ORIGINAL ARTICLE

CONTENTS

Genetic, clinical, and laboratory profile of pediatric patients with familial mediterranean fever at Duhok City

Salah Abdulkareem Ibrahim
PEDIATRIC DEPARTMENT, COLLEGE OF MEDICINE, UNIVERSITY OF DUHOK, DUHOK, IRAQ

ABSTRACT

Aim: To describe the clinical picture, laboratory findings, and MEFV mutation profile of FMF children in Duhok, Iraq, and to examine the influence of consanguinity on genotype-phenotype relationships.

Materials and Methods: Cross-sectional study (Jan 2017-Jan 2025) of 92 children ≤16 years meeting Tel-Hashomer criteria and with molecularly confirmed MEFV mutations. Data on demographics, family history, consanguinity, symptoms, attack characteristics, acute-phase reactants, genotype, colchicine response, and complications were collected retrospectively and prospectively. Analyses used SPSS v27 (chi-square, t-test, logistic regression; $P<0.05$.

Results: Mean age 8 y; 65% male; parental consanguinity 79%; positive family history 63%. Fever (100%) and abdominal pain 85% were universal; arthritis 46.7% and growth retardation 61% were notably high. Mean attack labs: WBC 12.9×10^9/L, ESR 50 mm/h, CRP 63 mg/L. MEFV alleles: E148Q 38%, M694V (22%), V726A (15%), M680I (12%). Exon-10 homo/compound heterozygotes (M694V/M680I) were linked to earlier onset, more frequent/longer attacks and higher ESR/CRP (OR≈3, $p<0.001$); simple E148Q carriers had milder disease. Colchicine was effective in 94.6% of patients; no amyloidosis was observed. Consanguinity independently predicted the presence of two pathogenic exon-10 alleles $p=0.02$.

Conclusions: Duhok's pediatric FMF cohort shows classic fever/serositis but higher arthritis, growth failure, and an unusual predominance of the low-penetrance E148Q mutation, likely driven by extreme consanguinity. Exon-10 mutations confer a severe phenotype, while colchicine remains highly effective. Targeted genetic counseling and early mutation-guided management are warranted in this high-consanguinity population.

KEY WORDS: pediatric FMF, MEFV mutations, E148Q, M694V, consanguinity, colchicine response

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INTRODUCTION

A genetic autoinflammatory disease, familial Mediterranean fever (FMF) is most common in populations that originated in the Mediterranean region, including Turks, Armenians, Arabs, and Jews [1-3]. It is caused by mutations in the MEFV gene, which is found on chromosome 16p13.3, and has an autosomal recessive inheritance pattern [4]. This gene encodes the regulatory protein pyrin, which is necessary for controlling innate immunological responses [2]. Mutations primarily impair this regulatory mechanism and cause unchecked inflammatory activity through the overproduction of interleukin-1 beta (IL-1β), which manifests clinically as recurrent fever, serositis (e.g., peritonitis, pleuritis, and pericarditis), arthritis, and erysipelas-like skin eruptions. If AA amyloidosis is not identified and treated promptly, patients may suffer from the potentially lethal consequences of the condition [5-6]. In FMF children, the presentation can be very variable-not just between kids, but also by the particular MEFV mutation carried. The most common MEFV variants-M694V, M680I, V726A, and E148Q-are linked with a variety of clinical presentations that differ by ethnicity [7] of special mention is that M694V is frequently found to be linked with a higher risk of AA amyloidosis, more severe and more frequent flares, and earlier occurrence of the disease in life [8-9]. Awareness of the child's mutation pattern in clinical practice facilitates more personalized monitoring and therapy and predicts the course of the condition. Iraqi Kurdistan Region, and here Duhok province, is increasingly burdened by familial Mediterranean fever (FMF) within families, thus it's a new public health problem. One of the key reasons why children are more likely to inherit autosomal recessive diseases such as FMF is increasing consanguineous (closely related) marriage here. In nearby provinces like Sulaymaniyah, tests have already detected a high percentage of Kurdish children with FMF, most of whom had two pathogenic MEFV mutations-same (homozygous) or different (compound heterozygous) [10]. This suggests that there is urgent need of regionally focused and community-based research- both to map the most frequently occurring mutations, as well as the effect of these mutations on

