careful.

Continuing exercise without rest and recovery time, despite stiffness and pain, can lead to hyperactivity, and the warning signs of illness, injury, burnout, and performance impairments are all the rage. Excessive exercise may cause muscle pain and other symptoms. From the digestive system to the urinary system, it is possible that the rest of the body is affected, and the symptoms of reduced movement will slowly disappear.

McCrae CS analysis predicts the difference between the survival of sepsis and the serum metabolome of patients with sports injuries, and found that the two have significant differences in fatty acid transport and oxidation, gluconeogenesis, and citric acid circulation pathways, thereby guiding the personalized treatment of patients with sports injuries [1]. Appleton SL uses metabolomics methods to discover the metabolic phenotypes of surgical patients and realize real-time personalized diagnosis, thereby improving the selectivity of diagnosis and treatment [2]. Kuwahara K found through gene expression analysis that puerarin in Pueraria lobata is an antagonist of Rev-erbα, which relieves exercise hyperhomocysteinemia in a circadian rhythm [3]. However, the specific mechanism of action needs further study. Wheaton AG found that the cardiotoxicity of aconite has circadian rhythm, and the ablation of Bmal1 will abolish the rhythm of aconite in liver metabolism [4]. Rao MN found through research that melatonin can effectively improve the changes in sleep patterns and energy metabolism in rats caused by circadian rhythms, thereby improving sleep quality [5]. Walker W H points out that disruption of biorhythms is significantly associated with a variety of psychiatric disorders, such as depression, anxiety, and bipolar disorder [6]. Moreover, the disturbance of biological rhythm can easily lead to metabolic diseases [7]. Adjusting biological rhythm can improve the treatment effect of many diseases [8].

Molecular mechanisms in circadian rhythms play a significant role in regulating physiology [9,10]. The Poh J study found that the expression levels of rhythm genes cry1, cry2, PPARα, and per2 were significantly up-regulated under the condition of animals ingesting sea cucumber saponin during the bright period, and at the same time up-regulated the expression of liver fatty acid synthesis and oxidation, cholesterol synthesis, and reverse transport related genes throughout the cycle level [11]. This study shows that sea cucumber saponins can regulate the expression of circadian clock genes, but the specific molecular mechanism remains to be studied in depth. The Lo J study found that resveratrol can improve the expression of CLOCK and Bmal1 by activating the rhythmic expression of SIRT1, and improve the circadian rhythm of lipid metabolism [12]. Kaplan J compound Zhenzhu Tiaozhi prescription can improve the blood lipid level of 14 models, increase insulin sensitivity, and regulate the rhythm of liver cry1, PPARα gene expression [13]. Chen C found that Shenqi compound regulates the circadian rhythm by up-regulating the expression of clock genes cry1 and Dbp to regulate the secretion of insulin, maintain the steady state of glucose metabolism in the body, and prevent type 2 diabetes [14]. Ravassard P found that the mechanism of Shenghui Decoction for improving Alzheimer's disease may be through up-regulating the expression of Bmal1 gene to improve circadian rhythm disorders [15].

Based on the biological rhythm estimation method, this paper uses the Google data analysis platform to calculate and analyze the relationship between the injury period and biological rhythm of these samples. First, according to the biological rhythm estimation method, the Google data analysis platform is used to calculate and analyze the relationship between the injury period of these samples and the biological rhythm. Then from the perspective of biomolecular analysis, the relationship between the athlete's biological rhythm and sports injury, as well as the effect of circadian rhythm changes on bioavailability and drugs.

2. Biorhythm and calculation principle

2.1. Biorhythm

The rotation and revolution of the earth will cause constant and temporary changes in the environment: constant changes include day and night alternations, seasonal alternations, and year changes; temporary changes are caused by sudden changes in the environment, including sunlight, humidity, and temperature changes [16]. In order to adapt to this change in the environment, most organisms including plants, animals, and fungi have evolved circadian biological systems [17]. This biological system adapts to environmental changes through biological behaviors such as mammalian sleep and wakefulness, body temperature, cell metabolism and hormone release at the cellular, physiological and biochemical levels [18].

The circadian rhythm plays an important role in maintaining the homeostasis and health of the organism. The chronic destruction and imbalance of the circadian rhythm can lead to disorders of the central system, liver system and digestive system of the organism, which in turn induces various metabolic syndromes and inflammations [19]. Therefore, the circadian rhythm has an inherent regulatory effect on the health and homeostasis of the organism [20]. The generation and maintenance mechanism of the circadian rhythm. The generation of the circadian rhythm depends on the organism's own biological clock system and a complex regulatory network formed by clock-controlled genes. Under the control of this network, the organism produces a rhythmic oscillation with a cycle of about 24 hours [21]. The manifestation of this shock is that the transcription and expression of the core rhythmic genes of the circadian clock system show rhythmic activity, and it also makes the expression of downstream genes regulated and controlled by the circadian clock and the synthesis of some important functional proteins show rhythmic changes, thereby to achieve the role of regulating the body's overall metabolic system [22].

At present, there is basically a consensus on the generation and maintenance mechanism of circadian rhythm at the molecular level. It is generally believed that the driving of mammalian circadian rhythms mainly relies on a series of complex positive and negative feedback regulation mechanisms. The operation of this mechanism mainly includes three important core feedback loops: E-box and D-reaction elements and ROR response element (RORE) [23].

Among them, circuit 1: CLOCK and Bmal1 form a heterodimer to activate the transcription of CCGs through the E-box circuit, and induce the transcription of clock-controlled genes circadian protein (per) and cryptochrome (cry), which are inducers

of this feedback pathway. And the expression of induced genes presents negative feedback regulation, that is, as the expression of per and cry in the cytoplasm and their transfer to the nucleus after phosphorylation increases, cry and per proteins inhibit the activity of CLOCK and Bmal1 complexes and down-regulate the CCGs expression [24].

