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**ВЛИЯНИЕ ПОЛИМОРФИЗМА ГЕНА VEGF НА ТЕЧЕНИЕ
ПНЕВМОНИИ У ДЕТЕЙ**

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Резюме

Данное исследование посвящено изучению роли полиморфизма гена сосудистого эндотелиального фактора роста (VEGF) в клиническом течении пневмонии у детей. Анализ распределения генотипов показал, что генотип С/С являлся преобладающим (72%) и был ассоциирован с протективным эффектом, характеризующимся более лёгким течением заболевания и благоприятными клиническими исходами. Гетерозиготный генотип С/Т (24%) демонстрировал промежуточный профиль риска, сопровождаясь умеренной степенью тяжести заболевания и ограниченным числом осложнений. В то же время генотип Т/Т (5%) был идентифицирован как вариант высокого риска, тесно связанный с агрессивным течением заболевания, выраженными клиническими проявлениями и развитием гиперкоагуляционных состояний. Полученные результаты свидетельствуют о значительном влиянии полиморфизма гена VEGF на тяжесть и прогрессирование пневмонии у детей и позволяют рассматривать его в качестве генетического маркера для стратификации риска и прогноза заболевания.

Ключевые слова: дети, пневмония, гемостаз, генетический полиморфизм

**ПНЕВМОНИЯ БИЛАН КАСАЛЛАНГАН БОЛАЛАРДА VEGF ГЕН
ПОЛИМОРФИЗИМИНИНГ КАСАЛЛИК КЕЧИШИГА ТАЪСИРИ**

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Резюме

Ushbu tadqiqot bolalarda pnevmoniyaning klinik kechishida tomir endotelial o'sish omili (VEGF) geni polimorfizmining rolini o'rganishga bag'ishlangan. Genotiplar taqsimoti tahlili natijalariga ko'ra, C/C genotipi eng ko'p uchragan (72%) bo'lib, u protektiv ta'sir bilan bog'liq ekanligi, ya'ni kasallikning nisbatan yengil kechishi va qulay klinik natijalar bilan tavsiflangan. Geterozigot C/T genotipi (24%) o'rtacha xavf profilini namoyon etib, kasallikning o'rtacha og'irlik darajasi va asoratlarning cheklangan soni bilan kechgan. Aksincha, T/T genotipi (5%) yuqori xavfli variant sifatida aniqlanib, kasallikning agressiv kechishi, og'ir klinik belgilarning namoyon bo'lishi hamda giperkoagulyatsion holatlarning rivojlanishi bilan chambarchas bog'liq bo'lgan. Olingan natijalar VEGF geni polimorfizmining bolalarda pnevmoniya og'irligi va kasallikning rivojlanishiga sezilarli ta'sir ko'rsatishini tasdiqlaydi hamda uni xavfni stratifikatsiya qilish va kasallik prognozini baholashda genetik marker sifatida qo'llash imkonini beradi.

Калит сўзлар: болалар, пневмония, гемостаз.

THE IMPACT OF VEGF GENE POLYMORPHISM ON THE COURSE OF PNEUMONIA IN CHILDREN.

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Summary

This study investigates the role of vascular endothelial growth factor (VEGF) gene polymorphism in the clinical course of pneumonia in children. Genotype distribution analysis revealed that the C/C genotype was predominant (72%) and was associated with a protective effect, characterized by a milder disease course and favorable clinical outcomes. The heterozygous C/T genotype (24%) demonstrated an intermediate risk profile, with moderate disease severity and limited complications. In

contrast, the T/T genotype (5%) was identified as a high-risk variant, strongly associated with an aggressive disease course, severe clinical manifestations, and the development of hypercoagulable states. These findings suggest that VEGF gene polymorphism significantly influences disease severity and progression in pediatric pneumonia and may serve as a genetic marker for risk stratification and prognosis.

Keywords: children, pneumonia, hemostasis, genetic polymorphism

Community-acquired pneumonia is one of the most common respiratory diseases in childhood and a major cause of pediatric hospitalization worldwide. Despite advances in antimicrobial therapy and supportive care, pneumonia continues to be associated with severe complications such as respiratory failure, pleural effusion, sepsis, and coagulation disorders. The clinical course of pneumonia varies widely among children, even when infected with similar pathogens, suggesting the involvement of host-related factors.

