

# How to Assess Founder Effect in Patients with Congenital Factor XIII Deficiency

**Hojat Shahraki<sup>1</sup>, Akbar Dorgalaleh<sup>1</sup>, Majid Fathi<sup>2</sup>, Shadi Tabibian<sup>1</sup>, Shahram Teimourian<sup>3</sup>, Hasan Mollanoori<sup>3</sup>, Alireza khiabani<sup>4</sup>, Farhad Zaker<sup>1</sup>**

<sup>1</sup>Department of Hematology and Blood Transfusion, School of Allied Medicine, Iran University of Medical Sciences, Tehran, Iran

<sup>2</sup>Department of Medical Biotechnology, School of Allied Medicine, Iran University of Medical Sciences. Tehran- Iran

<sup>3</sup>Department of Medical Genetics, School of Medicine, Iran University of Medical Sciences, Tehran, Iran

<sup>4</sup>School of Medicine, Bam University of Medical Sciences, Bam, Iran

**Corresponding Author:** Farhad Zaker, Department of Hematology and Blood Transfusion, School of Allied Medicine, Iran University of Medical Sciences, Tehran, Iran

Tel: +98- 021-88652276

Fax: +98- 021-88652276

Email: farhadz20@yahoo.co.uk

Received: 18, May, 2019

Accepted: 27, Nov, 2019

## **ABSTRACT**

Congenital factor XIII (FXIII) deficiency is an extremely rare bleeding disorder (RBD) with estimated prevalence of one per 2 million in the general population. The disorder causes different clinical manifestations such as intracranial hemorrhage (ICH), recurrent miscarriage, umbilical cord bleeding, etc. High incidence of the disorder might be due to founder effect. To assess founder effect, haplotype analysis is an important step. For this purpose, suitable and reliable genetic markers such as microsatellites (Hum FXIIIA01 and HumFXIIIA02) and single nucleotide polymorphisms (SNP) are suggested. In the present study we tried to describe evaluation of founder effect in patients with congenital FXIII deficiency via haplotype analysis using suitable genetic markers.

**Keywords:** Factor XIII deficiency; Intracranial hemorrhage; Founder effect; Genetic markers

## **INTRODUCTION**

Factor XIII (FXIII) deficiency is a rare inherited disorders with an incidence of one per 2 million. The disorder is higher in some regions like Iran, Pakistan, Tunisia, Indian, etc.<sup>1,2</sup>. Patients with FXIII deficiency have different clinical manifestations like recurrent and delayed bleeding, intracerebral hemorrhage (ICH), umbilical cord blood (UCB), defected wound healing and recurrent miscarriages<sup>3,4</sup>. There are specific and common mutations of factor XIII gene in different geographic areas. Due to autosomal recessive pattern of inheritance and rate of consanguineous marriages, disease causing

mutations may inherited to children by their parents<sup>5</sup>. On the other words, the presence of a same mutation in different non-consanguineous families in a particular area may indicate a common ancestor or a founder effect. Founder effect causing mutation is called founder mutation. For example, Trp187Arg is a suitable example for FXIII deficiency associated with founder mutation in southeast Iran. These types of mutations usually occur in one or more founders of a new and different population and are inherited to next generations, which finally make a great alteration in DNA. In other words, pathogenic alleles will be displayed in next

Copyright © 2020 Tehran University of Medical Sciences. This work is licensed under a Creative Commons Attribution-Noncommercial 4.0 International license (<http://creativecommons.org/licenses/by-nc/4.0>). Non-commercial uses of the work are permitted, provided the original work is properly cited.

generations in homozygote form and probably founder effect could be the reason of high incidence disorder<sup>6,7</sup>. For assessment of founder effect if: 1) candidate microsatellites and single nucleotide polymorphisms (SNPs) are meaningfully different in patient and control groups, 2) a unique haplotype is observed in the majority of the patients, these can indicate genetic linkage between microsatellites and polymorphisms with causative mutation<sup>8-10</sup>. Our goal in the present study was to describe how founder effect influences FXIII deficiency in areas with particular mutation by using haplotype analysis and suitable genetic markers.