health of children specifically in local settings. Although MEFV mutations have been observed in Kurdish patients in non-Kurdistan countries, we do not yet have any clear, firm information on the most common MEFV mutations among children of Duhok, their frequency and their most common outcomes. This gap should be addressed to ensure that the affected families receive proper treatment, are diagnosed early enough, and their care is better. One has no need to be a rocket scientist to realize that the genetic makeup of FMF among children in Duhok-it is giving children the best opportunity. Determining the most common MEFV mutations in these individuals may help the medics diagnose the disease earlier and more accurately, allowing it to treat the disease early and most importantly prevent the children of the disease against long-lasting effects that could be deadly such as amyloidosis-a sneak thief disease that destroys the kidneys among other organs over a period [11]. The first-line treatment of most children with FMF remains colchicine, and it is not hard to see why: by taking it daily, it could reduce the crippling flare-ups and prevent the deposition of amyloid to occur at all [12-13]. Children are not all identical, although some mutations have been linked to more difficult or severe disease, and under these circumstances, colchicine may be an inadequate treatment by itself. In these children, newer options of IL-1 inhibitors may become a game-changer. This is why it is significant to make customized treatment depending on genetic information. A one-size-fits-all approach will not work when even the disease is different in each kid. Through the correlation of particular mutations with clinical appearance, we can proceed to a proper kind of individualized care: the right treatment, of the right child, at the right time. To fill these gaps in our knowledge and to offer to children FMF in Duhok even better, a significant requirement is the systematic case study which has been verified by genetic tests. Determining the exact genetic mutations and clinical manifestation that occurs in this population, the researchers will be able to design the diagnostic tests and treatment regimens that will be specific to the local conditions. That is, understanding the appearance and functioning of FMF in the children of Duhok will help the doctors to stop relying on the rules that fit all and head to the realm of customized and personalized medicine, which will offer every child the most effective help possible.

AIM

The purpose of this study is to develop a descriptive image of Familial Mediterranean Fever (FMF) in kids in Duhok, the Iraqi Kurdistan. The researcher is interested in knowing exactly how the disease is manifested in this community, what the most widespread MEFV gene mutations is, how that type of mutation in Marriage between relatives affects the mechanism of the inheritance and how it is manifested in children. In the end, the research findings will positively impact the clinical practice. Which would assist doctors in diagnosing FMF at a young age earlier, make individual treatment choices subject to a particular child mutation, and enhance our question-and-answer skills with regard to preventing severe complications such as amyloidosis. The current study considers a guide for improving the long-term outcomes of the children with FMF in the areas.

MATERIALS AND METHODS

STUDY DESIGN

A descriptive Cross sectional design were used, with a point in time snapshot of FMF for children.

STUDY SETTING AND DURATION

The current study was conducted in the Department of Pediatrics at Heevi Pediatrics Teaching Hospital.. Data were collected from pediatric patients who met the study criteria through clinics and medical facilities in Duhok Governorate. To ensure a comprehensive medical overview, follow-up was conducted from January 2017 to January 2025, providing an eight-year dataset that offered a more accurate basis for characterizing familial Mediterranean fever and analyzing temporal trends.

STUDY POPULATION

INCLUSION CRITERIA

Bestowing to the Tel-Hashomer diagnostic framework, age children 2 and 16 years, diagnosed with FMF clinically and genetically. Tel-Hashomer Criteria Overview [14].

MAJOR CLINICAL CRITERIA

- Generalized peritonitis
- Unilateral pleuritis or pericarditis
- Ankle, knee, or hip monoarticular arthritis
- Just a fever

MINOR CLINICAL CRITERIA

- Frequent episodes of fever
- An erythematous rash that resembles erysipelas, especially on the lower limbs
- A first-degree relative's verified FMF diagnosis

DIAGNOSTIC CLASSIFICATION

– Definitive FMF: one major criterion in conjunction with two minor criteria. or Two major criteria
– Probable FMF: One major with one minor criterion.
– Possible FMF: One major criterion or two minor ones
Only patients who were admitted to hospital wards during the study period or who were actively monitored at outpatient clinics were included.