Circuit 2: RORα, β, γ, and REV-erbα/β are the targets of CLOCK and Bmal1 heterodimers. CLOCK and Bmal1 heterodimers activate the transcription of RORs, and REV-erbs regulate Bmal1 through negative feedback by combining with RORE transcription.

Circuit 3: Dbp and E4BP4 proteins regulate the expression of genes including Per through D-box. Produce rhythmic shocks, and then regulate the body's metabolic homeostasis.

2.2. Biorhythm estimation method

Biorhythm Estimation Method refers to techniques used to predict or estimate the cyclic patterns of various physiological and psychological functions in living organisms. These methods are often employed to track and interpret natural cycles such as sleep-wake cycles, hormonal fluctuations, and other periodic biological processes. The goal is to understand how these rhythms influence behavior, mood, and performance over time. Human biorhythm is periodic, and the period can be digitally calculated and its calculation model can be found to evaluate the biorhythm of different athletes [25]. Theta sequences are thought to play a key role in spatial navigation and the encoding of memories. During activities like exploring a new environment or learning a task, the hippocampus generates a sequence of neural activations that help to encode the order and spatial arrangement of experiences. These sequences are critical for forming coherent memories and for the ability to navigate through space. In this paper, the theta sequence is used as the calculation method, and its encoding characteristics and mechanism are calculated as follows: Let x be the total number of days from birth (Gregorian calendar) to a certain day for a person, then:

$$X = age \times 365 + leap + day \tag{1}$$

Then calculate with X:

$$f(x) = \frac{1}{Nh}\sum_{i=1}^{N} k\left(\frac{X_i - x}{h}\right) \tag{2}$$

$$k(x) = \frac{1}{\sqrt{2\pi}}\exp\left(-\frac{x^2}{2}\right) \tag{3}$$

$$P(x|n) = \frac{P(n|x) \times P(x)}{P(n)} \tag{4}$$

The above formula is the firing rate distribution of P(n|x) when it is at position x, P(x) represents the probability of being at position x within a certain period of time, and P(n) represents the firing rate of neurons during this period of time. Probability, usually a normalized coefficient. The final P(n|x) is the position probability distribution when the firing of the neuron is n. The basic characteristics of the theta sequence in the theta cycle, the cell clusters encoding the position near the current

position are discharged in sequence from back to front to produce a clear, orderly, and cross-neuronal sequential discharge, which is called theta sequence:

$$h_t = z_t \Theta h_{t-1} + (1 - z_t) \Theta h_t \tag{5}$$

$$s_j = \sum_i c_{ij} u_{(j|i)} \tag{6}$$

$$\sigma t = \frac{\sqrt{\frac{1}{n} \sum_{i=1}^{n} \left(FI_{it} - FI_{it} \right)^2}}{FI_{it}} \tag{7}$$

This sequence can represent a path trajectory near the location, so the theta sequence is a space-time compression sequence. The main verification methods of the convergence mechanism are the convergence model and the convergence model. Convergence refers to the dynamic change process of the deviation of biological rhythm development. Specifically, the convergence model is defined as follows:

$$w_G^{A_i A_j} = \max \left\{ 0, W_G \cdot \varepsilon \left(f_G^{A_i}, f_G^{A_j} \right) \right\} \tag{8}$$

$$u_{(j|i)} = w_{ij} A_i \tag{9}$$

$$M_n^{'} - H_{ys} > M_p \tag{10}$$

Among them, M represents the memory rhythm in different periods. The basic characteristics of theta sequence and its role in spatial memory have attracted the attention of researchers. First, in order to combine the sequential firing activity of the location cell cluster with the representation of the actual spatial location, the Bayesian formula is used to decode the actual spatial location represented by the theta sequence:

$$c_{ij} = \frac{e^{b_{ij}}}{\sum_k e^{b_{ik}}} \tag{11}$$

$$In\left(\frac{FI_{it}}{FI_{it} - 1} \right) = \alpha + \beta InFI_{it} - 1 + v_i + \zeta_t \tag{12}$$

$$r = \frac{\alpha}{1 - \beta} \tag{13}$$

The core idea is to use the firing rate of position cells and the firing pattern in a certain theta cycle to reconstruct the spatial position presented in the brain. Specifically, the firing rate of each location cell with location is taken as the prior probability, and the posterior probability that the cell cluster activated in a certain theta period characterizes the location is obtained by Bayesian formula, namely:

$$\tau = \frac{In(2)}{\theta} \theta = -\frac{1}{T} In(1 + \beta) \tag{14}$$

For each set of test cases, the currently commonly used relative deviation rate (PRD) is used to measure the accuracy of the algorithm. The PRD calculation formula is:

$$PRD(A) = \frac{C \max(A) - ref}{ref} \times 100\% \tag{15}$$

For each set of test cases, CPLEX and CIGA are used to solve them, and the maximum running time of CIGA is set ass, two indicators, PRD and success rate (SR) are used to test the optimality of CIGA. The calculation formula of SR is:

$$SR = \frac{Num - CIGA}{Num - all} \tag{16}$$

$$h_t = \tanh\left(w_c x_t + u_c\left(r_t \Theta h_{t-1}\right) + b_c\right) \tag{17}$$