### Diagnosis of factor XIII deficiency

Routine coagulation tests like bleeding time, prothrombin time, activated partial thromboplastin time, fibrinogen level and platelets count are normal<sup>11</sup>. The primary and the most commonly used test is clot solubility test. This is a qualitative test and is positive only in patients with a very low of FXIII<sup>1,12</sup>. Measuring FXIII activity is a decisive diagnosis<sup>13</sup>. Commercial ELISA kits are available for measuring of FXIII-A<sub>2</sub>B<sub>2</sub>, FXIII-A and FXIII-B antigenic levels<sup>14</sup>. Finally, genetic analysis can help to find associated mutations of FXIII gene. Carrier detection is very important to prevent marriage of these patients and to recognize FXIII suspected individuals in haplotype aspects<sup>15,16</sup>.

More than 170 mutations have been identified within *F13A* and *F13B* genes, most belongs to *F13A* subunit<sup>17,18</sup>. Sanger sequencing is the most common DNA sequencing method, but next-generation sequencing (NGS) is a more advanced sequencing technology, which can increase the rate of mutation detection<sup>16,19</sup>.

### Founder effect

Founder effect is one of the important topics in population genetics and it is one of the ways that nature uses to generate new species from primary populations<sup>10,20</sup>. In a simple word, sometimes, a few number of a large population immigrate to specific locations. Others cannot enter to these population to make change in their genetic pool that leads to lower genetic diversity and occurring of defected pathogenic mutation that is actually called founder

effect<sup>10</sup>. Over the time, new populations genetically and phenotypically become thoroughly differentiated from the primary population. Founder effect causing mutation is called founder mutation.

### Founder effect in congenital factor XIII deficiency

There are *F13A* common mutations in the different geographic areas. For example, Trp187Arg and Arg77His are common in Iran, Ser295Arg and c.2045G>A in Pakistan, c.869insC in Tunisia, Arg77Cys in Switzerland, and Arg661X in Finland<sup>3,7,21-33</sup>. In India, IVS1 A246G polymorphisms seems to be the most common FXIII polymorphisms<sup>34</sup>. The IVS5-1G>A mutation was observed in European countries, including Poland, Czech Republic, Turkish, Greek, UK, Macedonia and the Netherlands<sup>7,30,35,36</sup>. According to the inheritance pattern of mutation, disease-associated mutations may happen in previous generations. Presence of a same mutation in different non-consanguineous families in a special area may show common ancestor. For example, Trp187Arg is a suitable example for FXIII deficiency associated with founder mutation in southeast Iran<sup>37</sup>. These types of mutations usually occur in one or more founders of a new and different population and are inherited to next generation, and finally make great alterations in DNA. In other words, pathogenic alleles will be displayed in next generations in homozygote forms. One important population example is congenital FXI deficiency in Ashkenazi Jews<sup>38</sup>.

### How to evaluate association of founder effect and FXIII deficiency

We can use haplotype analysis in order to evaluate founder effect which is caused by inbreeding in populations of a certain area<sup>9,39</sup>. Haplotype is a combination of alleles in different locus of a chromosome that inherit together. In simple word, haplotype is a set of a mononucleotide polymorphisms like SNPs, microsatellites, variable number tandem repeats (VNTRs) on one chromosome of homologous chromosomes<sup>40,41</sup>. These markers are sequences of DNA and they inherit together due to their closeness to disease-associated gene, therefore if an individual or a group possesses a set of linked markers, the presence of

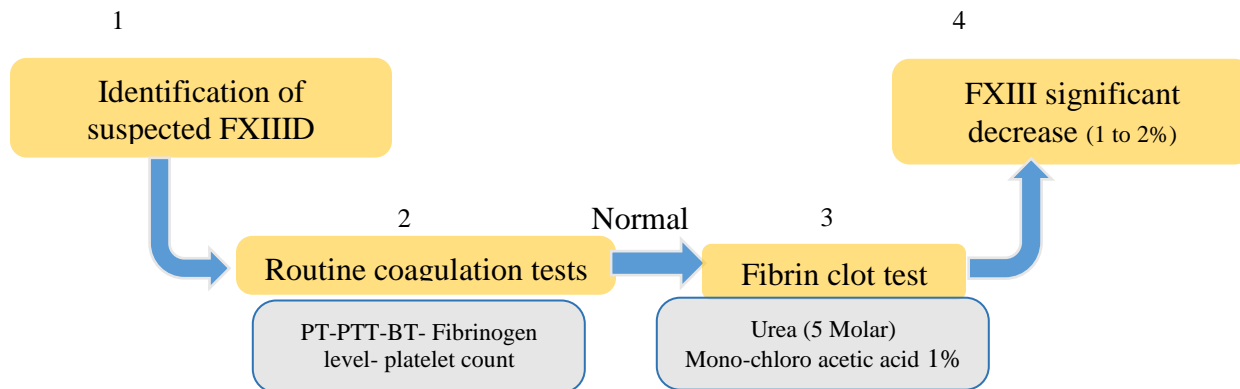
disease-associated gene in their genome is assumable. Therefore, haplotype analysis via SNP, microsatellite and VNTRs can be used to assess the association of founder effect with specific and considered mutation as the most incident type of FXIII deficiency causing mutation in particular region<sup>42,43</sup>. It's important that selected polymorphic markers should be informative and be close to disease-causing gene to achieve the best results<sup>44,45</sup>.

