

# MOLECULAR CHARACTERIZATION OF PAEDIATRIC IDIOPATHIC HYPEREOSINOPHILIA

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## ▶ To cite this version:

Maria Cristina Rapanotti, Roberta Caruso, Emanuele Ammatuna, Serena Zaza, Laura Trotta, et al.. MOLECULAR CHARACTERIZATION OF PAEDIATRIC IDIOPATHIC HYPEREOSINOPHILIA. British Journal of Haematology, 2010, 151 (5), pp.440. 10.1111/j.1365-2141.2010.08394.x hal-00586991

# HAL Id: hal-00586991 https://hal.science/hal-00586991v1

Submitted on 19 Apr 2011  $\,$ 

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Journal:	British Journal of Haematology				
Manuscript ID:	BJH-2010-00958.R1				
Manuscript Type:	Ordinary Papers				
Date Submitted by the Author:	21-Jul-2010				
Complete List of Authors:	Rapanotti, Maria Cristina; University of Rome, Department of Laboratory Medicine, Policlinico "Tor Vergata ", Rome, Italy; "Fondazione Santa Lucia" - IRCCS, Neuro-Oncohaematology Laboratory Caruso, Roberta; Bambino Gesu`"Children's Hospital," IRCCS, Hematology Unit Ammatuna, Emanuele; University of Rome "Tor Vergata", Department of Biopathology; "Fondazione Santa Lucia" - IRCCS, Neuro-Oncohaematology Laboratory Zaza, Serena; University of Rome "Tor Vergata", Department of Biopathology; "Fondazione Santa Lucia" - IRCCS, Neuro- Oncohaematology Laboratory Trotta, Laura; Bambino Gesu`"Children's Hospital," IRCCS, Hematology Unit Divona, Mariadomenica; University of Rome "Tor Vergata", Department of Medicine Laboratory; "Fondazione Santa Lucia" - IRCCS, Neuro-Oncohaematology Laboratory Funaro, Daria; Bambino Gesu`"Children's Hospital," IRCCS, Hematology Unit Divona, Mariadomenica; University of Rome "Tor Vergata", Department of Medicine Laboratory; "Fondazione Santa Lucia" - IRCCS, Neuro-Oncohaematology Laboratory Funaro, Daria; Bambino Gesu`"Children's Hospital," IRCCS, Hematology Unit Cicconi, Laura; University of Rome "Tor Vergata", Department of Biopathology Federici, Giorgio; University of Rome "Tor Vergata", Department of Biopathology De Rossi, Giulio; Bambino Gesu`"Children's Hospital," IRCCS, Hematology Unit Lo Coco, Francesco; University of Rome "Tor Vergata", Department of Biopathology De Rossi, Giulio; Bambino Gesu`"Children's Hospital," IRCCS, Hematology Unit Lo Coco, Francesco; University of Rome "Tor Vergata", Department of Biopathology; "Fondazione Santa Lucia" - IRCCS, Neuro- Oncohaematology Laboratory; University of Rome "Tor Vergata", Department of Biopathology; "Fondazione Santa Lucia" - IRCCS, Neuro- Oncohaematology Laboratory; University of Rome "Tor Vergata", Department of Medicine Laboratory				
Key Words:	Hypereosinophilia, CHILDHOOD HAEMATOLOGICAL MALIGNANCIES, CLONALITY, IgH, MOLECULAR DIAGNOSIS				



## MOLECULAR CHARACTERIZATION OF <u>PAEDIATRIC</u> IDIOPATHIC HYPEREOSINOPHILIA

\*Maria Cristina Rapanotti<sup>1,2,3</sup>, \*Roberta Caruso<sup>4</sup>, Emanuele Ammatuna<sup>2,3</sup>, Serena Zaza<sup>2,3</sup>, Laura Trotta<sup>4</sup>, Mariadomenica Divona<sup>2,3</sup>, Laura Cicconi<sup>2</sup>, Daria Funaro<sup>4</sup>, Giorgio Federici<sup>1</sup>, Sergio Amadori <sup>2</sup>, Giulio De Rossi <sup>4</sup>, Francesco Lo-Coco<sup>2,3</sup>