Among them, Num-CIGA represents the number of cases in which the optimal solution is obtained. Using this formula, the probability distribution of the real-time coding position of the brain can be decoded by the firing pattern of the neuron cluster in the theta cycle:

$$In\left(\frac{FI_{it}}{FI_{it}-1}\right) = \alpha + \beta InFI_{it} - 1 + \varphi X_{it} - 1 + v_i + \tau_t \tag{18}$$

$$k_{t1}[i] = \sum_j cos\left(w_i^1, w_j^2\right) \tag{19}$$

In order to further improve the accuracy of athlete biorhythm state prediction, this paper continues to use a comprehensive algorithm development framework. The framework first collects and preprocesses data such as athletes' birth dates and training competition schedules to calculate the periodic characteristics of biorhythms.

$$P(x) = sin\left(\frac{2\pi x}{T}\right) \tag{20}$$

Next, the theta sequence encoding mechanism of neuroscience is used to decode the actual spatial position in combination with Bayesian formulas to reconstruct the spatial representation in the brain.

$$P\left(n|x\right) = \frac{P\left(x|n\right)P\left(n\right)}{P\left(x\right)} \tag{21}$$

3. Objects and procedures

3.1. Object

This article uses a sample of 132 injured athletes with complete sample records from the Google data analysis platform as the research object. Each piece of data contains complete information such as physical rhythm, emotional rhythm, and intellectual rhythm at the time of sports injury. Criteria for sample selection: 1) Athletes have a clear record of sports injuries during the study period. 2) The athlete's biorhythm data (physical, emotional, and intellectual rhythms) were fully recorded at the time of injury. 3) The basic information of the athlete (age, gender, sport) is complete. The sample data extracted from the Google data analysis platform is stripped of invalid and missing items and integrated into a unified format.

3.2. Steps

First, according to the biological rhythm estimation method, the Google data analysis platform is used to calculate and analyze the relationship between the injury period of these samples and the biological rhythm. The platform mainly uses descriptive statistical analysis to reveal the distribution characteristics of sample basic

information and biorhythm data. Through correlation analysis, the potential relationship between biorhythm and sports injury was discussed. On this basis, a regression model was established to quantify the impact of biorhythm on sports injuries. Finally, the test set is used to verify the model, evaluate its accuracy and reliability, and ensure the robustness of the research results. Check the table to know the athlete's physical rhythm status on this day. As shown in **Table 1**, Y_1, Y_2, Y_3 are physical, emotional, and intellectual states, and Z is the positive remainder.

Table 1. Rhythm corresponds to Z-Y function table.

Z	Y1	Y2	Y3	Z	Y1	Y2	Y3
1	0.0000	0.0000	0.0000	8	0.9432	1.0000	0.9718
2	0.2698	0.2225	0.1893	9	0.8170	0.9747	0.9989
3	0.5196	0.4339	0.3717	10	0.6311	0.9010	0.9899
4	0.7308	0.6235	0.5406	11	0.3984	0.7818	0.9450
5	0.8879	0.7818	0.6901	12	−0.1362	0.4339	0.7557
6	0.9791	0.9010	0.8146	13	−0.3984	0.2225	0.6182
7	0.9977	0.9749	0.9097	14	−0.9432	0.0000	0.4852

For example, an athlete was born on 27 January 1980, and his elbow was sprained during training on 4 June 1992. What is the biorhythm state of the athlete on that day? The new perpetual calendar shows that the athlete was born to. A total of 12 years and 128 days have passed on this day, including four leap years, so according to the formula:

$$X = age \times 365 + leap + day = 12 \times 365 + 4 + 128 = 4512 \tag{22}$$

Divide x by 23, 28, and 33 to get the remainders to be 4, 4, and 24 respectively. Check **Table 1** to get:

$$Y_1 = 07308，\ Y_2 = 06235，\ Y_3 = 09899 \tag{23}$$

Then from the perspective of biomolecular analysis, the relationship between the athlete's biological rhythm and sports injury, as well as the effect of circadian rhythm changes on bioavailability and drugs.

4. Average incidence of injury in each period

4.1. Average incidence of injury in each period

As can be seen from the results in **Figure 1**, the low-tide period is an injury-prone period, but this does not take into account the random nature of the sport.

As shown in **Figure 2**, it is obviously wrong to compare the incidence of injury for 3 days of exercise with the incidence of injury for 10 days. Therefore, the relationship between the biological rhythm and sports injury obtained by the biological rhythm calculation method has a large error. The correct idea is shown in **Table 2**. The calculation of the relationship between biorhythms and sports injury needs to take into account multiple physiological cycles (physical, emotional, intellectual), and the interaction of these rhythms can lead to complex patterns of influence. The weighted

principle is used to consider the effect of various rhythm factors on the injury rate in each cycle, which can reflect the injury risk in different cycles more accurately.

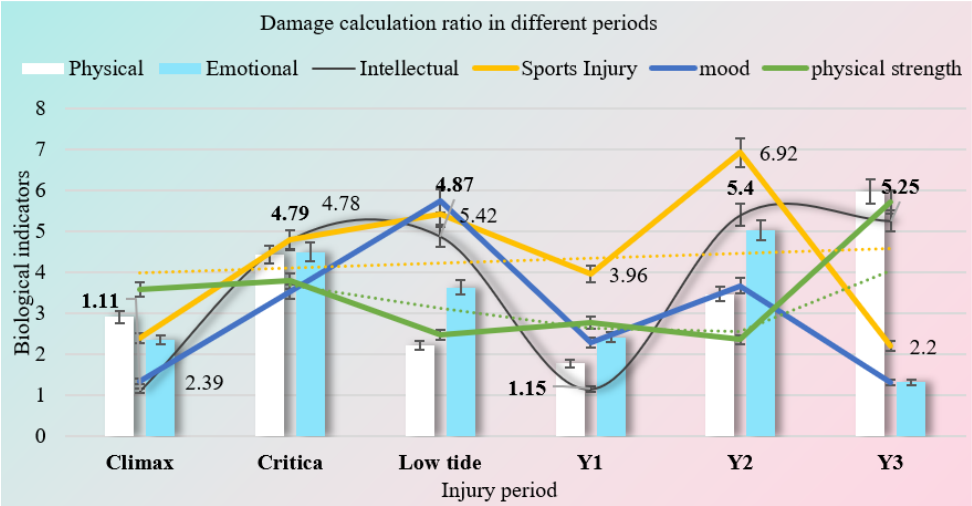

Figure 1. Damage calculation ratio in different periods.