### First step: Diagnosis of FXIII deficiency

-Providing questionnaires, including individual's characteristics such as age, gender, city of residence, family history, clinical symptoms

-Sample collection

-Routine coagulation tests: At first all FXIII deficiency suspected individuals have to be examined by common coagulation tests like bleeding time (BT), prothrombin time (PT), activated partial thromboplastin time (PTT), platelet count and fibrinogen level. Those patients with low FXIII level who showed a significant decrease (1 to 2%) should enter to molecular laboratory phase (Figure 1)<sup>2</sup>.



**Figure 1:** How to diagnose FXIII deficiency suspected individuals  
BT: Bleeding Time, PT: Prothrombin Time, PTT: Activated Partial Thromboplastin Time

### Second step: Detection of molecular defect in patients with congenital FXIII deficiency

- Bioinformatics studies: To find FXIII gene in NCBI data bank.  
- DNA extraction  
-Quantitative and qualification assessment of extracted DNA  
-Polymerase chain reaction-Restriction fragment length polymorphisms (PCR-RFLP): To select suitable restriction enzymes, after bioinformatics analysis based on candidate enzyme selected, different fragments of DNA are observable on electrophoresis gel, which indicates homozygote, heterozygote and normal gene (Table 1)<sup>46-48</sup>.

**Table 1:** Characteristics of important features most common mutation of congenital factor XIII deficiency

Most common mutation	Origin of patient	Chromosome location	Genotype	Type	Domain	Gene subunit	Functional information	References
Trp187Arg	Iran	Exon 4	Homozygous	Missense	Core	FXIII A-subunit	Steric clashes of arginine with side chains	(3, 6, 21, 22, 37, 49)
Arg77His	Iran	Exon 3	Homozygous	b-sandwich	Missense	FXIII A-subunit	Disruption of most H-bonds	(2, 21, 22, 47, 49)
Ser295Arg	Pakistan	Exon 7	Homozygous	Missense	Core	FXIII A-subunit	Incorrect folding resulting in an unstable FXIII polypeptide	(7, 24-27)
c.2045G>A	Pakistan	Exon 14	Homozygous	Splicing	Barrel 2	FXIII A-subunit	Probably splicing defect	(7, 25-27)
Arg77Cys	Switzerland	Exon 3	Homozygous	Missense	b-sandwich	FXIII A-subunit	Disruption of most H-bonds	(7, 30)
c.869insC	Tunisia	Exon 7	Homozygous	Frameshift	Core	FXIII A-subunit	Stop after 8 altered amino acid	(26, 28, 29)
Arg661X	Finland	Exon 14	Heterozygous	Nonsense	Barrel 2	FXIII A-subunit	Decrease of FXIII mRNA levels	(31-33)
IVS5-1G>A	European Countries: Netherland, Poland, UK, Czech Republic, Macrdonia, Greek, German and Turkish	Intron 5	Homozygous	Splicing	intronic	FXIII A-subunit	Effect on RNA splicing	(1, 2, 7, 30, 35, 36)
A246G	India	Intron 14	Heterozygous	Splicing	intronic	FXIII A-subunit	Probably splicing defect	(34)

**Third step: selection of suitable microsatellites**

Microsatellites are highly polymorphic and repetitive DNA sequences. These sequences are 2 to 6 base pair repeats that place along DNA<sup>50</sup>. Microsatellites are highly polymorphic and mutation prone. Because of microsatellite uniqueness in different populations and high number of them in the genome, they can be used as informative markers to investigate genetic association among human ethnics, population genetics and haplotype analysis<sup>39,51</sup>. There is a criterion named polymorphic informative content (PIC), which indicates allele frequency in the population and relates with mean repeat length. PIC < 0.7 represents that microsatellite is informative and this is important in microsatellite option<sup>45,52</sup>.