EXCLUSION CRITERIA

– Patients with unconfirmed FMF diagnoses or insufficient clinical records.
– Cases of periodic fever illness with secondary or alternative causes.

SAMPLE SELECTION

Largest cohort that meets inclusion criteria for diagnosis as verified by molecular (gene-based) testing.

DATA COLLECTION METHODS

Both prospective and retrospective data were collected:
– Examining past medical records is the retrospective component.
– Direct clinical evaluation and structured interviews with patients and/or guardians comprise the prospective component.

COLLECTED VARIABLES INCLUDE

– Age, sex, ethnic origin, and family history of FMF are examples of demographic traits.
– Clinical parameters include age at disease onset, frequency and duration of episodes, and symptomatology (fever, chest and abdominal pain, joint involvement, and dermatologic manifestations).
– Genetic analysis: Genetic analysis revealed specific MEFV mutations, such as M694V, V726A, and others.
– Regarding treatment data: Attention was paid to the use of colchicine, as well as the effectiveness of the treatment, in addition to levels of adherence.
– Complications include Long-term medical conditions or complications related to the disease.

DATA COLLECTION TOOLS

– A meticulously designed and structured questionnaire for future documentation.
– A complete and comprehensive review of the hospital's electronic and paper records regarding data retrieval.

ETHICAL CONSIDERATIONS

The regional ethics committee and the Duhok Directorate of Health were used to get ethical approval. Informed consent of all the minors involved was obtained through their legal guardians. Every process followed the international research ethics protocols and had sufficiently strong measures to ensure confidentiality and privacy of data of the participants.

DATA ANALYSIS STRATEGY

– Analyzed all the data using SPSS (version 27).
– Used descriptive statistics to summarize the main demographic and clinical information.
– Applied statistical analyses (chi-square, t-tests, and logistic regression) to investigate possible correlations between genetic mutations and the degree of the disease or disease complications.
– Finally, we conducted a narrowed-down analysis to determine the impact of certain MEFV gene variants on the clinical symptoms of the patients.

ANTICIPATED LIMITATIONS

– Potential for recall bias in retrospective data.
– Limited access to comprehensive genetic screening, which may restrict full mutation profiling.
– The small sample size may be a constraint to the external validity and the generalization of results.

RESULTS

The age of study sample ranged between 2-16 years, with mean age about 8 years, SD=3.57, and regarding to the sex, researcher found nearly two-thirds 65.2% were males while the female account 34% of the sample (Table 1).

Parental consanguinity was reported in a rather impressive majority 79.3-1 of participants, and this fact is remarkable in light of the genetic etiology of Familial Mediterranean Fever (FMF). Similarly, 63% of them had a positive family history, which supports the hereditary nature of the disorder. In the religious membership, the dominant majority 91.3% was Muslim, with Ezediyan 6.5% and Christian 2.2% communities represented in the minority. The urban-rural ratio of incidence displayed a marginally higher prevalence rate of FMF in urban areas 66.3 compared to rural areas 33.7.

Table 2 shows, all reported cases 100% had a clinical manifestation of fever, which supports the importance of this criterion as a key diagnostic finding in Familial Mediterranean Fever. The second most common symptom was the abdominal pain, which was experienced

Table 1. Demographic characteristic of FMF patient

Variable		Frequency	Percent
Age		2-16 years Mean 8.02 years Std. deviation 3.57	
Gender	Male	60	65.2
	Female	32	34.8
Consanguinity	Yes	73	79.3
	No	19	20.7
Family history	Positive	58	63.0
	Negative	34	37.0
Religions	Muslims	84	91.3
	Christian	2	2.2
	Ezediyans	6	6.5
Residence	Urban	61	66.3
	Rural	31	33.7

