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Contents

Thrice Monthly Volume 10 Number 25 September 6, 2022

MINIREVIEWS

8808	Ear, nose, and throat manifestations of COVID-19 and its vaccines				
	Al-Ani RM				

8816 Potential influences of religiosity and religious coping strategies on people with diabetes Onyishi CN, Eseadi C, Ilechukwu LC, Okoro KN, Okolie CN, Egbule E, Asogwa E

ORIGINAL ARTICLE

Case Control Study

8827 Effectiveness of six-step complex decongestive therapy for treating upper limb lymphedema after breast cancer surgery

Zhang HZ, Zhong QL, Zhang HT, Luo QH, Tang HL, Zhang LJ

Retrospective Study

8837 Hospital admissions from alcohol-related acute pancreatitis during the COVID-19 pandemic: A singlecentre study

Mak WK, Di Mauro D, Pearce E, Karran L, Myintmo A, Duckworth J, Orabi A, Lane R, Holloway S, Manzelli A, Mossadegh S

Indocyanine green plasma clearance rate and 99mTc-galactosyl human serum albumin single-photon 8844 emission computed tomography evaluated preoperative remnant liver

Iwaki K, Kaihara S, Kita R, Kitamura K, Hashida H, Uryuhara K

Arthroscopy with subscapularis upper one-third tenodesis for treatment of recurrent anterior shoulder 8854 instability independent of glenoid bone loss

An BJ, Wang FL, Wang YT, Zhao Z, Wang MX, Xing GY

Evaluation of the prognostic nutritional index for the prognosis of Chinese patients with high/extremely 8863 high-risk prostate cancer after radical prostatectomy

Yang F, Pan M, Nie J, Xiao F, Zhang Y

Observational Study

8872 Chlorine poisoning caused by improper mixing of household disinfectants during the COVID-19 pandemic: Case series

Lin GD, Wu JY, Peng XB, Lu XX, Liu ZY, Pan ZG, Qiu ZW, Dong JG

Mental health of the Slovak population during COVID-19 pandemic: A cross-sectional survey 8880 Kralova M, Brazinova A, Sivcova V, Izakova L



Contents

Thrice Monthly Volume 10 Number 25 September 6, 2022

Prospective Study

8893 Arthroscopic anatomical reconstruction of lateral collateral ligaments with ligament advanced reinforcement system artificial ligament for chronic ankle instability

Wang Y, Zhu JX

SYSTEMATIC REVIEWS

8906 How to select the quantitative magnetic resonance technique for subjects with fatty liver: A systematic review

Li YW, Jiao Y, Chen N, Gao Q, Chen YK, Zhang YF, Wen QP, Zhang ZM

8922 Lymphocytic choriomeningitis virus: An under-recognized congenital teratogen Ferenc T, Vujica M, Mrzljak A, Vilibic-Cavlek T

CASE REPORT

8932	Alagille syndrome associated with total anomalous pulmonary venous connection and severe xanthomas: A case report			
	Zeng HS, Zhang ZH, Hu Y, Zheng GL, Wang J, Zhang JW, Guo YX			
8939	Colo-colonic intussusception with post-polypectomy electrocoagulation syndrome: A case report			
	Moon JY, Lee MR, Yim SK, Ha GW			

8945 Portal vein gas combined with pneumatosis intestinalis and emphysematous cystitis: A case report and literature review

Hu SF. Liu HB. Hao YY

8954 Quadricuspid aortic valve and right ventricular type of myocardial bridging in an asymptomatic middleaged woman: A case report

Sopek Merkaš I, Lakušić N, Paar MH

8962 Treatment of gastric carcinoma with lymphoid stroma by immunotherapy: A case report Cui YJ, Ren YY, Zhang HZ

- 8968 Gallstone associated celiac trunk thromboembolisms complicated with splenic infarction: A case report Wu CY, Su CC, Huang HH, Wang YT, Wang CC
- 8974 Extracorporeal membrane oxygenation for lung cancer-related life-threatening hypoxia: A case report Yoo SS, Lee SY, Choi SH
- 8980 Multi-disciplinary treatment of maxillofacial skeletal deformities by orthognathic surgery combined with periodontal phenotype modification: A case report Liu JY, Li GF, Tang Y, Yan FH, Tan BC

