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# Allogeneic hematopoietic stem cell transplantation for VEXAS syndrome - UK experience

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Key Words:	CMML, MDS, VEXAS Syndrome, HSCT



# Allogeneic hematopoietic stem cell transplantation for VEXAS syndrome - UK experience

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#### **KEYWORDS**

VEXAS syndrome

Allogeneic hematopoietic stem cell transplantation

- Myelodysplastic syndrome
- Chronic myelomonocytic leukaemia

VEXAS (Vacuoles, E1-ligase, X-linked, Auto-inflammatory, Somatic) syndrome, is an acquired, progressive systemic auto-inflammatory disorder with overlapping rheumatological and haematological features(1, 2). It is caused by myeloid-restricted somatic mutations in *UBA1*, the gene which encodes E1 ubiquitin ligase. VEXAS is associated with significant morbidity and reduced life expectancy. Current treatment options are limited to symptomatic control, with corticosteroids being universally effective and JAK inhibitors showing promising results. Allogeneic hematopoietic stem cell transplantation (HSCT) has been proposed as potentially curative option in selected patients. The experience of HSCT in VEXAS is limited to few case reports(3, 4). Here, we describe four additional cases of VEXAS in whom HSCT was performed. We also report on the incidence of undiagnosed VEXAS in patients with MDS and chronic myelomonocytic leukaemia (CMML) who underwent BMT for haematological indications.

Clinical features of four VEXAS patients who underwent HSCT (mean follow up 13.5 months; range 0.4-40 months) are summarised in Table 1 (detailed clinical vignettes provided in supplements). Three patients P1, P2 and P3 were diagnosed with VEXAS prior to transplantation, with the transplant indication being severe and poorly controlled inflammatory illness. Patient 4 was identified retrospectively, after undergoing HSCT for what was thought to be MDS. Patients 1 and 3 were also included in a recent cohort study, although this did not report on their outcomes following HSCT (1, 2).

The average age of disease onset for these patients was 59 years (range 49-64), which is younger than expected for VEXAS, as described in two recent, large cohort studies which demonstrated an average age of 66 and 67 years (2, 5). Patients 1 and 2 had a UBA1 p.Met41Val variant recently found to be associated with a worse outcome (2). Patients 1, 3 and 4 were also transfusion dependent, a feature associated with more severe disease (2). All three patients transplanted for an inflammatory indication had previously failed multiple DMARD's, whilst patient 4 had only received corticosteroids. Outcomes following HSCT were variable. Patient 1 died from sepsis and multiorgan failure in the early post-transplant period (day +11). Patient 2 survived the transplant with good engraftment and full donor chimerism, but recovery was complicated by hemophagocytic lymphohistiocytosis, aseptic encephalitis and Epstein Barr Virus reactivation within 2 months of transplant, and subsequent extensive chronic graft versus host disease requiring systemic treatment, and recurrent bacterial

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infections, the sequelae of which have resulted in a Karnofsky performance score of 40. Patient 3 achieved disease control with no molecular evidence of VEXAS, however developed severe post-transplant myelitis resulting in paraplegia, urinary and faecal incontinence, and passed away 11 months post-transplant from infectious complications. Patient 4 is the only one who at the time of writing (40 months post-transplant) remains alive and in good health.

Previous studies have reported VEXAS patients being transplanted in the absence of a prior diagnosis, including one of the patients we report here (P4). We therefore speculated about the incidence of undiagnosed VEXAS cases amongst patients with myeloid disorders who had undergone HSCT. To this end, we studied patients from a single centre, with a diagnosis of MDS or CMML, who were transplanted in the last 10 years, for whom historical pre-HSCT bone marrow DNA samples were available.

We identified 44 patients in total, 34 MDS and 10 CMML. Historical, pre-HSCT bone marrow DNA samples were available for all patients. We performed deep sequencing of the whole *UBA1* gene (for method please see supplements). To date, all pathogenic mutations associated with VEXAS have been confined to exon 3, with Methionine-41 (Met41) being a particularly important site (1, 2). No patients demonstrated any of the known pathogenic mutations in *UBA1*, but 4 patients were found to have rare variants outside exon 3 that have not been previously reported and have unknown functional consequences. The variants identified (and variant allele frequencies) were: c.2554-1G>T (0.5), c.2554-8C>T (0.4), c.2374C>T:p.Gln792Ter (0.14) and c.1321G>A:p.Glu441Ter (0.8). However, none of the patients carrying these variants had any inflammatory symptoms. Three had a diagnosis of MDS, whilst the patient with c.1321G>A, p.Glu441Ter variant was diagnosed with CMML.

A failure to find any typical cases of VEXAS across the entire transplanted cohort was likely predictable. Very few patients had any inflammatory symptoms or disease manifestations classically associated with VEXAS (Table 2). The MDS features were also different. Ferrada et al. reported that MDS was diagnosed in 31% of the total cohort, who were retrospectively found to have VEXAS (2). On review, these patients typically had low risk disease, have a much lower frequency of MDS associated gene mutations and show no evidence of progression to acute myeloid leukaemia (2, 6) consistent with UBA1 mutations being the main driver of cytopenias and bone marrow morphological changes not a distinct MDS. The other haematological manifestations which are almost universal in VEXAS, such as macrocytic anaemia (close to 100%), were seen in only 32% of patients in our cohort, although other types of anaemia (e.g. microcytic) were more common.