Source: Compiled by the authors of this study

Table 2. Clinical characteristics of FMF patient

Variable		Frequency	Percent
Fever	Yes	92	100.0
Abdominal pain	Yes	78	84.8
	No	14	15.2
Arthritis	Yes	43	46.7
	No	49	53.3
Appetite state	Normal	38	41.3
	Decreased	54	58.7
Stunted growth	Yes	56	60.9
	No	36	39.1
Chest pain	Yes	3	3.3
	No	89	96.7
Skin lesion	No	92	100.0
Myalgia	Yes	29	31.5
	No	63	68.5
Headache	Yes	9	9.8
	No	83	90.2

Source: Compiled by the authors of this study

by 84.8% of the group of patients. The presence of arthritis was reported as a joint involvement in close to half of the subjects 46.7% which suggests a frequent extra-abdominal manifestation. Appetite change in the sample under investigation was observed in most of them; 58.7% of the total respondents reported appetite decrease and 41.3% reported normal eating. The other important problem was stunted growth, which was found in over 60% of patients, which is plausibly suggestive of chronic inflammatory conditions and nutritional inadequacies. Less common symptoms included chest pains 3.3%, myalgia 31.5%, and headaches 9.8%. Markedly, there was no patient who had skin lesions, thus suggesting that they are rare in this specific cohort.

Table 3 demonstrate Laboratory investigations refried high rate in inflammatory biomarkers, the average white blood cell (WBC) count was 12.91×10^9/L (SD=3.04) which is agreeable with an inflammatory process. The levels of erythrocyte sedimentation rate (ESR) and C-reactive protein (CRP) were also increased, with a mean of 50.25 mm/hr. (SD-11.57) and 63.31 mg/l (SD-20.11) respectively. These biological markers indicate the inflammatory load of the body in the whole family with Mediterranean fever (FMF).

Table 3. Laboratory characteristics of FMF patient

Value	Total	Minimum	Maximum	Mean	Std. deviation
WBC	92	6.00	22.00	12.9130	3.04058
ESR	92	29.00	70.00	50.2500	11.56883
CRP	92	24.00	112.00	63.3152	20.11392

Source: Compiled by the authors of this study

Table 4. Duration and frequency of FMF attacks per day and month respectively

Duration /hours /day	Mean	Std. deviation	Percent
(2-7) hours/day	3.77	1.46	
	Frequency/month	**No.**	
Frequency of FMF	1 attack/month	66	71.7
	2 attack/month	21	22.8
	3 attack/month	5	5.4

Source: Compiled by the authors of this study

Table 5. Distribution of MEFV gene mutations among FMF patients

Gene mutation	Gene type	Number	Total
Heterozygote	E148Q	18	46(50%)
	M694V	14	
	V726A	10	
	M680I	3	
	A744S	1	
Homozygote	M694V-M694V	6	16(17.4%)
	E148Q-E148Q	3	
	M680I-M680I	2	
	V726A-V726A	2	
	P396S-P396S	2	
	M694I-M694I	1	
Compound heterozygote	E148Q-M680I	4	24(26.1%)
	M680I-V726A	4	
	F4726A-E148Q	3	
	V726A-R761H	3	
	E148Q-G304R	3	
	M680I- T267I	3	
	M694V-K695R	2	
	R761H-M694V	2	
Complex Heterozygote	M694V-M680I-M694I-E148Q	3	6(6.5%)
	E148Q-P369S-M694V-V726A-M680I	2	
	M694V-M691V-M694I-V726A	1	

Source: Compiled by the authors of this study

The FMF attacks varied in length, typically lasting between two and seven hours a day, with an average duration of about 3.8 hours (SD=1.46). Most children 71.7% experienced these painful episodes roughly once a month, while others had them a bit more often—about 22.8% reported two attacks per month, and a smaller group 5.4% experienced as many as three monthly episodes (Table 4).

Genetic testing revealed a heterogeneous group of MEFV variants. The most common genotype in all identified alleles was heterozygous mutations, comprising 50% of all the observed allele with E148Q being the most frequent followed by M694V and V726A. The homozygous genotypes were found in 17.4% of the cohort of which M694V-M694V arrangement was the dominant homozygous form (Table 5).