8990 X-linked recessive Kallmann syndrome: A case report Zhang P, Fu JY

8998 Delayed complications of intradural cement leakage after percutaneous vertebroplasty: A case report Ma QH, Liu GP, Sun Q, Li JG



.	World Journal of Clinical Cases
Conten	Thrice Monthly Volume 10 Number 25 September 6, 2022
9004	Coexistent Kaposi sarcoma and post-transplant lymphoproliferative disorder in the same lymph nodes after pediatric liver transplantation: A case report
	Zhang SH, Chen GY, Zhu ZJ, Wei L, Liu Y, Liu JY
9012	Misdiagnosis of pancreatic metastasis from renal cell carcinoma: A case report
	Liang XK, Li LJ, He YM, Xu ZF
9020	Discoid medial meniscus of both knees: A case report
	Zheng ZR, Ma H, Yang F, Yuan L, Wang GD, Zhao XW, Ma LF
9028	Simultaneous laparoscopic and arthroscopic excision of a huge juxta-articular ganglionic cyst compressing the sciatic nerve: A case report
	Choi WK, Oh JS, Yoon SJ
9036	One-stage revision arthroplasty in a patient with ochronotic arthropathy accompanied by joint infection: A case report
	Wang XC, Zhang XM, Cai WL, Li Z, Ma C, Liu YH, He QL, Yan TS, Cao XW
9044	Bladder paraganglioma after kidney transplantation: A case report
	Wang L, Zhang YN, Chen GY
9050	Total spinal anesthesia caused by lidocaine during unilateral percutaneous vertebroplasty performed under local anesthesia: A case report
	Wang YF, Bian ZY, Li XX, Hu YX, Jiang L
9057	Ruptured splenic artery aneurysms in pregnancy and usefulness of endovascular treatment in selective patients: A case report and review of literature
	Lee SH, Yang S, Park I, Im YC, Kim GY
9064	Gastrointestinal metastasis secondary to invasive lobular carcinoma of the breast: A case report
	Li LX, Zhang D, Ma F
9071	Post-bulbar duodenal ulcer with anterior perforation with kissing ulcer and duodenocaval fistula: A case report and review of literature
	Alzerwi N
9078	Modified orthodontic treatment of substitution of canines by first premolars: A case report
	Li FF, Li M, Li M, Yang X
9087	Renal cell carcinoma presented with a rare case of icteric Stauffer syndrome: A case report
	Popov DR, Antonov KA, Atanasova EG, Pentchev CP, Milatchkov LM, Petkova MD, Neykov KG, Nikolov RK
9096	Successful resection of a huge retroperitoneal venous hemangioma: A case report
	Qin Y, Qiao P, Guan X, Zeng S, Hu XP, Wang B
9104	Malignant transformation of biliary adenofibroma combined with benign lymphadenopathy mimicking advanced liver carcinoma: A case report
	Wang SC, Chen YY, Cheng F, Wang HY, Wu FS, Teng LS



.	World Journal of Clinical Cases
Conten	Thrice Monthly Volume 10 Number 25 September 6, 2022
9112	Congenital hepatic cyst: Eleven case reports
	Du CX, Lu CG, Li W, Tang WB
9121	Endovascular treatment of a ruptured pseudoaneurysm of the internal carotid artery in a patient with nasopharyngeal cancer: A case report
	Park JS, Jang HG
9127	Varicella-zoster virus meningitis after spinal anesthesia: A case report
	Lee YW, Yoo B, Lim YH
9132	Chondrosarcoma of the toe: A case report and literature review
	Zhou LB, Zhang HC, Dong ZG, Wang CC
9142	Tamsulosin-induced life-threatening hypotension in a patient with spinal cord injury: A case report
	Lee JY, Lee HS, Park SB, Lee KH
9148	CCNO mutation as a cause of primary ciliary dyskinesia: A case report
	Zhang YY, Lou Y, Yan H, Tang H
9156	Repeated bacteremia and hepatic cyst infection lasting 3 years following pancreatoduodenectomy: A case report
	Zhang K, Zhang HL, Guo JQ, Tu CY, Lv XL, Zhu JD
9162	Idiopathic cholesterol crystal embolism with atheroembolic renal disease and blue toes syndrome: A case report
	Cheng DJ, Li L, Zheng XY, Tang SF
9168	Systemic lupus erythematosus with visceral varicella: A case report
	Zhao J, Tian M
	LETTER TO THE EDITOR

Imaging of fibroadenoma: Be careful with imaging follow-up 9176 Ece B, Aydın S



Contents

Thrice Monthly Volume 10 Number 25 September 6, 2022

ABOUT COVER

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The primary aim of World Journal of Clinical Cases (WJCC, World J Clin Cases) is to provide scholars and readers from various fields of clinical medicine with a platform to publish high-quality clinical research articles and communicate their research findings online.