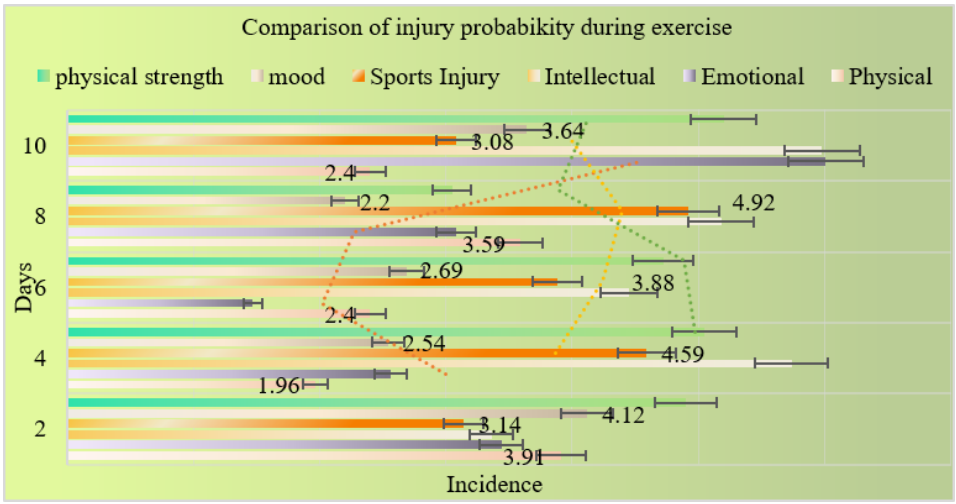

Figure 2. Comparison of injury probability during exercise.

Table 2. The weighted principle calculates the daily average incidence of each period.

Item	Physical	Emotional	Intellectual	Sports Injury	mood	physical strength
Climax	2.91	2.35	1.11	2.39	1.34	3.58
Critica	4.42	4.49	4.79	4.78	3.52	3.78
Low tide	2.22	3.63	4.87	5.42	5.74	2.47
Y1	1.77	2.41	1.15	3.96	2.28	2.77
Y2	3.46	5.02	5.4	6.92	3.67	2.35
Y3	5.96	1.31	5.25	2.2	1.32	5.71

These findings are consistent with some conclusions in the existing literature. Previous research has also shown that different cycles of biorhythms have a significant impact on the body's physiological function, with low periods particularly prone to

decreased athletic performance and increased risk of injury [26]. However, this paper further quantifies the specific impact of different biorhythm cycles on sports injuries through the weighted average method, which provides more detailed data support for future research.

4.2. Significance test of sports injury incidence in different periods

This article uses a sample of 132 injured athletes from a university with complete sample records from the Google data analysis platform as the research object. Each piece of data contains complete information such as physical rhythm, emotional rhythm, and intellectual rhythm at the time of sports injury. The statistics of sports injuries are shown in **Table 3**.

Table 3. Statistical table of athletes' biorhythm and sports injury.

Rhythm	Number of injuries	Climax		Critical period		Low tide	
		frequency	Incidence	frequency	Incidence	frequency	Incidence
Physical	64	31	48%	15	23%	18	28%
Emotional	64	20	31%	28	43%	16	25%
Intellectual	64	19	29%	35	54%	10	15%

As shown in **Table 4**, sampling surveys or biological rhythms can cause differences in the incidence of injuries in different periods. It can be seen that biological rhythms are closely related to sports injuries.

Table 4. Average daily damage frequency during critical period.

Days	Physical	Emotional	Intellectual	Sports Injury	mood	physical strength
2	3.91	3.44	3.36	3.14	4.12	4.9
4	1.96	2.56	5.74	4.59	2.54	5.05
6	2.4	1.47	4.45	3.88	2.69	4.72
8	3.59	3.08	5.18	4.92	2.2	3.05
10	2.4	6.01	5.98	3.08	3.64	5.2

As shown in **Figure 3**, the difference between the high tide period and the low tide period is not large. Therefore, the same method can be used to predict the injury rate of sports injuries. Although exercise biorhythms are closely related to sports injuries, intellectual rhythms do not seem to be related to sports injuries. The incidence of injury in different periods is shown in **Table 5**.