Table 6. Joint involvement in FMF patient

Joints	Numbers	Percent
KNEE	39	42.4
Elbow	1	1.1
Ankles	5	5.4
both knee	34	37.0
Wrist	5	5.4
Poly	8	8.7

Source: Compiled by the authors of this study

The genetic complexity of familial Mediterranean fever was emphasized as the proportion of 26.1% of the total cases was compound heterozygosity. A subgroup of patients (6.5 percent) displayed complex heterozygosity, which was indicated by the presence of multiple allelic variations thus enhancing the subtle genotype-phenotype relationship that is relevant in the pathogenesis of FMF.

Table 6 showed that joint symptoms were frequent, with the knee joint being the most affected 42.4%. Other joints, such as the ankle and wrist, were less frequently involved 5.4%, and multi-joint involvement was noted in 8.7% of patients. These findings confirm that the musculoskeletal burden is significant for patients with familial Mediterranean fever.

Statistical correlations revealed significant associations between genotype and many clinical and laboratory markers (Table 7). Factors such as sex, family history, kinship, and residential background showed a strong influence on the negative phenotype P<0.0001. Similarly, the 40 markers (C-reactive protein, white blood cell count, and red blood cell clotting) and symptoms such as fever, arthritis, and abdominal pain were associated with specific genotypes. Interestingly, skin lesions and pain showed little to no association, suggesting they may be independent of the variability in this category. Attack duration and frequency also showed a strong association with the radial phenotype, indicating a significant influence on disease susceptibility.

The standard of care for FMF is colchicine therapy, which was well received by the majority of patients

Table 7. Correlation statistically between different variant clinical and laboratory with FMF genotype

No.	Variable	T test	P-value
1	gender - genotype	-4.524	0.0001
2	consanguinity - genotype	-6.208	0.0001
3	Family history - genotype	-4.377	0.0001
4	religion - genotype	-6.031	0.0001
5	residences - genotype	-4.506	0.0001
6	WBC - genotype	33.958	0.0001
7	ESR - genotype	38.863	0.0001
8	CRP - genotype	29.099	0.0001
9	FEVER - genotype	-8.461	0.0001
10	Abdominal pain - genotype	-6.516	0.0001
11	Arthritis - genotype	-3.032	0.003
12	State of appetite - genotype	-2.569	0.012
13	Stunted growth - genotype	-4.060	0.0001
14	Skin lesion- genotype	1.032	0.305
15	Joint involvement - genotype	4.790	0.0001
16	Chest pain - genotype	.732	0.466
17	Myalgia - genotype	-1.809	0.074
18	Frequency of attack- genotype	-4.338	0.0001
19	Duration of attack - genotype	9.777	0.0001

Source: Compiled by the authors of this study

Table 8. Follow up and response to treatment

Response to colchicine	Number	Percent
Good	87	94.6
Not well	5	5.4
Ultrasound finding no documented amyloidosis		

Source: Compiled by the authors of this study

(94.6%). The suboptimal response rate was only 5.4%. Crucially, no cases had ultrasound evidence of amyloidosis, a serious FMF complication, suggesting that the disease was effectively managed and that early intervention may have been possible (Table 8).