<sup>1</sup> Department of Laboratory Medicine, Policlinico "Tor Vergata", Rome, Italy
 <sup>2</sup>Department of Biopathology, University of Tor Vergata
 <sup>3</sup>Laboratorio di Neuro-Oncoematologia, Fondazione Santa Lucia, Rome, Italy
 <sup>4</sup>Hematology Unit-"Bambino Gesu"Children Hospital, IRCCS, Rome, Italy

\*These authors have equally contributed to this work

RUNNING TITLE: Molecular features of paediatric hypereosinophilia

#### **Corresponding author: Maria Cristina Rapanotti, PhD** Department of Laboratory Medicine Policlinico "Tor Vergata " University of Rome Viale Oxford 81 - 00133 - Rome - Italy

Tel: 39 06-20902169 Fax: 39 06-20902359 E-mail: <u>cristinarapanotti@yahoo.it</u>

\*These authors have equally contributed to this work

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## Summary

Hypereosinophilic <u>syndromes</u> (HES) include a group of heterogeneous diseases <u>characterized</u> by the persistent increase of the <u>number of eosinophils in blood and bone marrow</u>. Few cases of <u>paediatric</u> hypereosinophilia (pHES) have been described in the literature. Early identification of pHES <u>that may evolve</u> towards a lymphomyeloproliferative disease is relevant in light of prognostic and therapeutic implications. Molecular features of 10 pHES patients were analysed at presentation and during their clinical outcome, <u>including</u> analysis of *BCR-ABL* and *FIP1L1/PDGFRA* fusion genes, <u>quantitation of Wilm's tumour suppressor gene copy number and clonality of T-cell receptor</u> and immunoglobulin heavy chain (IgH). All patients had normal karyotype and germ line T-cell receptor configuration. Five children showed IgH clonality at presentation: of these, <u>two</u> developed a <u>B non-Hodgkin lymphoma and a B-lineage acute lymphocytic leukaemia</u> at <u>six</u> and 12 months, respectively, <u>two spontaneously reverted</u> to a polyclonal IgH profile during the follow-up, and the last one persisted with pHES without B-clonal evolution after 19 months. One patient <u>had</u> a *PDGFRA/FIP1L1* fusion and achieved hematologic and molecular remission after imatinib therapy. IgH rearrangement <u>was observed</u> to be a frequent molecular feature of pHES <u>in children</u> and may precede <u>B-cell clonal</u> expansion and evolution into B-cell malignancies.

#### Introduction

Hypereosinophilic <u>syndromes</u> (HES) include a group of heterogeneous diseases characterized by the persistent increase of eosinophil numbers in the peripheral blood and the bone marrow (Chusid *et al.*, 1975; Brito-Bapapulle *et al.*, 2003, Bain *et al.*, 2004, Gleich and Leiferman, 2009). HES is predominantly a disease of males (<u>male:female</u> ratio 9:1) and is usually diagnosed between the ages of 20 and 50 years. Tissue infiltration by eosinophils is responsible for the end-organ damage <u>that</u> results from the activity of proteins released by the eosinophil granules. A major change in the new WHO 2008 classification was the reorganization of chronic eosinophilic <u>leukaemia</u> CEL/HES into "<u>CEL</u> not otherwise specified (CEL, NOS)" and <u>"myeloid</u> and lymphoid neoplasms with eosinophilia associat<u>ed</u> with *PDGFRA*, *PDGFRB*, and *FGFR1* abnormalities" (Klion *et al.*, 2006; Bain *et al.*, 2009).

The relevance of identifying PDGFR-rearranged eosinophilic disorders is related to the efficacy of treatment with imatinib mesylate, (Cools *et al.*, 2004; Gotlib *et al.*, 2004; Helbig *et al.*, 2008). However, the myeloproliferative CEL, NOS are <u>also</u> frequently responsive to imatinib, suggesting that other as yet unrecognized mutations affecting tyrosine kinases may underlie their pathogenesis (Salem *et al.*, 2003).