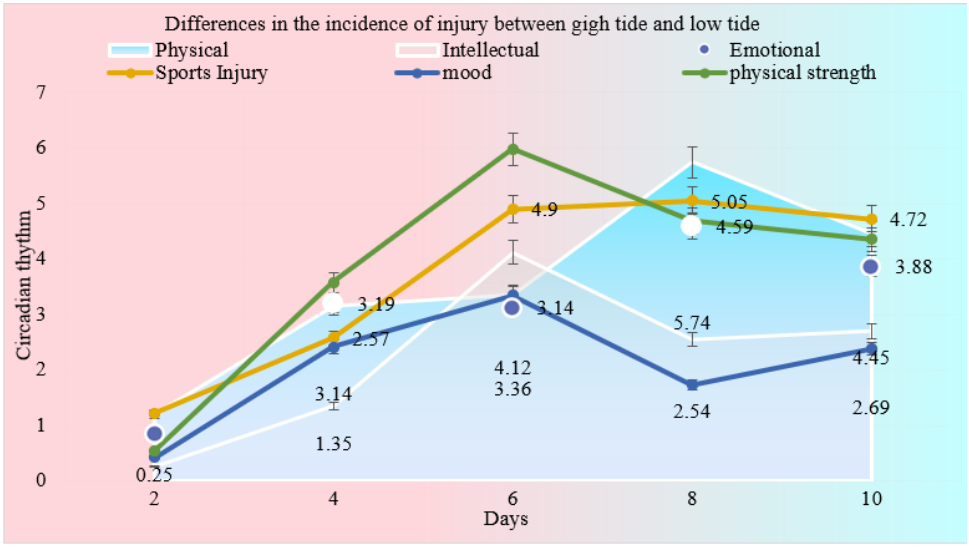

Figure 3. Differences in the incidence of injury between high tide and low tide.

Table 5. The incidence of injury in different periods.

Biological factors	Injury	Climax	Low tide	Critical period	Sports Injury
Mood	0.47	1.96	0.77	0.73	0.81
Physical strength	3.7	2.39	1.87	3.42	1.18
Intelligence	5.51	3.47	3.05	5.39	4.43

As shown in **Figure 4**, the circadian rhythm and the biological clock system participate in the metabolic regulation process of various systems in the body. More than 600 liver metabolites are in harmony with the rhythm, indicating that there is a very close relationship between the biological clock system and metabolism. The two may be connected through a series of metabolic sensors.

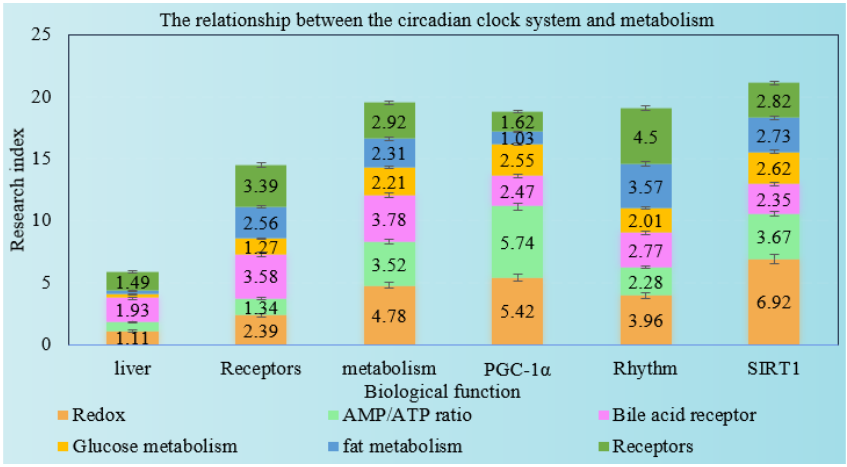

Figure 4. The relationship between the circadian clock system and metabolism.

As shown in **Table 6**, Krüppel-like factor 10 (KLF-10), peroxisome proliferator-activated receptor (PPAR) and Rev-erb regulate the expression of 5Bmal1. The level of NAD+ can affect the activity of Silent Information Regulator 1 (SIRT1) and deacetylate factor 1α (PGC-1α) protein, which leads to the co-activation of PGC-1α-mediated Bmal1 expression and ROR. From the perspective of biomolecules,

deacetylated per2 is degraded in the form of β-transduction repeat compatible protein (β-TrCP), the binding ability of deacetylated Bmal1 and E-box is reduced, and the rhythm regulator PPAR1 is regulated by unknown factors. The activity of PPAR family members is usually regulated by ligands (such as fatty acids and their derivatives) and cofactors, including heterodimer formation with RXR (retinal X receptor). CLOCK is regulated by ribosylation when the AMP/ATP ratio is higher than 30%, liver kinase B (LKB) phosphorylates AMP-activated protein kinase (AMPK), and phosphorylated AMPK phosphorylates cry1 and targets the degradation of F-box leucine-rich repeat protein. According to the whole gene transcription analysis, about 15% of the genes show rhythmic oscillations, transcription factors that have been proven to regulate the output of the biological clock mainly include: Dbp, E4BP4, transcription enhancer factor (TEF), hepatic leukemia factor (HLF), KLF10 and KLF15, etc. CLOCK protein itself is also regulated by a variety of post-translational modifications such as acetylation and phosphorylation, which not only regulate its activity, but also affect the stability of its complex with BMAL1 and the transcriptional efficiency of downstream genes.

Table 6. The corresponding recognition sequence in the promoter is combined to regulate.

Physiological	Redox	AMP/ATP ratio	Bile acid receptor	Glucose metabolism	fat metabolism	Receptors
liver	1.11	0.73	1.93	0.29	0.32	1.49
Receptors	2.39	1.34	3.58	1.27	2.56	3.39
metabolism	4.78	3.52	3.78	2.21	2.31	2.92
PGC-1α	5.42	5.74	2.47	2.55	1.03	1.62
Rhythm	3.96	2.28	2.77	2.01	3.57	4.5
SIRT1	6.92	3.67	2.35	2.62	2.73	2.82

As shown in **Figure 5**, in mammals, there are multiple clock systems in the body's circadian rhythm. The synchronization adjustment of these clocks depends on the SCN. The secretion and normal movement of the body play a very important role. It is generally believed that the circadian rhythm system affects the body's metabolism changes through the system instructions issued by the SCN or some rhythm oscillators in the surrounding tissues.