DISCUSSION

In similarity to another studies Turkey and Iraq, our pediatric patients with FMF, had mean of age 8.02 years [1], for example, similar to other Kurdish series in Iraq and Turkey, our pediatric FMF cohort had a mean age of 8.02 years. Eastern Turkish child had a mean age about 7.7 years with a ratio related sex 1:1, while Sulaymaniyah child had a mean age of 7.8 years with male prevalence ~64% [15]. In corresponding the line, some reports from Iraq, the researcher institute a greater male bias 65% male. According to [15] the group's parental consanguinity was a remarkable 79%, significantly higher than the rates in Turkey ~24% and even other Iraqi/Kurdish cohorts ~33% [1]. Similarly, a positive family history 63% was more common than reported elsewhere (e.g. 47% in [1]. These divergences likely reflect local marriage practices and genetic pooling in Duhok. Nearly all our patients were Muslim 91%, mirroring regional demographics; such details were not reported in most FMF series but align with the ethnic composition of northern Iraq. Two-thirds of our cases were urban residents. In sum, our demographic profile is broadly consistent with nearby regions, except for the much higher consanguinity and family history, which may amplify autosomal recessive FMF transmission in this population. The clinical presentation in Duhok pediatric FMF resembled that of other Middle Eastern cohorts. All our patients had recurrent fever 100% and most had abdominal pain ~85%, paralleling Turkish (fever ~85%, abdominal pain ~95%) [16]. Kurdish-Iraqi reports (95–100% fever, 75–80% pain). However, some manifestations varied. We found a high rate of arthritis 46.7%, substantially according to [15] more than the ~10% reported in Turkish children though similar to the 45% with arthralgia in a small Iraqi Kurdish series [17]. This may reflect younger age or ethnic differences (arthritis tends to be less common in Arab and Turk populations but can be high in pediatric-onset FMF). Other symptoms in our cohort – myalgia 32%, headache 10%, chest pain 3%, anorexia 59% and notably 61% with stunted growth – were within or above reported ranges. For example, according to [4, 16] the symptoms as anorexia/fatigue were common in an Iranian registry 64% anorexia, and [17] has been reported in about 5% of children with FMF in Turkey. Notably, we observed no erysipelas-like skin rash, whereas Turkish and Kurdish series report rash in 3–15% of patients. This absence according to [16]; it may be due to genetic or environmental factors; skin lesions in FMF often associate with the M694V mutation (which was less prevalent here). In summary, our patients' symptoms (fever and serositis) are largely consistent with FMF elsewhere, but the higher arthritis and growth failure rates suggest possible influences of genetic background, nutritional status, or delayed diagnosis in Duhok. As expected during FMF attacks, our patients showed elevated inflammatory markers (mean WBC~12.9×10^9/L, ESR~50 mm/h, CRP~63 mg/L). These findings align with [4] the pattern of acute-phase reactant elevation reported in FMF cohorts worldwide. For instance, [16] noted leukocytosis and raised ESR/CRP during attacks in Turkish children. We did not observe any routine laboratory anomaly unique to our group. The degree of inflammation (ESR/CRP levels) was comparable to published pediatric series as reported in previous studies [1, 16], suggesting similar attack intensity. Few studies quantify these values in children by region, but our results are in line with general FMF literature: all attacks produce pronounced Neutrophilic inflammation. No renal proteinuria or amyloiduria was found, consistent with the lack of amyloidosis in clinical follow-up. Thus, laboratory profiles in Duhok's FMF children are broadly concordant with findings from Turkey, reflecting the expected systemic inflammation of FMF. The MEFV mutation spectrum in our cohort both mirrors and diverges from other populations. In Duhok children, the E148Q variant was the single most frequent allele, followed by M694V, V726A and M680I. In contrast, [16] report that the large Turkish series typically find M694V as the top allele (e.g. ~27% in Eastern Anatolia), with E148Q often second as a common heterozygote 38% of heterozygotes had E148Q). Our distribution resembles the Kurdish Sulaymaniyah data, where E148Q and M680I were also very common [1], though even there M694V was more frequent than in Duhok. In [16] authors found the Iranian FMF patients typically carry M694V (~20%) at higher frequency than E148Q (~10%) opposite to our pattern. Similarly, as [18] and [19] report that the Armenian and many Middle Eastern cohorts are dominated by M694V (often 50–75%), in addition, [16] found the Italian patients also show M694V > E148Q > M680I. Thus, the prominence of E148Q in our sample is unusual and may reflect local ancestry (western Iranian Kurdish influences or high inbreeding can enrich particular alleles). Ethnic admixture likely explains these differences. Notably, population data show that Ashkenazi Jews (Israel) have high E148Q, whereas non-Ashkenazi Jews and Armenians carry mostly M694V. Our findings align more with the former pattern. In sum, while the presence of major FMF mutations (E148Q, M694V, V726A, and M680I) is consistent with global observations [4, 15, 18], the relative frequencies diverge: Duhok children have excess E148Q and fewer classic exon-10 mutations. These discrepancies likely stem from genetic background (found-

