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Screening of the most common MEFV mutations in a Large Cohort of Egyptian Patients with Familial Mediterranean Fever

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Abstract

Background and aim**:** Familial Mediterranean fever (FMF) is the most common monogenic auto-inflammatory disease (AID) characterized by self-limited inflammatory attacks of fever and serosal tissues inflammation. FMF is caused by mutations in the *MEFV* gene coding for pyrin, which is a component of inflammasome functioning in inflammatory response. The objectives of the investigation were to evaluate the clinical symptoms and screen the most common *MEFV* variants in the Egyptian FMF patients.
Methods: 818 FMF patients were enrolled in this study based on clinical criteria. Three different screening molecular methods were used; ARMs, strip assay and direct Sanger sequencing.
Results: The most frequent clinical presentations of the patients were abdominal pain, fever and arthritis. Most of the patients responded to colchicine therapy. *MEFV* gene mutations were detected in 50.7% of the patients. The most common mutations were; M694I (27.59%), M762A (16.84%), M680I (16.02%), E148Q (10.34%) and M694V (9.33%).
Conclusion: This is the largest study on FMF from Egypt. Exon 10 of the *MEFV* gene recorded hot spot variants in the studied Egyptian FMF patients. We suggest screening for exon 10 as the first step in molecular characterization of FMF patients. Although none of the mutations in exon 10 and 2 were detected in 49.3% of our patients, despite all of them suffered from FMF symptoms and responded well to colchicines. This study recommends full sequencing to *MEFV* gene in these patients which may help to discover new mutations in Egyptian FMF patients and to design a local diagnostic kit.

Keywords: Familial Mediterranean fever; MEFV gene, mutations, auto-inflammatory disease

Introduction

Familial Mediterranean fever (OMIM: 249100) is the most frequent monogenic auto-inflammatory disease (AID) round the world. In 2006, more than 100000 FMF patients have been reported (Onen, 2006). Reporting FMF cases were concentrated in the eastern Mediterranean but after establishing the diagnosis of the disease, worldwide carrier rates become as high as 1:5 (Onen, 2006, Lidar and Livneh, 2007 and Wekell et al., 2013). FMF is associated with recurrent cycles of fever and short attacks of serosal inflammation (Drenth et al., 2001). The most critical complication of FMF is amyloidosis, and it is responsible for long-standing morbidity and mortality (Twig et al., 2014). The symptoms and severity of FMF vary among patients even those in the same family. The absence of pathognomonic signs makes