Location of the gene causing hyperimmunoglobulinemia D and periodic fever syndrome differs from that for familial mediterranean fever

Received: 8 June 1994 / Revised: 27 June 1994

Abstract The hyperimmunoglobulinemia D and periodic fever (hyper-IgD) syndrome is typified by recurrent febrile attacks with abdominal distress, joint involvement (arthralgia/arthritis), headache, skin lesions, and an elevated serum IgD level (>100 U/ml). This familial disorder has been diagnosed in 56 subjects worldwide. As the hyper-IgD syndrome resembles familial Mediterranean fever, one could speculate that both result from mutations in the same gene. The gene causing familial Mediterranean fever (MEF) has been located on chromosome 16p. We have studied 10 families with 19 affected and 28 non-affected subjects. The clinical findings and IgD determinations from these families are compatible with autosomal recessive inheritance. Using highly polymorphic markers surrounding the MEF gene, only negative Lod scores were obtained, whereas haplotype analysis excluded this locus as the cause of the hyper-IgD syndrome. In addition, no indication for linkage was obtained with markers from other candidate gene regions on chromosomes 17q and 14q.

Introduction

The hyperimmunoglobulinemia D and periodic fever syndrome (hyper-IgD) is a rare entity characterized by recurrent attacks of fever (Van der Meer et al. 1984). Symptoms start at an early age and persist throughout life (Drenth et al. 1994a). Diagnosis is made by using clinical criteria allowing distinction from other periodic fever syndromes, such as familial Mediterranean fever (FMF), adult-onset Still’s disease, and juvenile chronic arthritis (Drenth et al. 1994a). Typically, the attacks occur every 4–8 weeks and last 3–7 days; they are accompanied by abdominal distress (vomiting, diarrhoea, and pain), joint involvement (arthralgia/arthritis), skin lesions, headache, and lymphadenopathy (Drenth et al. 1994a, b; Van der Meer et al. 1984). All patients have a persistently elevated polyclonal serum IgD level (>100 U/ml) (Hiemstra et al. 1989). The pathogenesis of the hyper-IgD syndrome remains an enigma and consequently therapy is solely supportive. So far, 56 patients (29 male/27 female) from nine countries have been diagnosed. Autosomal recessive inheritance is suggested by the finding that in seven families, two or more sibs are affected, whereas the parents are unaffected. Serum IgD measurements in one family revealed high values in patients and low values in unaffected members (<100 U/ml), supporting the concept of autosomal recessive inheritance (Reeves and Mitchell 1984).

The febrile attacks of the hyper-IgD syndrome and FMF have much in common, despite some clinical differences, such as lymphadenopathy (rare in FMF), serositis (rare in hyper-IgD syndrome), and amyloidosis (not seen in hyper-IgD syndrome). Both syndromes are typified by recurrent abdominal distress, articular symptoms, and skin manifestations.

There are also similarities in the biochemical changes that accompany attacks, namely, high erythrocyte sedimentation rate, leukocytosis, and high levels of C-reactive protein (Drenth et al. 1994a; Meyerhoff 1980). In view of these similarities, it could be speculated that FMF and the hyper-IgD syndrome are variants of one condition (Feder-spiel and Tonz 1987; Majeed and Barakat 1989), and that both syndromes are allelic and produced by defects in the same gene. Initially, in Israeli families of North African and Iraqi (non-Askhenazi) descent, linkage was indicated between FMF and markers on chromosome 17q22-q24 (Aksentijevich et al. 1993a). A maximum multipoint Lod score of 3.27 was reached approximately 10 centimorgans (cM) telomeric to D17S40. Subsequent linkage studies...
have however failed to support chromosome 17q as the location for the responsible gene (Aksentijevich et al. 1993a). In the same non-Askhenazi Israeli families, the gene causing FMF (the MEF gene) could be mapped to the short arm of chromosome 16 (Pras et al. 1992). Using marker D16S84 (16p13.3), a lod score of 9.17 was reached at a recombination frequency (θ) of 0.04. These results also pertain to Armenian families suffering from FMF (Shohat et al. 1992). Refined mapping with highly polymorphic markers resulted in the localization of the MEF gene less than 1 cM centromeric from D16S246 (Aksentijevich et al. 1993b; Levy et al. 1993). Such accurate localization allows us to examine the role of the MEF gene in the hyper-IgD syndrome.