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CASE REPORT

Alagille syndrome associated with total anomalous pulmonary venous connection and severe xanthomas: A case report

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Abstract

BACKGROUND

Alagille syndrome (ALGS) is an autosomal dominant genetic disorder caused by mutations in the JAG1 or NOTCH2 gene. It is characterized by decreased intrahepatic bile ducts associated with a variety of abnormalities in many other organ systems, such as the cardiovascular, skeletal, and urinary systems.

CASE SUMMARY

We report a rare case of ALGS. A 1-month-old male infant presented with sustained jaundice and had a rare congenital heart disease: Total anomalous pulmonary venous connection (TAPVC). Sustained jaundice, particularly with cardiac murmur, caught our attention. Laboratory tests revealed elevated levels of alanine aminotransferase, aspartate aminotransferase, gamma-glutamyl transpeptidase, total bilirubin, and total bile acids, indicating serious intrahepatic cholestasis. Imaging confirmed the presence of butterfly vertebra at the seventh thoracic vertebra. This suggested ALGS, which was confirmed by genetic testing with a c.3197dupC mutation in the JAG1 gene. Ursodiol was administered immediately after confirmation of the diagnosis, and cardiac surgery was performed when the patient was 1.5 month old. He recovered well after treatment and was discharged at the age of 3 mo. At the age of two years, the patient returned to our clinic because multiple cutaneous nodules with xanthomas appeared, and their size and number increased over time.

CONCLUSION

We report a unique case of ALGS associated with TAPVC and severe xanthomas. This study has enriched the clinical manifestations of ALGS and emphasized the association between JAG1 gene and TAPVC.



Key Words: Alagille syndrome; JAG1 gene; Notch signaling pathway; Total anomalous pulmonary venous connection; Severe xanthomas; Case report

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Core Tip: Total anomalous pulmonary venous connection (TAPVC) and severe xanthomas are rarely reported in Alagille syndrome (ALGS) patients. These two symptoms have never appeared in the same patient at the same time. Here, we report a unique case of ALGS associated with TAPVC and severe xanthomas. This study has enriched the clinical manifestations of ALGS and emphasized the association between JAG1 gene and TAPVC.

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INTRODUCTION

Alagille syndrome (ALGS, OMIM 118450) is a multiple system disorder that affects the face, eyes, liver, heart, bones and other organs[1-3]. ALGS is due to biallelic mutations in the Notch signaling pathway ligand JAG1 (JAGGED1) in 94% of patients and Notch receptors (NOTCH2) in 1%-2% of patients[4-6]. ALGS can be clinically diagnosed if three of the following features are present: Cardiac murmur, posterior embryotoxon (eye abnormalities), butterfly-like vertebrae, renal abnormalities, and characteristic faces in the presence of bile duct paucity on liver biopsy[7,8]; or at least 4 of the 5 major features if liver biopsy is not performed [9,10]. In some atypical cases, molecular confirmation of ALGS diagnosis is valuable^[7].

A high percentage (97%) of ALGS patients have cardiac murmur[11,12], including branch pulmonary artery stenosis, peripheral pulmonary stenosis, tetralogy of Fallot (TOF), valvar pulmonic stenosis, atrial septal defect, ventricular septal defect, coarctation of the aorta, and similar issues[13]. To our knowledge, the association of total anomalous pulmonary venous connection (TAPVC) and ALGS has never been reported in any article, but it was reported in a conference by Sanchez-Lara et al[14].

CASE PRESENTATION

Chief complaints

A 20-day-old male neonate with unknown cause of jaundice since birth and TAPVC was referred to our hospital.

History of present illness

The patient had jaundice and TAPVC since birth, without a history of other ailments.