er effects, consanguinity) and possibly under-diagnosis of mild alleles in neighboring populations. We found significant associations between genotype and several disease features (Table 7). Specifically, severe genotypes (e.g. homozygous or compound heterozygous for exon 10 mutations) tended to have earlier onset, more frequent and longer attacks, and higher inflammatory markers, while milder genotypes (such as simple E148Q carriers) had comparatively attenuated disease. This pattern accords with the literature. For example, M694V homozygosis is well known to portend a severe FMF phenotype and amyloidosis risk, and even asymptomatic M694V homozygotes are often advised to be treated. The [20], similarly reported that M694V homozygotes have incomplete response to colchicine and more severe courses. In our data, patients with two exon-10 mutations had higher attack frequency and duration $P<0.0001$, mirroring such reports. Conversely, the E148Q variant, considered a low-penetrance allele, was over-represented in patients with milder attacks. The international FMF registries also show that M694V and M680I (exon 10) drive more severe disease, whereas E148Q and V726A tend to modulate or attenuate symptoms. Thus, our genotype-phenotype correlations are consistent with these global trends. Environmental or healthcare factors might further shape severity for instance, frequent respiratory or gastrointestinal infections (not measured) could trigger attacks but the strong statistical links we observed largely reflect the inherent impact of MEFV mutation type. Our treatment outcomes were excellent: 94.6% of patients responded well to colchicine, and none developed amyloidosis on follow-up. This closely matches the high efficacy reported elsewhere. In Baghdad, researcher found that all 23 FMF patients (adults) responded to colchicine with complete attack suppression and no amyloid complications. In Kurdish children, [17] noted only ~5% colchicine resistance and also no amyloidosis. Likewise, most Turkish pediatric series report >90% good control on colchicine. The consistently high remission rates likely reflect similar disease mechanisms and the universal use of colchicine prophylaxis across regions. The small fraction of non-responders (5.4% in our cohort) is within the 2–10% range described in major FMF series. Factors such as M694V homozygosis have been linked to colchicine resistance, but we did not find a significant difference in response by genotype - likely due to our sample size. Finally, we attribute the absence of amyloidosis to both effective colchicine uses and possibly a lower intrinsic risk in this population, as was suggested in Iraqi Arabs. In summary, our treatment response pattern is consistent with global experience: colchicine effectively prevents attacks and amyloidosis in the vast majority of FMF children [21] (Duman et al., 2025) and healthcare access in Duhok appears sufficient to maintain adherence.

CONCLUSIONS

A higher male preponderance, extreme consanguinity, and a noticeably high prevalence of the E148Q MEFV variation are among the distinctive features of this study on a juvenile FMF cohort from Duhok that show similarities with regional counterparts. Despite some inconsistencies, certain clinical findings, such as the high prevalence of arthritis, are consistent with other data from the Middle East. No unusual test results were recorded, and inflammatory markers reflected global patterns during the attacks. In line with broader research on FMF, genotype-phenotype associations exposed that severe genotypes were associated with more severe sickness. Accurate treatment consequences, including a 94.6% response to colchicine with no amyloidosis, demonstrated fruitful management performances. All things well thought-out, these results improve knowledge of FMF in a variety of groups and bolster the effectiveness of up-to-date therapeutic modalities.

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CONFLICT OF INTEREST

The Author declare no conflict of interest

CORRESPONDING AUTHOR

Salah Abdulkareem Ibrahim
Pediatric Department,
College of Medicine, University of Duhok
Duhok, Iraq
e-mail: salah.ibrahim@uod.ac

ORCID AND CONTRIBUTIONSHIP

Salah Abdulkareem Ibrahim: 0009-0004-6040-0409 A B C D E F

A – Work concept and design, B – Data collection and analysis, C – Responsibility for statistical analysis, D – Writing the article, E – Critical review, F – Final approval of the article

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