**Materials and methods**

**Patients**

The present study included 10 families with members suffering from the hyper-IgD syndrome (Fig. 1). Seven families originate from the Netherlands (nos. 2, 5, 8–10), the other three families are from the United Kingdom (no. 6), France (no. 1), and Spain (no. 7), respectively. There were no consanguineous marriages. In total, 19 affected and 28 non-affected family members were investigated. The clinical data pertaining to these patients have been published elsewhere and the diagnosis of hyper-IgD syndrome was made according to published criteria (Drenth et al. 1994a). Briefly, the patients suffer from life-long recurrent self-limiting attacks of fever, with no known antigenic triggers, lasting 3–7 days and accompanied by one or a combination of the following symptoms: abdominal distress (vomiting, diarrhea, pain), skin manifestations, arthralgia/arthritis, and/or lymphadenopathy. A detailed family history and pedigree were obtained by interviewing each patient; a comprehensive medical history was also taken from each unaffected family member. Immunoglobulin D concentrations were measured by enzyme-linked immunosorbent assay with a detection limit of 1 U/ml. The study was approved by the Medical Ethics Committee of the University Hospital St Radboud, Nijmegen.

**DNA analysis**

Blood was sampled from relevant family members, and genomic DNA was isolated according to the method of Miller et al. (1988). The markers studied were D16S418, D16S423, D16S283, and D16S291 (chromosome 16p13.3), D17S515 (chromosome 17q22-24), and D14S78 (chromosome 14q32-33).

All markers were analyzed using polymerase chain reaction amplification of genomic DNA (50 ng) in a 15-ml reaction mixture containing 200 μM of each dATP, dGTP, dTTP, 0.6 μCi 32P-dCTP (10 mCi/ml, 3000 Ci/mmol), 1 × Supertaq buffer [10 mM TRIS-HCl pH 9.0, 50 mM KCl, 1.5 mM MgCl2, 0.1% Triton X-100, 0.01% (w/v) gelatin] and 0.06 U Supertaq (HT Biotechnology, United Kingdom) overlayed with mineral oil. After an ini-

---

**Fig. 1** Ten hyper-IgD families studied for linkage analysis with polymorphic markers. In total, 19 affected patients and 33 non-affected family members were present. Results of IgD measurements in U/ml are shown for each individual. Note the high serum IgD concentrations in patients (>100 U/ml) and the low values for unaffected individuals (<100 U/ml)
The genetic distances (sex averaged) are given in cM according to the microsatellite markers examined in the current study (Aksentijevich et al. 1993a). Multi-point linkage analysis indicates that the most likely position of the gene was at 10cM telomeric to D17S40. However, linkage analysis in our families with the marker D17S515, which has been mapped at this location (NIH/CEPH collaborative mapping group 1992), resulted in a negative lod score (Table 1). A region of about 30cM surrounding this marker locus was excluded; this argues against the 17q region as the location of the gene for hyper-IgD syndrome.

Another candidate locus is the immunoglobulin heavy chain gene cluster on chromosome 14q32.3 (Hofker et al. 1989). The high serum IgD concentration persists during the entire disease course of FMF and also during the development of FMF. These findings exclude the MEF gene as the cause for hyper-IgD syndrome in these families. After the exclusion of the MEF gene, we decided to test two other candidate regions.

Markers from the region 17q22-q24 have previously shown linkage with the disorder in a subset of MEF families (Aksentijevich et al. 1993a). Multi-point linkage analysis indicates that the most likely position of the gene was at 10cM telomeric to D17S40. However, linkage analysis in our families with the marker D17S515, which has been mapped at this location (NIH/CEPH collaborative mapping group 1992), resulted in a negative lod score (Table 1). A region of about 30cM surrounding this marker locus was excluded; this argues against the 17q region as the location of the gene for hyper-IgD syndrome.

Another candidate locus is the immunoglobulin heavy chain gene cluster on chromosome 14q32.3 (Hofker et al. 1989). The high serum IgD concentration persists during the entire disease course of FMF and also during the development of FMF. These findings exclude the MEF gene as the cause for hyper-IgD syndrome in these families. After the exclusion of the MEF gene, we decided to test two other candidate regions.

