# The role of E148Q in FMF

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### **Familial Mediterranean Fever** (FMF)

#### Acute attacks of fever accompanied by:

- Peritonitis
- Pleuritis
- **Arthritis**
- Erysipelas like erythema



Frequency of Attacks
 From twice a week to once every
 couple of years

**Precipitating Factors** Infections, trauma, physical activity, menstrual period, mental stress, unknown factors



![](_page_4_Picture_0.jpeg)

#### **Disease Distribution**

# North African Jew Iraqi Jews Armenians Turks

#### Middle eastern Arab

Ashkenazi Jews

The disease is one of the most common Mendelian disorder in world

Hundreds of thousands of FMF patients world wide

The disease is by far the most common Mendelian disorder in Israel with more than 15,000 patients

#### **Colchicine Treatment**

Until the mid 70's - no effective treatment Prophylactic colchicine first introduced

Patients resistant to colchicinetreated today with II-1Inhibitors

![](_page_7_Picture_3.jpeg)

# The FMF Gene (MEFV) mRNA-3700 bp long Encodes a 781 amino acid protein (Pyrin)

![](_page_8_Figure_1.jpeg)

### **FMF patients with a single mutation Mutation analysis in FMF patients reveal:**

60-65% two mutations
20-25% one mutation
5-10% no mutations

The most common single mutation genotype found is M694V/null

#### **MEFV** Mutations

♦ <u>M694V</u>	<b>K695R</b>	R42W	Y688X
♦ <u>V726A</u>	A744S	E230K	T681I
• <u>E148Q</u> •	<b>V704I</b>	E148V	M680L
<b>E167D</b>	<b>G687E</b>	L110P	S675N
<b>P369S</b>	<b>T267I</b>	R408Q	R653H
<b>M680I</b>	<b>F479L</b>	I591T	M640Del
<b>M694I</b>	<b>I692Del</b>	R761H	

E148Q In FMF a Mutation or a Polymorphism ?

# In the Far East carrier rate of 25% in control samples.

No difference in the frequency of this variant between cohorts of patients and controls

#### One of the most common ways to differentiate between a mutation and a polymorphism is to assess its frequency in patients vs. controls

![](_page_12_Picture_1.jpeg)

	Patients (Zaks 2003)	Healthy Controls
E148Q	58	163
	766	2639
Total	824	2802
	7.04%	5.81%

PV=0.2280

	Patients (Zaks 2003)	Healthy Controls
V726A	122	141
	702	3877
Total	824	4018
	14.8%	3.5%

![](_page_14_Picture_1.jpeg)

# No functional assay For FMF mutations

![](_page_15_Picture_1.jpeg)

#### **IN-FEVERS DATA BASE**

## E148Q is defined as a variant of unknown significance (VOUS)

(http://fmf.igh.cnrs.fr/infevers)

### **Through out the years**

We all shared the feeling that E148Q has a functional effect but the game changing evidence was missing

#### Penetrance

No. of symptomatic patients with a given genotype Total\_no. of individuals with that genotype

**Full Penetrance = 1.0** 

# What is the penetrance of the disease in patients with the M694V/E148Q genotype

What is the penetrance of the disease in patients with the M694V/null genotype

Compare the penetrance of M694V/E148Q to the penetrance of M694V/null

![](_page_22_Picture_0.jpeg)

# To determine the penetrance of the M694V/null and M694V/E148Q genotypes in adult FMF patients.

Functional role for E148Q in the disease

### **Calculating penetrance**

1. Direct calculation: Genotype 100,000 individuals, look for the M694V/E148Q and M694V/null genotypes and see how many of them have FMF.

2. Indirect relative penetrance calculation

#### **Methods**

Find a population group in which FMF and these 2 mutations are very prevalent.

Assess the allele frequencies of these two variants in a large control group.

Calculate the expected frequencies of the M69V/M694V, M694V/null and M694V/E148Q genotypes.

**Construct a cohort of at least 100 consecutive FMF patients who came for genetic analysis, all belonging that population group.** 

Assuming a penetrance of 100% for the M694V/M694V genotype:

The ratio between the calculated frequencies of the 3 genotypes and the actual frequencies of these 3 genotypes obtained from the patient cohort will be used to determine the penetrance of M694V/null and M694V/E148Q.

#### **North African Jewish population (NAJ)**

We shall assess the carrier rates for M694V and E148Q in NAJ from three previous studies (over 500 controls).

The expected frequencies of the M69V/M694V, M694V/null and M694V/E148Q genotypes were calculated.

We will construct a cohort of at least 100 consecutive patients with FMF, all of NAJ decent who came for genetic analysis.

The ratio between the calculated frequencies of the 3 genotypes and the actual frequency obtained from the patient cohort was used to determine the penetrance of M694V/null and M694V/E148Q.

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