A diagnosis of CEL, NOS requires evidence of clonality of the eosinophils. Since in many cases it is impossible to define clonality, the diagnosis of idiopathic HES is still made. The diagnosis of idiopathic HES is based on exclusion criteria and frequently remains doubtful because of the lack of genetic markers (Brito-Bapapulle et al., 2003). Early discrimination between idiopathic HES confined to an unidentified reactive process and hypereosinophilia accompanied by a clonal proliferation eventually evolving into a lymphoproliferative disease is relevant in light of its obvious prognostic and therapeutic implications (Smith et al., 2004; Roche-Lestienne et al., 2005). In the latter case, the hypereosinophilia is the result of a primitive T or B lymphoid disorder and can be considered as an epiphenomenon. Long-term evolution of this form of hypereosinophilia is often complicated by <u>T-cell</u> lymphoma or <u>leukaemia</u>, indicating that T cells are involved in the pathogenesis of these disorders (Raghavar et al., 1987; Cogan et al., 1994; Roufosse et al., 2000; Bank et al., 2001; Roumier et al., 2003). Evolution into <u>B-cell</u> malignancies has been occasionally reported both in adults and in childhood (Blatt et al., 1992; Urtasùn et al., 2001; Bernasconi, 2001; Hill et al., 2003; Wynn et al., 2003; Horigome et al., 2005; Rapanotti et al., 2005; Bhatti et al., 2009). Finally, the expression level of WT1 has been recently investigated as an additional marker to the standard parameters so far considered in the diagnosis of CEL, NOS in the adult population,

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 and <u>it seems to be particularly useful in cases where standard molecular and cytogenetic analyses</u> are not informative (Cilloni *et al.*, 2007).

Few\_cases of pHES have been described in the literature (Blatt *et al.*, 1992; Urtasùn *et al.*, 2001; Bernasconi, 2001; Hill *et al.*, 2003; Scheinfeld *et al.*, 2003; Wynn *et al.*, 2003; Chien *et al.*, 2004; Horigome *et al.*, 2005; Rapanotti *et al.*, 2005; Rives *et al.*, 2005; Farruggia *et al.*, 2009). pHES <u>has</u> <u>a</u> slight male predominance and <u>shows a</u> distinct biologic and clinical course <u>compared with the</u> adult forms. The disease in children is commonly associated with chromosomal abnormalities, including trisomy 8 and gene rearrangements <u>that</u> may involve *ABL* (Brito-Bapapulle *et al.*, 2003, Bain *et al.*, 2004). In addition, pHES has <u>also</u> been described in association with acute lymphoblastic <u>leukaemia</u>, while the abnormal fusion *FIP1L1/PDGFRA* <u>has rarely been found</u> (Rives *et al.*, 2005), and evolution of idiopathic HES into a B-cell neoplasia has been only occasionally described (Blatt *et al.*, 1992; Jain *et al.*, 2000; Urtasùn *et al.*, 2001; Bernasconi, 2001; Hill *et al.*, 2003; Scheinfeld *et al.*, 2003; Wynn *et al.*, 2003; Chien *et al.*, 2004; Horigome *et al.*, 2005; Rapanotti *et al.*, 2005, D'Angelo *et al.*, 2008). Here, we report the molecular and clinical features of 10 pHES studied at diagnosis and during follow up.

#### **Patients and methods**

#### Patients and healthy donors

Between November 2001 and October 2007, 10 children (<u>six</u> males and <u>four</u> females) with marked hypereosinophilia lasting for at least <u>six</u> months were observed at the <u>Division of Haematology</u>, <u>Bambino Gesù Children's Hospital of Rome</u>. The main clinical and laboratory features at the time of presentation are summarized in Table 1. <u>The</u> median absolute number of eosinophils was 10.1/mm<sup>3</sup> (range 1.5–70.8/mm<sup>3</sup>). Five patients presented with <u>anaemia</u>, while <u>the</u> platelet count was normal in all but one patient (UPN6). In three cases (UPN2, UPN4 and UPN5), there were no signs of organ involvement at diagnosis.