Markers from the region 17q22-q24 have previously shown linkage with the disorder in a subset of MEF families (Aksentijevich et al. 1993a). Multi-point linkage analysis indicates that the most likely position of the gene was at 10cM telomeric to D17S40. However, linkage analysis in our families with the marker D17S515, which has been mapped at this location (NIH/CEPH collaborative mapping group 1992), resulted in a negative lod score (Table 1). A region of about 30cM surrounding this marker locus was excluded; this argues against the 17q region as the location of the gene for hyper-IgD syndrome.

Another candidate locus is the immunoglobulin heavy chain gene cluster on chromosome 14q32.3 (Hofker et al. 1989). The high serum IgD concentration persists during the entire disease course of FMF and also during the development of FMF. These findings exclude the MEF gene as the cause for hyper-IgD syndrome in these families. After the exclusion of the MEF gene, we decided to test two other candidate regions.

Markers from the region 17q22-q24 have previously shown linkage with the disorder in a subset of MEF families (Aksentijevich et al. 1993a). Multi-point linkage analysis indicates that the most likely position of the gene was at 10cM telomeric to D17S40. However, linkage analysis in our families with the marker D17S515, which has been mapped at this location (NIH/CEPH collaborative mapping group 1992), resulted in a negative lod score (Table 1). A region of about 30cM surrounding this marker locus was excluded; this argues against the 17q region as the location of the gene for hyper-IgD syndrome.

Another candidate locus is the immunoglobulin heavy chain gene cluster on chromosome 14q32.3 (Hofker et al. 1989). The high serum IgD concentration persists during the entire disease course of FMF and also during the development of FMF. These findings exclude the MEF gene as the cause for hyper-IgD syndrome in these families. After the exclusion of the MEF gene, we decided to test two other candidate regions.

Markers from the region 17q22-q24 have previously shown linkage with the disorder in a subset of MEF families (Aksentijevich et al. 1993a). Multi-point linkage analysis indicates that the most likely position of the gene was at 10cM telomeric to D17S40. However, linkage analysis in our families with the marker D17S515, which has been mapped at this location (NIH/CEPH collaborative mapping group 1992), resulted in a negative lod score (Table 1). A region of about 30cM surrounding this marker locus was excluded; this argues against the 17q region as the location of the gene for hyper-IgD syndrome.

Another candidate locus is the immunoglobulin heavy chain gene cluster on chromosome 14q32.3 (Hofker et al. 1989). The high serum IgD concentration persists during the entire disease course of FMF and also during the development of FMF. These findings exclude the MEF gene as the cause for hyper-IgD syndrome in these families. After the exclusion of the MEF gene, we decided to test two other candidate regions.

Markers from the region 17q22-q24 have previously shown linkage with the disorder in a subset of MEF families (Aksentijevich et al. 1993a). Multi-point linkage analysis indicates that the most likely position of the gene was at 10cM telomeric to D17S40. However, linkage analysis in our families with the marker D17S515, which has been mapped at this location (NIH/CEPH collaborative mapping group 1992), resulted in a negative lod score (Table 1). A region of about 30cM surrounding this marker locus was excluded; this argues against the 17q region as the location of the gene for hyper-IgD syndrome.

Another candidate locus is the immunoglobulin heavy chain gene cluster on chromosome 14q32.3 (Hofker et al. 1989). The high serum IgD concentration persists during the entire disease course of FMF and also during the development of FMF. These findings exclude the MEF gene as the cause for hyper-IgD syndrome in these families. After the exclusion of the MEF gene, we decided to test two other candidate regions.

Markers from the region 17q22-q24 have previously shown linkage with the disorder in a subset of MEF families (Aksentijevich et al. 1993a). Multi-point linkage analysis indicates that the most likely position of the gene was at 10cM telomeric to D17S40. However, linkage analysis in our families with the marker D17S515, which has been mapped at this location (NIH/CEPH collaborative mapping group 1992), resulted in a negative lod score (Table 1). A region of about 30cM surrounding this marker locus was excluded; this argues against the 17q region as the location of the gene for hyper-IgD syndrome.

Another candidate locus is the immunoglobulin heavy chain gene cluster on chromosome 14q32.3 (Hofker et al. 1989). The high serum IgD concentration persists during the entire disease course of FMF and also during the development of FMF. These findings exclude the MEF gene as the cause for hyper-IgD syndrome in these families. After the exclusion of the MEF gene, we decided to test two other candidate regions.