As shown in **Table 7**, the nuclear orphan receptor Rev-erba can specifically inhibit the expression of Bmal1, based on the tetracycline dependence of Rev-erba to construct a model without liver biological clock function. Analysis of the whole genome spectrum of the liver showed that of 350 genes with stable circadian rhythm accumulation, less than 10% of them showed rhythm accumulation with high amplitude. This indicates that these rhythm genes are dependent on the local oscillator in the liver cells, rather than on the signal of the SCN system. The remaining single-oscillation mRNA transcripts continue to oscillate daily, with no obvious fluctuations in phase and amplitude. These genes may be regulated by the SCN region to transmit rhythmic signals to the core clock-controlled genes of hepatocytes and participate in the rhythmic metabolism of the liver. This indicates that metabolic changes caused by

changes in the eating rhythm will affect the circadian rhythm of the biological clock. The above shows that metabolic changes will affect the changes of key rhythm genes and regulatory factors in the biological rhythm system. This change is processed by the core master regulator of the biological clock SCN and fed back to the body's metabolic receptors to adjust the corresponding changes. In addition, in the peripheral biological system, the seismic oscillator can independently regulate the local biological metabolic rhythm.

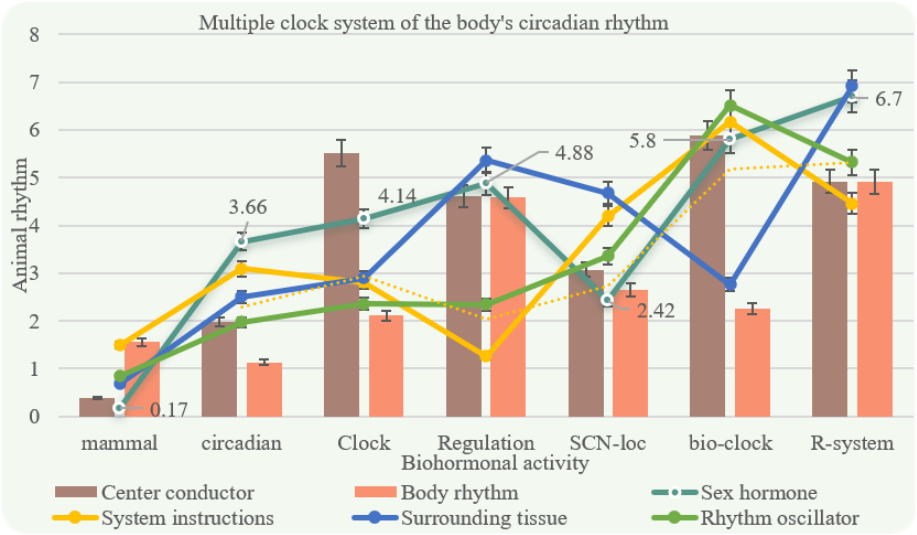

Figure 5. Multiple clock systems of the body's circadian rhythm.

Table 7. Nuclear orphan receptor Rev-erba can specifically inhibit the expression of Bmal1.

Item	Center conductor	Body rhythm	System instructions	Surrounding tissue
mammal	0.39	1.56	1.49	0.68
circadian	1.98	1.13	3.09	2.51
Clock	5.51	2.11	2.81	2.9
Regulation	4.62	4.58	1.26	5.36
SCN-loc	3.07	2.65	4.19	4.68
bio-clock	5.88	2.25	6.16	2.76
R-system	4.92	4.91	4.46	6.91

As shown in **Figure 6**, these regulatory factors and regulatory elements are widely present in liver and body adipose tissue, and are regulated by the biological clock system and exhibit rhythmic expression. Among them, Rev-erb and ROR are the core biological clock components that directly participate in the regulation of lipid metabolism in the body. Others such as Per2, Cry, liver X receptor (LXR) and farnesol X receptor (FXR) in this process through stimulation or inhibiting the production of molecular ligands helps. It can not only regulate lipoprotein metabolism and the differentiation of fat cells to maintain the steady state of lipid metabolism, but also inhibit the expression of apolipoprotein C to reduce the level of ultra-low density lipoprotein in the blood. Rev-erbα regulates lipid synthesis by mediating key

regulatory elements in the process of lipid synthesis, including SREBP and its target genes fatty acid synthase, ACCα, etc.

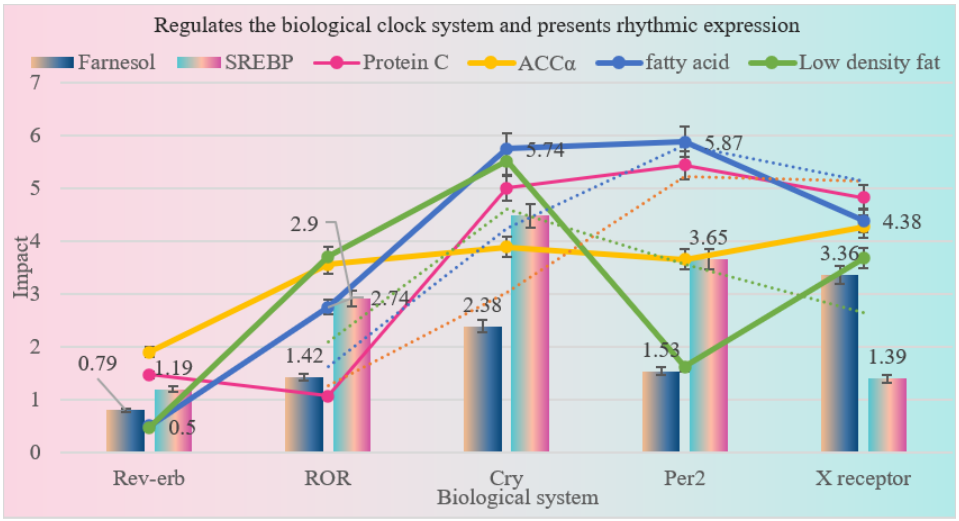

Figure 6. Regulates the biological clock system and presents rhythmic expression.