Eosinophil infiltration in the bone marrow at presentation ranged from 21.5% to 80% (median 35%). Cardiac involvement was documented by echocardiography and <u>electrocardiography (EKG)</u> in four patients who presented with chronic cardiac tamponade and pleural effusion, sinus tachycardia, restrictive cardiomyopathy and pancarditis with mitral valvular insufficiency, respectively (UPN3, UPN6, UPN7 and UPN8). Three patients (UPN3, UPN7 and UPN9) presented with pulmonary involvement with interstitiopathy, pleural effusion and asthmatic bronchitis. All but two patients (UPN1 and UPN10) started therapy with steroids (prednisone 1 mg/kg/day) followed

by  $\alpha$ -interferon up to <u>1 MIU</u> three times a week. All patients were followed up at regular intervals with periodic clinical controls and standard laboratory and instrumental evaluation.

#### Clinical and laboratory exams

Bone marrow (BM) aspirate and complete clinical chemistry, including serum immunofixation and IgE count assessed by the PRIST method, and allergic tests (RAST method), were performed in all patients together with blood culture, virological investigations and immunophenotype. Instrumental examinations including chest radiography, abdomen ultrasound, total body computed tomography scan, EKG and echocardiography were carried out to exclude the causes of secondary hypereosinophilia and to evaluate end-organ damage. Immunophenotype was performed by flow cytometry <u>at onset</u> in all cases. The following monoclonal antibodies were used for the characterization of potential abnormal T or B clonal population: CD19, CD10, CD20, CD22, CD24, HLADR, CD3, CD7, CD5, CD4, CD8, CD79a, CD13, CD33, CD34 and TdT.

Genetic studies included conventional karyotyping on bone-marrow-derived G-banded metaphases. Molecular biology analysis was performed by RT-PCR to identify the presence of the *BCR-ABL* and *FIP1L1/PDGFRA* fusion genes (vanDongen *et al.*, 1999; Bacher *et al.*, 2006). In order to assess the clonality of IgH and TCR repertoires, BM genomic DNA was extracted from bone marrow mononuclear cells. TCR clonality was performed by DHPLC sequencing of the TCR $\beta$  genomic region (Cave *et al.*, 1994). IgH clonality analysis was performed on BM genomic DNA by amplifying CDRI, CDRII and CDRIII regions of the heavy chain immunoglobulin genes (IgH-PCR). Amplification of the CDRIII region was performed using CA1 and CA2 primers, respectively, the "consensus primers" for variable and joining regions of the heavy chain (Nizet *et al.*, 1991). Amplifications of CDRI and CDR II were performed using oligo-degenerate sequence primers mapping the frameworks FR2 and FR3, as previously described (Diss *et al.*, 1993).

Quantitative *WT1* assessment (RQ-PCR) and fluorescence measurement were performed on the ABI PRISM 7700 Sequence Detection System (PE Applied Biosystem, Epster City, CA, USA) as described by Cilloni and co-workers (2007).

#### Control populations

Blood samples from 30 healthy donors were taken from the Transfusion Centre as a negative control population. Bone marrow aspirates from 25 B-ALL and peripheral blood from 25 chronic lymphocytic leukaemia (CLL) patients were used <u>as positive controls</u>, all of which had a monoclonal IgH profile and a polyclonal TCR $\beta$  repertoire. To assess the prevalence of IgH rearrangement<u>in</u> chronic myeloid neoplasms, we analysed a cohort of 10 patients affected by

chronic myeloid leukaemia (CML) (<u>five patients</u>), essential thrombocytemia (three patients) and chronic myelomonocytic leukaemia (two patients), <u>all of which demonstrated polyclonal IgH</u>.

#### Results

#### Diagnostic findings

Biological and clinical features at onset are summarized in <u>Table 1</u>. Immunophenotype analysis <u>was</u> normal in all but one patient (UPN9), who showed <u>a</u> very low proportion <u>of T-helper lymphocytes</u>, <u>with a CD4/CD8 ratio of 0.5%</u>. The CD4/CD8 ratio was normal <u>in all other</u> patients. All patients expressed CD33/CD13 antigens in their myeloid compartments, whereas <u>the</u> CD34 marker was never expressed. All patients <u>had a</u> normal karyotype.