-Candidate microsatellite: based on previous studies and bioinformatics analysis in NCBI databank and FXIII Database, 2 microsatellites could be selected in *F13A* gene (Table 2).

-Microsatellite Hum FXIII A01 has repeated sequence of AAAG in chromosomal location of 6p24-25 and in 5`UTR(-2775/ATG) region<sup>44,53</sup>.

-Microsatellite Hum FXIII A02 has repeated sequence of AC (poly AC) in chromosomal location of 6p24-25 and in intron 8 region<sup>29</sup>.

For visiting the most practical microsatellites in details, go to <http://www.cstl.nist.gov/biotech/strbase>.

- DNA extraction
- Quantitative and qualitative assessment of extracted DNA
- PCR along labeled primers with fluorescent substance (FAM)
- Capillary electrophoresis
- Data analysis using Gene marker software

**Fourth step: Selection of suitable SNPs for haplotype analysis**

SNPs occur with frequency of 1% in general population and they span all the human genome, because of this, these markers are widely used in

diagnosis of different cancers and congenital genetic disorders<sup>40,54,55</sup>.

-Candidate SNPs: SNPs are selected after bioinformatics analysis in NCBI database. Candidate SNPs should be verified by Hapmap project, Cluster, 1000 genomes project and frequency databases. Furthermore, these SNPs are mostly locate in FXIII gene (6:6144077-6320590). It is better to select SNPs with global minor allele frequency (Global MAF) near to 0.5 to have fewer differences between SNPs allele incidence (Table 3)<sup>9,40,42</sup>.

- DNA extraction
- Qualitative and quantitative assessment of extracted DNA
- PCR
- Sequencing or PCR-RFLP
- Data analysis by CLC sequencer and Chromas software

**Fifth step: Haplotype analysis**

After data analysis, we have to determine similarity of haplotypes in FXIII deficiency patients. Generally microsatellites are more reliable markers than SNPs<sup>9,44,45</sup>. On the other hand, larger number of genetic markers in a study results in more reliable and informative results. The important point is that in haplotype analysis, shorter distances between genetic markers and considered mutations will achieve to more reliable results. We can differentiate haplotypes by comparing results of patients and normal individuals<sup>56</sup>. Schematic figure of chromosomal location of candidate SNPs and STRs for FXIII haplotype analysis are shown in Figure 2.

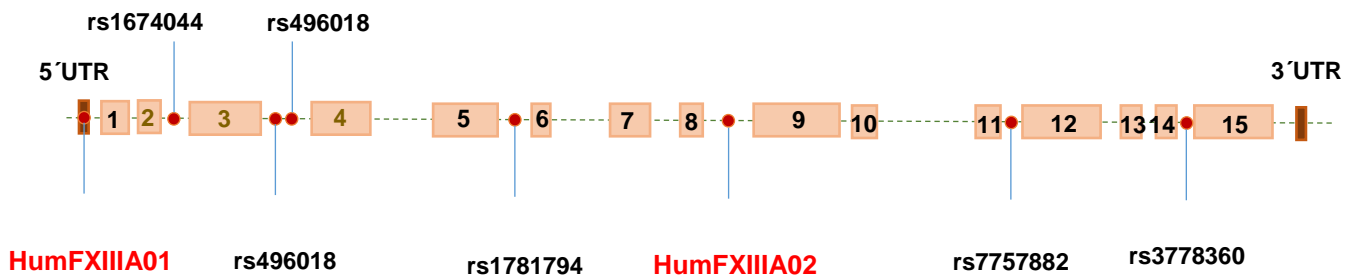
**Table 2:** Features of Hum FXIII A01 and Hum FXIII A02 microsatellites

Microsatellite	Human FXIII A01 (FXIII A01)	Human FXIII A02 (FXIII A02)
Repeat sequence	AAAG	AC
Chromosomal location	6p24-25	6p24-25
Gene bank accession	M21986	-
Expected range of allele	281-331	204-236
PCR primers	5'-TTTTCTCTGCCTTCCCATGT-3' 3'-ATGCCATGCCAGATTAGAAA-5'	5'-GAGGTTGCACTCCAGCCTTT-3' 3'-CCCCAGTGCAGTGTTTTAT-5'
Primer concentration	0.1 Micromolar	0.1 Micromolar

\* No accession number was reported for this STR and it was mentioned in article <sup>29</sup>.