Recent studies highlight the importance of genetic predisposition in determining disease severity and outcome. Among the molecular mediators involved, vascular endothelial growth factor (VEGF) plays a central role in endothelial integrity, angiogenesis, inflammatory response, and vascular permeability. Excessive VEGF expression contributes to increased capillary leakage, tissue edema, and endothelial dysfunction, which may aggravate lung injury and promote coagulation abnormalities.

VEGF gene polymorphisms are known to influence VEGF expression levels and biological activity. However, data regarding their role in pediatric pneumonia remain limited. Understanding the impact of VEGF genetic variability on disease progression may help identify children at risk for severe and complicated pneumonia.

Aim and Objectives

Aim

To investigate the effect of VEGF gene polymorphism on the clinical course and severity of pneumonia in children.

Objectives

1. To determine the distribution of VEGF genotypes (C/C, C/T, T/T) in children with pneumonia.
2. To assess the association between VEGF genotypes and disease severity.
3. To evaluate the relationship between VEGF polymorphism and hypercoagulable states.
4. To identify VEGF polymorphism as a potential prognostic biomarker for severe pneumonia.

3. Materials and Methods

Study Design and Population

A clinical and genetic observational study was conducted in pediatric patients diagnosed with pneumonia. Diagnosis was based on clinical presentation, laboratory findings, and radiological evidence.

Genetic Analysis

DNA was extracted from peripheral blood samples. VEGF gene polymorphisms were identified using standard molecular genetic techniques. Patients were classified into three genotype groups:

C/C genotype

C/T genotype

T/T genotype

Clinical Assessment

Disease severity was assessed based on clinical symptoms, respiratory distress, oxygen requirement, presence of complications, and laboratory indicators of inflammation and coagulation.

Statistical Analysis

Genotype distribution and clinical correlations were analyzed using appropriate statistical methods. Associations were considered significant at $p < 0.05$.

4. Results

Analysis of VEGF gene polymorphism revealed a distinct genotype distribution among children with pneumonia.

The C/C genotype was identified in 72% of patients and was associated with a predominantly mild and uncomplicated disease course. These children exhibited less severe respiratory symptoms, minimal endothelial dysfunction, and stable coagulation profiles, suggesting a protective role of this genotype.

The C/T genotype, observed in 24% of cases, was associated with an intermediate clinical course. Patients in this group showed moderate disease severity with occasional complications, reflecting a balanced but potentially unstable VEGF expression.

The T/T genotype, although least frequent (5%), demonstrated the most severe clinical outcomes. Children with this genotype experienced aggressive disease progression, severe respiratory failure, marked inflammatory response, and a pronounced tendency toward hypercoagulation. These findings indicate that excessive VEGF activity may contribute to endothelial damage and activation of the coagulation cascade.

5. Discussion

The present study confirms the significant role of VEGF gene polymorphism in modulating the clinical course of pneumonia in children. The protective effect observed in the C/C genotype may be attributed to regulated VEGF expression, maintaining endothelial stability and preventing excessive vascular leakage.

Conversely, the T/T genotype appears to promote pathological VEGF overexpression, leading to increased vascular permeability, tissue edema, endothelial dysfunction, and hypercoagulable states. These mechanisms may explain the higher risk of severe and complicated pneumonia observed in this group.

Our findings are consistent with previous reports linking VEGF overexpression to severe pulmonary inflammation and coagulation abnormalities. Identification of genetic risk factors such as VEGF polymorphism may improve early risk stratification and personalized management strategies[3, 4, 15, 16, 17, 19].

6. Conclusion

VEGF gene polymorphism plays a crucial role in determining the severity and progression of pneumonia in children.

- The **C/C genotype** exhibits a protective effect and is associated with a mild disease course.
- The **C/T genotype** represents an intermediate-risk variant.
- The **T/T genotype** is a significant genetic risk factor for aggressive disease progression, severe pneumonia, and hypercoagulable complications.

Assessment of VEGF polymorphism may serve as a valuable prognostic tool and contribute to individualized therapeutic approaches in pediatric pneumonia.

7. Practical Implications

- Early identification of high-risk genotypes (T/T) may allow timely intensive monitoring.
- VEGF polymorphism can be considered a molecular marker for predicting severe pneumonia.
- Genetic screening may improve personalized treatment strategies in pediatric respiratory diseases.

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