<u>Molecular analysis</u> documented a B-clonal disorder showing a monoclonality of the IgH-CDRII region (framework FR2) in 5/10 patients (UPN1, UPN2, UPN7, UPN8 <u>and</u> UPN9). *FIP1L1/PDGFRA* transcript was found in one patient (UPN6) <u>who</u> was diagnosed as having a myeloid neoplasm with eosinophilia and abnormalities of *PDGFRA*. <u>TCR rearrangements</u> were not detected in any of the <u>patients</u>. Quantitative *WT1* <u>analysis</u> was performed in 6/10 patients at presentation (UPN4, UPN5, UPN6, UPN8, UPN9 and UPN10). Over-expression of *WT1* (cut-off > <u>90</u> copies) was detected in 3/6 patients (UPN 4, UPN5 and UPN8).

#### Patient follow-up

A spontaneous reduction of eosinophils with normalization of total blood cell count was observed in <u>two</u> patients (UPN1 and UPN10). Two patients (UPN 4 and UPN 5) were treated with steroid therapy <u>that resulted in</u> a reduction of the eosinophil count within 15 and 20 days, <u>respectively</u>, from treatment initiation, while in <u>another</u> two patients <u>reversion was achieved after</u> the withdrawal of a neurological drug (Clobazam) and surgical correction of a congenital anomaly of the thoracic duct, respectively (UPN2 and UPN3, 7 and 2 months, respectively). B-cell clonality was detected at onset in patients UPN1 and UPN2 and converted spontaneously to <u>a</u> polyclonal profile in subsequent follow-up bone marrow aspirates.

Patient UPN6 started therapy with Imatinib (400 <u>mg/day)</u> and is now in continuous complete molecular and haematological remission with a follow-up of 36 months. <u>Six months after diagnosis</u>, <u>patient UPN7 developed a B- NHL</u> showing the same monoclonal rearrangement IgH-CDRII (framework FR2) documented at the onset.

Patient UPN8 was treated for one year with steroids and  $\alpha$ -interferon, achieving a decrease of hypereosinophilia prior to development of <u>B-lineage ALL</u>. The patient was treated according to the

AIEOP LAL 2006 protocol, <u>eventually</u> obtaining complete remission, which is currently maintained at a follow-up of 24 months. Karyotype and T-cell configuration were normal and polyclonal, respectively, in both UPN7 and UPN8. Patient UPN9, who showed monoclonality <u>in the IgH-</u> CDRII region both at onset and in follow-up marrow samples without any evidence of a Blymphoid malignancy, is still under treatment with  $\alpha$ -interferon because of skin and lung involvement at onset. She had complete regression of organ involvement after a follow-up of 19 months.

#### Discussion

According to the scarce <u>existing</u> literature on pHES, most patients with persistent <u>hypereosinophilia</u> do not <u>show</u> known molecular lesions at presentation. <u>Hence</u>, diagnostic refinement of the disease remains difficult, and frequently malignancy of hypereosinophilia may be defined only after a careful clinical and biologic follow-up (Blatt *et al.*, 1992; Jain *et al.*, 2000; Urtasùn *et al.*, 2001; Bernasconi, 2001; Hill *et al.*, 2003; Scheinfeld *et al.*, 2003; Wynn *et al.*, 2003; Chien *et al.*, 2004; Horigome *et al.*, 2005; Rapanotti *et al.*, 2005; Rives *et al.*, 2005, D'Angelo *et al.*, 2008). Moreover, to the best of our knowledge, no studies have systematically analysed TCR and IgH clonality in a sizable number of pHES.