**Table 3:** Features of candidate Single Nucleotide Polymorphism (SNPs)

SNP	rs3024317	rs4960181	rs63778360	rs7757882	rs1781794	rs1674044
Number	1	2	3	4	5	6
Chromosomal location	6:6319146	6:6269065	6:6150132	6:6189967	6:6241547	6:6310481
Hap map	✓	✓	✓	✓	✓	✓
Intron Site	3	3	14	11	6	2
Frequency	✓	✓	✓	✓	✓	✓
Global MAF	0.4688	0.4854	0.4842	0.4553	0.4888	0.4535
1000 G	✓	✓	✓	✓	✓	✓
Cluster	✓	✓	✓	✓	✓	✓

Figure 2. Schematic figure of chromosomal location of candidate microsatellites and SNPs of *F13A* gene

**CONCLUSION**

When we are evaluating impact of founder effect in congenital FXIII deficiency, we have to notice that if:

- Candidate microsatellites and SNPs were meaningfully different in patients and control groups
- A unique haplotype was observed in most of the patients
- These can indicate genetic linkage between microsatellites and polymorphisms with considered

mutation and subsequently this genetic linkage can imply a kind of founder effect for the disease, which means that previous generations increased FXIII deficiency via consanguineous marriage. Generally, it is considered some circumstances like consanguineous marriage; ethnic and place of residence can prominently increase pathogenic mutations, founder effect and subsequently raise FXIII deficiency.