History of past illness

There was no history of past illness.

Personal and family history

There was no family history of other genetic diseases. The father showed characteristic facial features: A prominent forehead, deep-set eves with mild hypertelorism, pointed chin, and saddle-shaped nose with a bulbous tip.

Physical examination

Physical examination revealed an infant weight of 3.2 kg. Jaundiced skin and sclera were observed along with a triangular appearance. The patient showed the same characteristic facial features as his father (Figure 1). He had abnormalities in both eyes (Figure 2) (posterior embryotoxon). No positive signs were found in the lungs. Abnormal sounds and murmurs were audible upon heart auscultation. The liver was palpable with a soft edge 4.0 cm below the right costal margin.





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Figure 1 The patient shows characteristic faces of Alagille syndrome: Prominent forehead, deep-set eyes, mild hypertelorism, pointed chin, and saddle shape nose with a bulbous tip. A: Front image; B: Side image.



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Figure 2 Posterior embryotoxon. A: Posterior embryotoxon in left eye; B: Posterior embryotoxon in right eye. L: Left; R: Right.

Laboratory examinations

Biochemical analysis showed increased levels of serum gamma-glutamyl transpeptidase, total bilirubin (TBil), direct bilirubin (DBil), and total bile acids (TBAs), indicating cholestasis (Table 1).

Imaging examinations

X-ray didn't discover obvious skeletal deformities (Figure 3A), while Chest computed tomography (CT) angiography clearly shows that butterfly vertebra at the seventh thoracic vertebrae (Figure 3B). CT angiography showed that four pulmonary veins (PVs) joined together and drained into the vertical vein (VV). The VV flowed into the dilated left innominate vein (LIV), then into the superior vena cava (SVC), and finally into the right atrium (RA) (Figure 4).

Further diagnostic work-up

Based on these findings, ALGS was suspected and confirmed by genetic testing. A heterozygous variant (c.3197dupC) in the *JAG1* gene was identified (Figure 5). This is a frame shift mutation, and it has been reported previously[10]. It is expected that the protein products encoded by this gene will be cut off prematurely, which is considered pathogenic.

FINAL DIAGNOSIS

Based on the clinical, imaging, and genetic findings, the final diagnosis was ALGS.

TREATMENT

After a clear diagnosis of ALGS, the patient began ursodiol treatment, which he has been tolerating very well. The patient underwent surgical correction of his cardiac murmur at the age of 1.5 mo. He responded well to treatment and was discharged 1.5 mo later.



Table 1 Biochemical alterations over time of the patient when he was in hospital										
Biochemical indices	February 26, 2017	March 5, 2017	March 11, 2017	March 20, 2017	March 27, 2017	April 3, 2017	April 9, 2017			
ALT (5-40 U/L)	107	198	266	527	256	324	444			
AST (5-40 U/L)	221	382	457	620	233	378	525			
GGT (8-50 U/L)	573		1015	1186	1065	1125	1114			
ALP (20-500 U/L)	440		390	418	200	197	262			
TP (60.0-83.0 g/L)	55.1	65.1	60.6	57.7	45.9	53.3	52.2			
Alb (35.0-55.0 g/L)	36.5	40.2	38.2	38.8	30.4	34.3	35.5			
Tbil (2-19 µmol/L)	242.4	241.4	254.0	469.6	235.4	295.6	294.5			
Dbil (0-6 µmol/L)	165.5	163.6	133.1	245.9	149.0	138.7	124.4			
Ibil (2.56-20.9 µmol/L)	76.9	77.8	120.9	223.7	86.4	156.9	170.1			
TBA (0-10 µmol/L)	100	116.0	74.0	104.0	94.0	113.0	133.3			

ALT: Alanine aminotransferase; AST: Aspartate aminotransferase; GGT: Gamma-glutamyl transferase; ALP: Alkaline phosphatase; TP: Total protein; Alb: Albumin; Tbil: Total bilirubin; Dbil: Direct bilirubin; Ibil: Indirect bilirubin; TBA: Total bile acid.



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Figure 3 X-ray and computed tomography examination. A: X-ray didn't discover obvious skeletal deformities; B: Chest computed tomography clearly showed that butterfly vertebra at the seventh thoracic vertebrae.