As shown in **Table 8**, in Bmal knockout white fat, the rhythmic loss of ATGL and HSL expression indicates that lipid hydrolysis is controlled by the core rhythm genes of the biological clock system. These studies indicate that lipid synthesis and metabolism are regulated by the core rhythm Bmal1, and are mainly completed by the transcription and regulation of a series of clock-controlled genes mediated by Rev-erb, PPAR and ROR. However, the specific molecular mechanism of the lipid metabolism rhythm, the transcription factors and the regulatory elements under the control of the biological clock system, and the interactions between them are still relatively vague, and a large number of molecular biology experiments are needed to prove it.

Table 8. Lipid synthesis rhythm and metabolic rhythm are affected by core rhythm.

Item	Farnesol	Protein C	SREBP	ACCα	fatty acid	Low density fat
Rev-erb	0.79	1.46	1.19	1.89	0.5	0.47
ROR	1.42	1.06	2.9	3.55	2.74	3.7
Cry	2.38	5	4.47	3.88	5.74	5.51
Per2	1.53	5.43	3.65	3.65	5.87	1.61
X receptor	3.36	4.82	1.39	4.26	4.38	3.67

4.3. Regulation of circadian rhythms on the movement system at the biomolecular level

As shown in **Figure 7**, the biological clock regulates the body's energy metabolism through the regulation of key energy metabolism steps and participants. The realization of this regulation depends on the combination of rate-limiting enzymes, nuclear receptors, nutrient sensors and other proteins and the biological clock. Studies have found that the activation of AMPK can lead to an increase in NAD+ levels. It can be inferred that the expression of AMPK and SIRT1 has an associated mechanism, and the process of body energy metabolism is regulated by the biological clock system.

Studies have shown that the biological clock system and clock-control genes can finely regulate the metabolism of nutrients in the body, and changes in the circadian rhythm have a certain influence on the metabolism of the digestive system of the body.

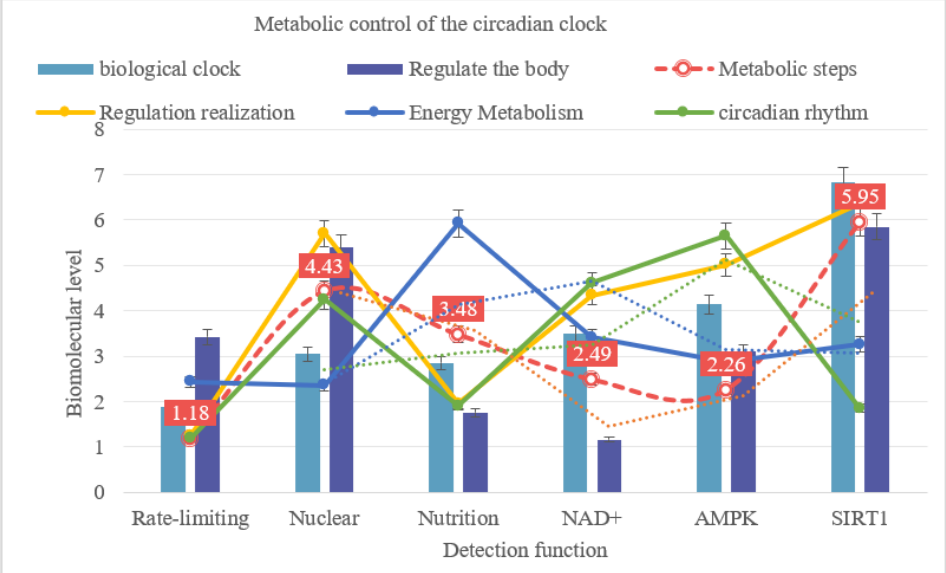

Figure 7. Metabolic control of the circadian clock.

As shown in **Figure 8**, circadian rhythm changes have a certain impact on bioenergy availability and drug effects. P glycoprotein (P-gp) is a transport protein and is encoded by the multi-drug resistance (Mdr) gene. Research found that the expression of Mdr1amRNA and P-gp protein in the mouse intestine fluctuates day and night, and the expression of P-gp contributes to the dose-dependent absorption of digoxin. Mechanism studies have shown that the expression of P-gp is regulated by Bmal1 through the circadian clock system output genes HLF and E4BP4. In summary, the circadian clock system regulates the synthesis of rhythmic functional proteins such as Dbp, glucose transporter, PEPT1, etc. through the associated expression of AMPK and SIRT1, thereby regulating digestive system energy metabolism and oral drug absorption.