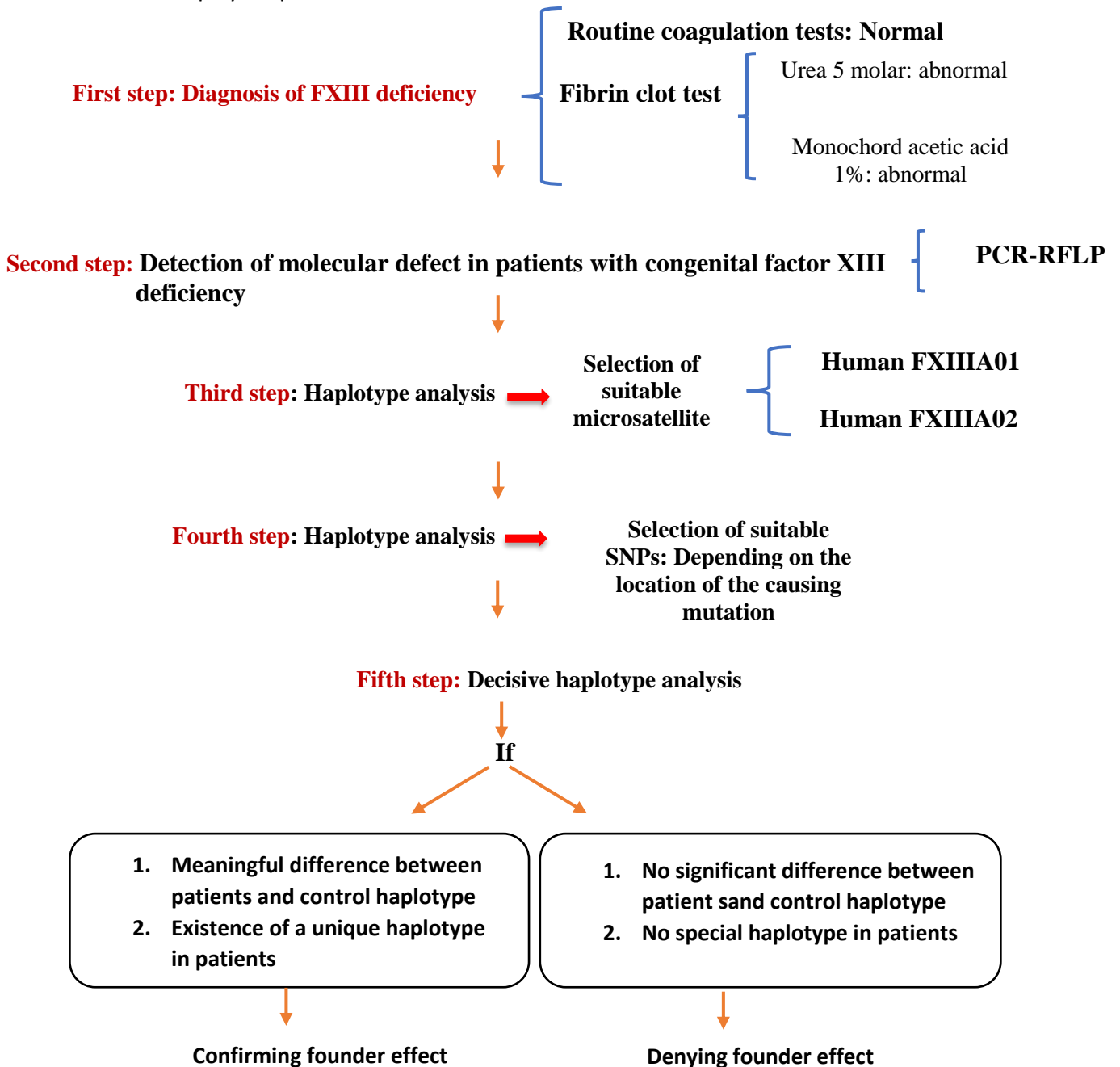


Figure 3: Evaluating association of founder effect with FXIII deficiency by step-by-step diagnostic algorithm

## Funding

This study was supported by Grant No. 94-05-31-27408 from Iran University of Medical Sciences.

## CONFLICTS OF INTEREST

There are no conflicts of interest.