OUTCOME AND FOLLOW-UP

The patient did not attend regular follow-up visits at our hospital; thus, no follow-up data were obtained. He returned to our clinic due to severe xanthomas at the age of two years (Figure 6). Laboratory tests revealed increased levels of alanine aminotransferase, 339 U/L; aspartate aminotransferase, 396 U/L; alkaline phosphatase, 998 U/L; Tbil, 138.5 µmol/L; Dbil, 112.3 µmol/L; TBAs, 270.2 umol/L; total cholesterol level, 39.9 mmol/L; and triglyceride levels, 3.79 mmol/L.

DISCUSSION

Protein Jagged-1 encoded by the JAG1 gene is one of the ligands of the Notch receptor[1]. Notch signaling pathway plays an important role in cardiovascular development[15,16]. It coordinates the morphogenesis of the cardiac chambers and valves, and regulates the formation of the cardiac outflow tract[11,12]. Therefore, malformations related to right ventricular outflow tract obstruction (RVOTO), such as stenosis at some level of the pulmonary tree and TOF, have accounted for more than 80% of cardiac murmurs in these patients [13,16]. However, a few patients have other cardiac murmurs, such as valvar pulmonic stenosis, atrial septal defect, ventricular septal defect, patent ductus arteriosus, or double-chambered RV[16].

Our patient was confirmed to have ALGS by clinical examination and genetic testing. His cardiac murmur, TAPVC, has never been reported in any article on ALGS. TAPVC is a rare cardiac murmur in which the PVs fail to return to the RA. The incidence of this rare entity is approximately 7-9 per 100000





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Figure 4 The classic hemodynamic features of total anomalous pulmonary venous connection type I. LIV: Left innominate vein; VV: Vertical vein; SVC: Superior vena cava.



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Figure 5 Gene analysis results of the family. A: Next generation sequencing result of the patient; B-D: Sanger sequencing results of the patient, the mother and the father.



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Figure 6 Xanthomas seen in the surface of hands and feet. A and B: Hands; C: Feet.

live births or 0.7%-1.5% of all congenital heart diseases[17-20]. TAPVC is divided into four major types. Type I: Supracardiac (approximately 55%), as in this case, which is the most common type. The PVs confluence behind the left atrium, then drain into the LIV through the VV, then into the SVC or sometimes into the azygos vein, and finally into the RA[17]. Type II: Intracardiac (approximately 30%),



all PVs drain directly into the RA or through the common trunk of the PVs to the coronary sinus[21,22]. Type III: Infracardiac (approximately 12%), after confluence behind the LA, the PVs pass the diaphragmatic esophageal hiatus through the VV, then flow into the portal vein or its branches[21,22]. Type IV: Mixed (approximately 3%), the PVs enter the RA through multiple channels[21,22].

AG1 gene mutations are mainly associated with the development of RVOTO, which is a spectrum of diseases associated with the pulmonary valve, branches of the pulmonary artery, and the RV[16]. Thus, stenosis at some level of the pulmonary tree and TOF are the most common causes of cardiac murmur in ALGS patients. However, a number of other types of cardiac murmur have been discovered in ALGS patients. This indicates that JAG1 mutations have a multifaceted impact on cardiac development. TAPVC has not been reported in ALGS patients in any article; however, Sanchez-Lara et al[14] reported three ALGS patients at the 2006 ASHG Annual Meeting[14]. Therefore, at least five ALGS patients and three mutation sites have been found to be associated with TAPVC. We suspect that JAG1 is closely associated with TAPVC.

Biliary stricture is the main feature in most ALGS patients, and unusual structures can cause cholestatic liver disease. The dysfunctional liver often leads to an increase in serum total cholesterol and triglycerides. Thus, hypercholesterolemia is attributable to cholestasis and may finally lead to severe xanthomas^[23]. Although some medicines have been reported to improve liver function in ALGS patients, the only way to resolve the problem is liver transplantation.

CONCLUSION

Bile duct paucity is the main characteristic feature in most cases of ALGS. Here, we report a more fatal and rarer feature, TAPVC, which requires surgical correction at an early age. We also report the unusual finding of severe xanthomas. These findings suggest that JAG1 gene may be a pathogenic gene of TAPVC. Further research should be carried out to prove this hypothesis.

FOOTNOTES

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