Markers from the region 17q22-q24 have previously shown linkage with the disorder in a subset of MEF families (Aksentijevich et al. 1993a). Multi-point linkage analysis indicates that the most likely position of the gene was at 10cM telomeric to D17S40. However, linkage analysis in our families with the marker D17S515, which has been mapped at this location (NIH/CEPH collaborative mapping group 1992), resulted in a negative lod score (Table 1). A region of about 30cM surrounding this marker locus was excluded; this argues against the 17q region as the location of the gene for hyper-IgD syndrome.

Another candidate locus is the immunoglobulin heavy chain gene cluster on chromosome 14q32.3 (Hofker et al. 1989). The high serum IgD concentration persists during the entire disease course of FMF and also during the development of FMF. These findings exclude the MEF gene as the cause for hyper-IgD syndrome in these families. After the exclusion of the MEF gene, we decided to test two other candidate regions.

Markers from the region 17q22-q24 have previously shown linkage with the disorder in a subset of MEF families (Aksentijevich et al. 1993a). Multi-point linkage analysis indicates that the most likely position of the gene was at 10cM telomeric to D17S40. However, linkage analysis in our families with the marker D17S515, which has been mapped at this location (NIH/CEPH collaborative mapping group 1992), resulted in a negative lod score (Table 1). A region of about 30cM surrounding this marker locus was excluded; this argues against the 17q region as the location of the gene for hyper-IgD syndrome.

Another candidate locus is the immunoglobulin heavy chain gene cluster on chromosome 14q32.3 (Hofker et al. 1989). The high serum IgD concentration persists during the entire disease course of FMF and also during the development of FMF. These findings exclude the MEF gene as the cause for hyper-IgD syndrome in these families. After the exclusion of the MEF gene, we decided to test two other candidate regions.
non-symptomatic periods, and other serum immunoglobulins such as IgA and IgG3 can also be elevated in patients with hyper-IgD syndrome. One could therefore speculate that a mutation at the Ig-locus might interfere with the regulation of several members of the gene cluster. Although such a mutation would be anticipated to act dominantly, we have performed linkage analysis with the marker D14S78, which is located an estimated distance of 8 cM from the Ig-locus. Although the Ig-locus cannot be firmly excluded (Table 1), the negative Lod score would not support the presence of a mutation in the immunoglobulin heavy chain gene cluster causing hyper-IgD syndrome.

In summary, linkage analysis in 10 families with the hyper-IgD syndrome demonstrates that, despite many of the symptoms of the hyper-IgD syndrome being similar to FMF, the MEF gene can be unequivocally excluded as the primary disease locus for the hyper-IgD syndrome. This finding firmly establishes that the hyper-IgD syndrome and FMF are two distinct genetic disorders. Furthermore, we have found no indication of linkage with markers on chromosome 17q (foregoing evidence suggested linkage with FMF) or 14q (immunoglobulin heavy chain cluster). The localization of the gene may require a search with markers equally spaced along the entire human genome.
Acknowledgements  J.P.H. Drenth is a recipient of a Dutch Organization for Scientific Research fellowship for Clinical Investigators (KWO 900-716-065).

Appendix

Members of the International Hyper IgD study group are as follows: J.P.H. Drenth, J.W.M. van der Meer, C.M.R. Weemaes, University Hospital St Radboud, Nijmegen, The Netherlands; J.W.J. Bijlsma, University Hospital Utrecht, E.R. de Graeff-Meeder, Wilhelmina Children’s Hospital, Utrecht, The Netherlands; M. Alcalay, Hospital Jean Bernard, Poitiers, France; C. Chapelon-Abric, Hospital Pitié Salpétrière; M.F. Kahn, Hospital Bichat, A.M. Prieur, Hospital Necker Enfants Malades, J. Sibilia, Hospital St. Louis, Paris, France; C. Morand, Hospital Augustin Morvan, Brest, France; R.J. Powell, Queen’s Medical Centre, Nottingham, United Kingdom; R. Topaloglu, U. Saatçi, Hacettepe Children’s Hospital, Ankara, Turkey; M. Alcalay, Hospital Jean Bernard, Poitiers, France; C. Chapelon-Abric, Hospital Pitié Salpétrière; M.F. Kahn, Hospital Bichat, A.M. Prieur, Hospital Necker Enfants Malades, J. Sibilia, Hospital St. Louis, Paris, France; C. Morand, Hospital Augustin Morvan, Brest, France; R.J. Powell, Queen’s Medical Centre, Nottingham, United Kingdom.

The underlined members of the study group provided blood samples and clinical data from their patients and families.

References