## REFERENCES

- Dorgalaleh A, Tabibian S, Hosseini MS, et al. Diagnosis of factor XIII deficiency. *Hematology*. 2016;21(7):430-9.
- Dorgalaleh A, Tabibian S, Hosseini S, et al. Guidelines for laboratory diagnosis of factor XIII deficiency. *Blood Coagul Fibrinolysis*. 2016;27(4):361-4.
- Naderi M, Dorgalaleh A, Alizadeh S, et al. Clinical manifestations and management of life-threatening bleeding in the largest group of patients with severe factor XIII deficiency. *Int J Hematol*. 2014;100(5):443-9.
- Levy JH, Greenberg C. Biology of Factor XIII and clinical manifestations of Factor XIII deficiency. *Transfusion*. 2013;53(5):1120-31.
- Karimi M, Bereczky Z, Cohan N, et al. Factor XIII deficiency. *Semin Thromb Hemost*. 2009; 35(4): 426-38.
- Trinh CH, Sh ElSayed W, Eshghi P, et al. Molecular analysis of sixteen unrelated factor XIII deficient families from south-east of Iran. *Br J Haematol*. 2008;140(5):581-4.
- Ivaskevicius V, Seitz R, Kohler HP, et al. International registry on factor XIII deficiency: a basis formed mostly on European data. *Thromb Haemost*. 2007;97(06):914-21.
- Vieira MLC, Santini L, Diniz AL, et al. Microsatellite markers: what they mean and why they are so useful. *Genet Mol Biol*. 2016;39(3):312-28.
- Stram DO, Seshan VE. Multi-SNP haplotype analysis methods for association analysis. *Methods Mol Biol*. 2012;850:423-52.
- Pulst SM. Genetic linkage analysis. *Arch Neurol*. 1999;56(6):667-72.
- Dorgalaleh A, Kazemi A, Zaker F, et al. Laboratory Diagnosis of Factor XIII Deficiency, Routine Coagulation Tests with Quantitative and Qualitative Methods. *Clin Lab*. 2016;62(4):491-8.
- Dorgalaleh A, Tabibian S, Shams M, et al. Laboratory diagnosis of factor XIII deficiency in developing countries: an Iranian experience. *Lab Med*. 2016;47(3):220-6.
- Jennings I, Kitchen S, Woods T, et al. Problems relating to the laboratory diagnosis of factor XIII deficiency: a UK NEQAS study. *J Thromb Haemost*. 2003;1(12):2603-8.
- Dorgalaleh A, Rashidpanah J. Blood coagulation factor XIII and factor XIII deficiency. *Blood Rev*. 2016;30(6):461-75.
- Peyvandi F. Carrier detection and prenatal diagnosis of hemophilia in developing countries. *Semin Thromb Hemost*. 2005; 31(5):544-54.
- Peyvandi F, Jayandharan G, Chandy M, et al. Genetic diagnosis of haemophilia and other inherited bleeding disorders. *Haemophilia*. 2006; 12 Suppl 3:82-9.
- Hsieh L, Nugent D. Factor XIII deficiency. *Haemophilia*. 2008;14(6):1190-200.
- Biswas A, Ivaskevicius V, Seitz R, et al. An update of the mutation profile of Factor 13 A and B genes. *Blood Rev*. 2011;25(5):193-204.
- Palla R, Peyvandi F, Shapiro AD. Rare bleeding disorders: diagnosis and treatment. *Blood*. 2015;125(13):2052-61.
- Ferreira MA. Linkage analysis: principles and methods for the analysis of human quantitative traits. *Twin Res*. 2004;7(5):513-30.
- Eshghi P, Cohan N, Lak M, et al. Arg77His and Trp187Arg are the most common mutations causing FXIII deficiency in Iran. *Clin Appl Thromb Hemost*. 2012;18(1):100-3.
- Naderi M, Dorgalaleh A, Alizadeh S, et al. Molecular analysis of the largest group of patients with factor XIII deficiency in southeast of Iran. *Blood*. 2013;122(21):4780.
- Peyvandi F, Tagliabue L, Menegatti M, et al. Phenotype-genotype characterization of 10 families with severe a subunit factor XIII deficiency. *Hum Mutat*. 2004; 23(1):98.
- Anwar R, Gallivan L, Miloszewski KJ, et al. Factor XIII deficiency causing mutation, Ser295Arg, in exon 7 of the factor XIII gene. *Thromb Haemost*. 2000;84(10):591-4.
- Anwar R, Gallivan L, Richards M, et al. Factor XIII deficiency: new nonsense and deletion mutations in the human factor XIII gene. *Haematologica*. 2005;90(12):1718-20.
- Vysokovsky A, Saxena R, Landau M, et al. Seven novel mutations in the factor XIII A-subunit gene causing hereditary factor XIII deficiency in 10 unrelated families. *J Thromb Haemost*. 2004;2(10):1790-7.
- Aslam S, Standen G, Khurshid M, et al. Molecular analysis of six factor XIII-A-deficient families in Southern Pakistan. *Br J Haematol*. 2000;109(2):463.
- El Mahmoudi H, Amor M, Gouider E, et al. Small insertion (c. 869insC) within F13A gene is dominant in Tunisian patients with inherited FXIII deficiency due to ancient founder effect. *Haemophilia*. 2009;15(5):1176-9.
- Louhichi N, Medhaffar M, Hadsalem I, et al. Congenital factor XIII deficiency caused by two mutations in eight Tunisian families: molecular confirmation of a founder effect. *Ann Hematol*. 2010;89(5):499-504.
- Schroeder V, Meili E, Cung T, et al. Characterisation of six novel A-subunit mutations leading to congenital factor



XIII deficiency and molecular analysis of the first diagnosed patient with this rare bleeding disorder. *Thromb Haemost.* 2006;95(01):77-84.