In the present series, 6/10 patients with hypereosinophilia fulfilling the criteria of persistent (> 6 mos) and elevated (>  $1.5 \times 10^{9}$ /L) eosinophil count had molecular evidence of WBC clonality, including monoclonal IgH rearrangement in <u>five</u> patients and *FIP1L1/PDGFRA* fusion in <u>one</u>. The remaining <u>four</u> patients <u>showed</u> polyclonal B- and T-cell repertoires and had no detectable cytogenetic and molecular aberrations. We note however that lesions other than the *FIP1L1/PDGFRA* fusion have been reported in adults with hypereosinophilia. These may involve *PDGFRA*, *PDGFRB* and *FGFR1* through other fusions and point mutations (Klion *et al.*, 2006; Teffery *et al.*, 2006; Bain *et al.*, 2009). Unfortunately, we were not able to search for these alterations in the present series because of the lack of adequate material.

B-cell clonality was the most frequently detected alteration in our pHES patients (50%). In particular, in two cases (UPN7 and UPN8) a monoclonal rearrangement of the IgH-CDRII was already detectable in the marrow <u>at six</u> and 12 months, respectively, prior to the development of a B-cell lymphoproliferative disorder, clearly indicating clonal evolution. While the origin of the neoplastic proliferation from the same clone detected at diagnosis is documented by the same IgH rearrangement, it remains unclear whether a second undetected alteration might have <u>occurred that</u> contributed to successive clonal expansion and overt lymphoproliferative disease. However, our

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results also suggest that detection of B-cell clonality at presentation does not invariably imply subsequent development of a neoplastic lymphoproliferative disease, as shown by the two patients with clonal IgH that did not show any progression in successive clinical and molecular evaluations. In an attempt to interpret these latter findings, we can hypothesize that B-cell clonality might, in these patients, remain under the control of the immune system and be extinguished after the stimulus has ceased. Interestingly, as shown in UPN2, IgH clonality might accompany a clearly reactive and transient pHES, whereby a drug used for the underlying <u>neurological</u> disease was most likely responsible for the prolonged hypereosinophilia. Precursor B-acute lymphoblastic leukaemia/lymphoma with exaggerated eosinophilia is a rare entity, with less than 50 cases including adult and paediatric populations reported since 1973, when it was first described by Spitzer and Garson (Spitzer et al., 1973; D'Angelo et al., 2008). The most common cytogenetic abnormality encountered in ALL with eosinophilia is the t(5;14), which is characterized by overproduction of interleukin 3 (IL-3) (Meeker et al., 1990). The latter entity is now included as "B lymphoblastic leukaemia/lymphoma with t(5;14); IL-3-IgH" in the new WHO classification of lymphoid neoplasms published in 2008 (Meeker et al., 1990, Swerdlow et al., 2008). In this case, eosinophilia is secondary to overproduction of IL-3 by the lymphoblasts, resulting from activation of the <u>IL-3 gene</u> on chromosome 5 after its translocation adjacent to the <u>IgH gene</u> on <u>chromosome</u> 14 (Meeker et al., 1990).

IgH rearrangement was present in <u>five of our</u> cases at the time of diagnosis of hypereosinophilia, was associated with <u>a</u> normal karyotype and antedated the development of a B-cell disease by several months in the two cases (UPN7 and UPN8) <u>where this occurred</u>.

In our study, we were not able to find a correlation between the level of hypereosinophilia at presentation and its possible <u>aetiology</u>. In addition, even if the WHO classification <u>does not</u> include *WT1* analysis in the diagnostic screening of <u>hypereosinophilic</u> syndrome, a supplementary role of this assay has recently been reported for <u>the</u> adult population (Cilloni *et al.*, 2007). <u>With respect to the question of whether WT1</u> expression in children is different from that in adults, we did not find any correlation between *WT1* expression levels and the differential diagnosis of <u>HES, CEL, NOS or</u> reactive <u>disease</u>.

In conclusion, although though the study of a limited series, our results suggest that HES in children has distinct biologic and clinical features compared with adult cases, indicating a different underlying disease and molecular pathogenesis. In addition, we suggest that, besides the identification of <u>T-cell</u> clonality, IgH rearrangement should be taken <u>into</u> consideration during the diagnostic characterization of <u>paediatric hypereosinophilia</u>.