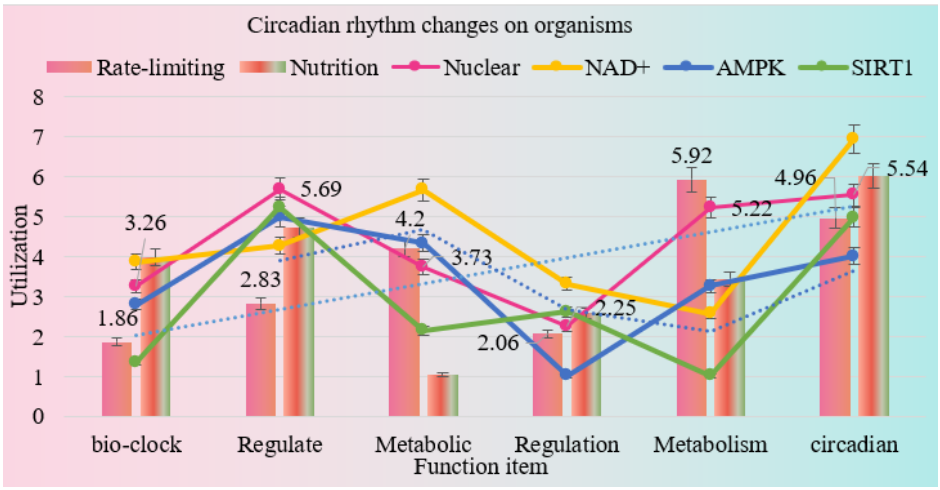

Figure 8. Circadian rhythm changes to bioavailability.

As shown in **Figure 9**, the animal's urine pH, urine protein content, glomerular filtration rate, and renal plasma flow all present circadian rhythms. The rhythmic changes in the above physiological functions indicate that the renal function is regulated by the biological clock system. The dose-dependent nephrotoxicity of cisplatin in humans and animals may depend on the diurnal expression of Slc22a2 and OCT2 in the kidney. The nuclear receptor PPARα controlled by the night rhythm regulates the transcription of 12Slc22a2, thereby realizing the regulation of the circadian rhythm. In samples with PARbZip deficiency, the kidney expression of Mrp4 and Slc22a7 was significantly reduced. Therefore, the regulation of the circadian rhythm in the renal system may regulate the transcription of Slc22a2 by the nuclear receptor PPARα through the E-box and D-box circuits, and the transcription and synthesis of other functional proteins such as Slc9a3 and Slc22a7 to regulate the metabolic rhythm of the kidney.

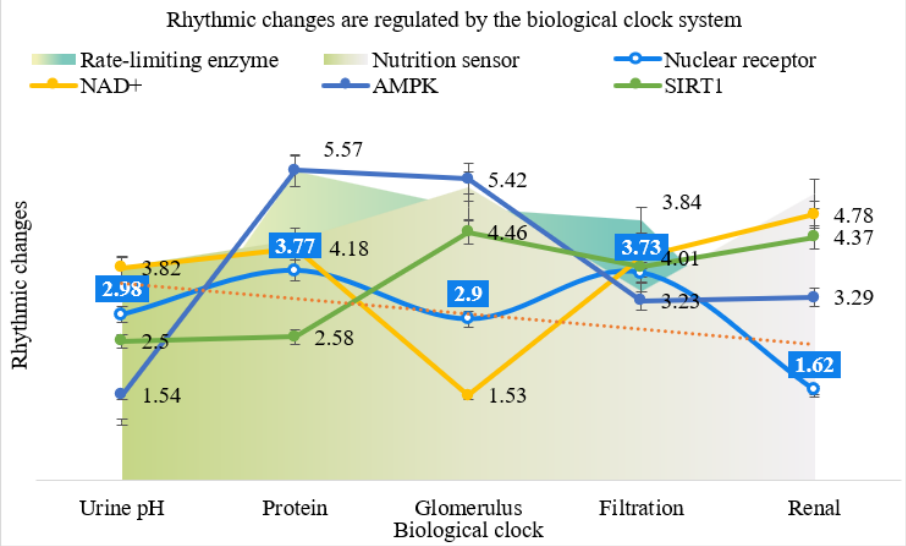

Figure 9. Rhythmic changes are regulated by the biological clock system.

In summary, the experimental data reveal the important role of circadian rhythm in energy metabolism, drug absorption and kidney function. The influence on drug absorption and metabolism provides an important theoretical basis and practical guidance for personalized drug design and treatment.

5. Conclusions

Conjugated bile acid reached its peak after food intake, followed by increased fibroblast growth factor (FGF19) and decreased bile acid secretion. However, no correlation with FGF19 was observed in non-conjugated bile acids. This phenomenon indicates that FXR plays a vital role in the synthesis and transportation of bile acids, and high-fat diet will significantly cause the expression level of FXRmRNA, indicating that there may be a negative feedback regulation mechanism between FXR and bile acids. The rhythmic metabolism of bile acids may be regulated in two ways. On the one hand, FXRmRNA negatively regulates the synthesis of bile acids by regulating the expression of FGF19. On the other hand, SHPmRNA negatively

regulates the expression of Cyp7a1 through the FXR/SHP pathway to regulate the metabolic rhythm of bile acids.

From the perspective of biological rhythms, on the basis of lowering blood pressure, anti-platelet, and regulating lipids, changing the medication time can significantly reduce the plasma hs-CRP level, increase the plasma adiponectin level, and significantly improve the blood pressure circadian rhythm ratio in sports injury patients. Taking it before going to bed makes the night-time drug concentration at a high level, thereby more effectively reducing the night-time blood pressure value, which is manifested by the decrease of hs-CRP and the increase of APN level. The lower the hs-CRP and the higher the APN increase, the better the prognosis of patients with sports injuries, and the two are negatively correlated. All in all, according to the relationship between circadian rhythm and sports injury, optimize the training plan and medication time, adjust the intensity and time of training, avoid high-intensity training when the body is least active or the least resilient, and use the "peak time" to train key skills and physical fitness tests. Make sure athletes get enough sleep, optimize sleep quality, and adjust training and competition times to fit natural sleep patterns. By implementing these specific strategies, sports performance can be improved more effectively and the overall health of athletes can be promoted.

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