31. Mikkola H, Yee VC, Syrjala M, et al. Four novel mutations in deficiency of coagulation factor XIII: consequences to expression and structure of the A-subunit. *Blood.* 1996;87(1):141-51.
32. Mikkola H, Syrjala M, Rasi V, et al. Deficiency in the A-subunit of coagulation factor XIII: two novel point mutations demonstrate different effects on transcript levels. *Blood.* 1994; 84(2):517-25.
33. Palotie A, Mikkola H, Muszbek L, et al. Molecular mechanisms of mutations in factor XIII A-subunit deficiency: in vitro expression in COS-cells demonstrates intracellular degradation of the mutant proteins. *Thromb Haemost.* 1997;77(06):1068-72.
34. Kulkarni BP, Nair SB, Vijapurkar M, et al. Molecular pathology of rare bleeding disorders (RBDs) in India: A systematic review. *PLoS one.* 2014;9(10):e108683.
35. Anwar R, Gallivan L, Miloszewski KJ, et al. Splicing and missense mutations in the human FXIII gene causing FXIII deficiency: effects of these mutations on FXIII RNA processing and protein structure. *Br J Haematol.* 1998;103(2):425-8.
36. Vreken P, Niessen RW, Peters M, et al. A point mutation in an invariant splice acceptor site results in a decreased mRNA level in a patient with severe coagulation factor XIII subunit A deficiency. *Thromb Haemost.* 1995;74(02):584-9.
37. Dorgalaleh A, Tabibian S, Shams M, et al. A unique factor XIII mutation in southeastern Iran with an unexpectedly high prevalence: Khash factor XIII. *Semin Thromb Hemost.* 2019 ;45(1):43-49.
38. Asakai R, Chung DW, Davie EW, et al. Factor XI deficiency in Ashkenazi Jews in Israel. *N Engl J Med.* 1991;325(3):153-8.
39. Butler JM. Short tandem repeat analysis for human identity testing. *Curr Protoc Hum Genet.* 2004;41(1): Chapter 14:Unit 14.8.
40. Chanock S. Candidate genes and single nucleotide polymorphisms (SNPs) in the study of human disease. *Dis Markers.* 2001;17(2):89-98.
41. Saint Pierre A, Génin E. How important are rare variants in common disease? *Brief Funct Genomics.* 2014;13(5):353-61.
42. Silberstein M, Weissbrod O, Otten L, et al. A system for exact and approximate genetic linkage analysis of SNP data in large pedigrees. *Bioinformatics.* 2012;29(2):197-205.
43. Panagiotou OA, Evangelou E, Ioannidis JP. Genome-wide significant associations for variants with minor allele

frequency of 5% or less—an overview: A HuGE review. *Am J Epidemiol.* 2010;172(8):869-889.

44. Kangsadalampai S, Coggan M, Caglayan SH, et al. Application of HUMF13A01 (AAAG) n STR polymorphism to the genetic diagnosis of coagulation factor XIII deficiency. *Thromb Haemost.* 1996;76(6): 879-82.
45. Li Y-C, Korol AB, Fahima T, et al. Microsatellites within genes: structure, function, and evolution. *Mol Biol Evol.* 2004;21(6):991-1007.
46. Frayling I.M. ME, Butler R. PCR-Based Methods for Mutation Detection. In: Tsongalis WBCJ. *Molecular Diagnostics.* Humana Press; 2006. p. 510.
47. Naderi M, Dorgalaleh A, Tabibian S, et al. Current understanding in diagnosis and management of factor XIII deficiency. *Iran J Ped Hematol Oncol.* 2013;3(4):164.
48. Dorgalaleh A, Farshi Y, Alizadeh S, et al. Challenges in implementation of ISTH diagnostic algorithm for diagnosis and classification of factor XIII deficiency in Iran. *J Thromb Haemost.* 2015;13(9):1735-6.
49. Dorgalaleh A, Assadollahi V, Tabibian S, et al. Molecular basis of congenital factor XIII deficiency in Iran. *Clin Appl Thromb Hemost.* 2018;24(2):210-6.
50. Hammond HA, Jin L, Zhong Y, et al. Evaluation of 13 short tandem repeat loci for use in personal identification applications. *Am J Hum Genet.* 1994;55(1):175.
51. Sprecher CJ, Puers C, Lins AM, et al. General approach to analysis of polymorphic short tandem repeat loci. *Biotechniques.* 1996;20(2):266-76.
52. Hearne CM, Ghosh S, Todd JA. Microsatellites for linkage analysis of genetic traits. *Trends Genet.* 1992;8(8):288-94.
53. Polymeropoulos M, Rath D, Xiao H, et al. Tetranucleotide repeat polymorphism at the human coagulation factor XIII A subunit gene (F13A1). *Nucleic Acids Res.* 1991;19(15):4306.
54. Twyman RM, Primrose SB. Techniques patents for SNP genotyping. *Pharmacogenomics.* 2003;4(1):67-79.
55. Norrgard K, Schultz J. Using SNP data to examine human phenotypic differences. *Nature Education.* 2008;1(1):85.
56. Shahraki H, Fathi M, Tabibian S, et al. Indirect Molecular Diagnosis of Congenital Factor XIII Deficiency by Candidate Microsatellites and Single Nucleotide Polymorphisms. *Iran J Ped Hematol Oncol.* 2020;10(2):114-30.