### Acknowledgements

The authors would like to thank Ms Pamela Paoletti and Ms Tara Mayte Suarez Viguria for their excellent and dedicated technical assistance. <u>This study was partially supported by</u> <u>Associazione Italiana contro la Ricerca sul Cancro (AIRC)</u>, <u>Associazione Italiana contro le</u> Leucemie (AIL) and Progetto Integrato Oncologia (PIO), Ministero della Salute.

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Table 1. Patient characteristics and biological features of bone marrow at presentation and clinical evolution.

U P N	Sex/Age (years)	Hb (g/dL)	<b>WBC</b> 10 <sup>3</sup> /mm <sup>3</sup>	Eos. count 10 <sup>3</sup> /mm <sup>3</sup>	PLT count 10 <sup>3</sup> /mm <sup>3</sup>	Eos. (%)	Signs of organ involvement at diagnosis	Karyotype	BCR-ABL and FIP1L1/PDGFRA analysis	TCRβ clonality	WT1 expression (cut-off < 90)	IgH clonality	Final diagnosis	Clinical evolution and treatment	IgH status at last follow up
1	M/2	10	63.2	45,496	248	80	Mild hepato- splenomegaly	46, XY	Negative	Polyclonal	N.A.	CDRII-IgH (FR2/JH)	Hypereosinophilia associated with IgH clonality	Normalization No treatment	Polyclonal
2	M/6	12.4	26	15,340	288	60	Absent	46, XY	Negative	Polyclonal	N.A.	CDRII-IgH (FR2/JH)	Hypereosinophilia associated with IgH clonality	Normalization Stop neurological drug/steroid α–interferon treatment	Polyclonal
3	M/10	12.7	4.5	1,512	274	30	Chronic cardiac tamponade and pleural effusion	46, XY	Negative	Polyclonal	N.A.	Polyclonal	Idiopathic HES	Normalization Surgical correction/steroid α–interferon treatment	Polyclonal
4	M/5	14.1	94.9	70,830	281	70	Absent	46, XY	Negative	Polyclonal	503	Polyclonal	Idiopathic HES	Normalization steroid α–interferon treatment	Polyclonal
5	F/15	12.8	13.9	6,950	130	80	Absent	46, XX	Negative	Polyclonal	240	Polyclonal	Idiopathic HES	Normalization steroid α–interferon treatment	Polyclonal
6	M/16	8.5	13.5	5,284	171	34	Lympho- adenomegaly splenomegaly, restrictive cardiomyopathy	46, XY	PDGFR A/FIP1L1 positive	Polyclonal	< 30	Polyclonal	MPN associated with PDGFRA rearrang ement	Myeloid neoplasm Imatinib therapy ↓ Complete remission + 36 mos	Polyclonal
7	M/1.4	7.8	52.6	31,022	18	30	Hepato- splenomegaly, sinus tachycardia, asthmatic bronchitis	46, XY	Negative	Polyclonal	N.A.	CDRII-IgH (FR2/JH)	Hypereosinophilia associated with IgH clonality	NHL-B High-grade NHL treatment ↓ Complete remission + 60 mos	Polyclonal
8	F/9	12.8	19.6	10,100	401	35	Pancarditis with mitral valvular insufficiency	46, XX	Negative	Polyclonal	1876	CDRII-IgH (FR2/JH)	Hypereosinophilia associated with IgH clonality	ALL-B AIEOP2006 treatment ↓ Complete remission 24 mos	Polyclonal
9	F/7	10.3	8,31	4,603	834	40	Interstitial pneumonia	46, XX	Negative	Polyclonal	< 30	CDRII-IgH (FR2/JH)	Hypereosinophilia associated with IgH clonality	Persistent HES α–interferon therapy + 19 mos	CDRII-IgH (FR2/JH) α-interferon therapy
10	F/1	10.3	67.6	49,920	301	22	Hepatomegaly	46, XX	Negative	Polyclonal	< 30	Polyclonal	Idiopathic HES	Normalization No treatment	Polyclonal

N.A.: not available; MPN: Myeloid neoplasm with eosinophilia and PDGFRA rearrangement