We report variable outcomes of HSCT in our VEXAS case series with 50% (2/4) overall survival but only 25% event free survival at current follow up. There are several potential explanations for this. Patient 1 underwent HSCT as a 'treatment of last resort' for a rapidly progressive, recalcitrant inflammatory disorder. The risk of poor outcome in such circumstances is invariably high, as reflected in his HCT-CI score of 6. Patient 2 was transplanted three years after the onset of symptoms and had received continuous immunosuppressive therapy including corticosteroids during this time. Patient 3 was transplanted almost 10 years after disease onset, during which time he had already developed several complications including renal impairment and steroid toxicity. In addition, he was exposed to several immunosuppressive therapies and had experienced several serious infections. It is unclear to what degree post-transplant complications were influenced by these factors. Nevertheless, the purported benefit of reduced corticosteroid use as a result of better control of his inflammatory illness was significantly offset by his pre-existing, iatrogenic adrenal insufficiency.

What these cases illustrate is the current lack of evidence informing the selection of VEXAS patients who will benefit from HSCT. The tools currently utilised in "classical" MDS and CMML to identify transplant candidates (IPSS, IPSS-R) would not be applicable in patients with VEXAS given the distinct bone marrow pathology and clinical manifestations. The only way to address these issues is through well-designed trials, alongside collection of detailed outcome data for all transplanted patients. An example of such a trial has been proposed by a team from the National Institutes of Health (USA) who are now recruiting patients for a Phase II study of allogeneic HSCT for subjects with VEXAS syndrome (7). An essential design of this trial could be adopted by other transplant centres internationally. This could lead to a larger platform trial to recruit more patients, test more treatment arms and provide results sooner.

Patient ID Genetics	1	in VEXAS patients	<b>D</b> 2	
Senetics	P1	P2	P3	P4
JBA1 mutation	p.Met41Val (c.121A>G)	p.Met41Val (c.121A>G)	p.Met41Thr (c.122T>C)	p.Met41Leu.(c.121
/AF (5%)	50	24	50	40
Demographics				
0 1	1	1		1
Gender	Male	Male	Male	Male
Age of onset	49	64	52	59
key inflammatory features				
			<b>1</b> 4	
ever	Yes	Yes	Yes	Yes
Veight loss	Yes	Yes	Yes	No
ikin involvement	Yes (Nodular)	Yes (Nodular)	Yes (Nodular)	Yes (Jessners Infilt
Chondritis	No	No	No	Yes (Ear)
Arthritis				. ,
	No	No	No	No
Pulmonary infiltrates	Yes	No	Yes	No
ΡE	No	Yes	No	No
TVC	No	No	No	No
Other	None	Periorbital oedema	Tubular interstitial nephritis	No
Rheumatological diagnosis	None	None	uSAID	Relapsing polychon
laematological disease				
0	No.	Na	Ne	Vee
MDS	Yes	No	No	Yes
Ayelofibrosis	No	No	No	No
MGUS/MM	No	No	No	No
ransfusion dependent	Yes	No	Yes	Yes
R-IPSS score	3		N/A	
	3	N/A	N/A	2.5
aboratory findings				
Macrocytic anaemia	Yes	Yes	Yes	Yes
hrombocytopenia	Yes	Yes	Yes	No
Veutropenia	No	No	No	No
ymphopenia	No	Yes	Yes	No
levated CRP	Yes	Yes	Yes	Yes
Bone marrow vacuoles	Yes	Yes	Yes	No
	tes	Tes	Tes	NU
Additional genetic aberrations (HTS				
and cytogenetics)	No	No	No	No
Freatment prior to HSCT				
reachient phor to hoer	1			
otal number of previous treatments	4	3	6	1
otal number of previous treatments				-
	CS,TOC, Anakinra, BAR,		CS, MTX, AZA, MMF,	
Туре	Colchicine	CS, MTX, HCQ	anakinra, TOC, BAR	CS
,pc				
			Severe injection site	
			reaction to anakinra,	
			infections (pneumonia,	
Complications	None	None	menigitis)	None
Allogeneic HSCT				
Age at transplant	F1	67	61	62
• •	51	67	61	62
Carnofsky performance scale (PS)	70	80	70	90
eattle HCT-CI score	6	3	3	N/A
	Single kidney with CKD,	TLCO 63%		Chondritis
	J , ,	1100 05%	Moderate pulmonary, mild	Chonufitis
	Deranged liver function,		hepatic impairment,	
	type II diabetes (on oral		obesity	
	hypoglycaemics)			
Comorbidities				
Conditioning regiment	FLU/BU, Thiotepa	FLU/MEL/CAM	FLU/TREO/CAM	FLU/BU/ATG
Donor	Haplo (son)	MUD	Sibling	MUD
Graft origin	PBSC	PBSC	PBSC	PBSC
GVH prophylaxis	CYC, TAC, MMF	CSA	CAM, CSA & MMF	ATG/CSA
	Salmonella houtenae in			
	blood cultures,		Bacterial, C difficile, SARS-	
nfectious complications	pseudomonas in sputum	EBV reactivation	CO-V2	No
pilotions				-
		HLH, aseptic encephalitis,	Metabolic acidosis peri-	
	N/A		transplant, myelitis & optic	Grade 1 GvHD
mmune complications/ GVHD		GvHD	neuropathy	
•				
Day 100 Donor chimerism CD3	N/A	100%	99%	100 (whole blood)
Day 100 Donor chimerism CD15	N/A	100%	100%	100 (whole blood)
•	1			
Duration of follow-up post HSCT	11 days	5 months	11 months	40 months
Alive	No	Yes	No	Yes
	Sepsis, multiorgan failure,			
		NI / A	Infaction	N/A
Second all all and the	cardiac arrest	N/A	Infection	N/A
Cause of death	11 days	5 months	11 months	40 months
Cause of death Event free survival (EFS)		4.5 months	11 months	40 months
vent free survival (EFS)	11 days			
event free survival (EFS) GRFS	11 days			Alive in remission
vent free survival (EFS)	11 days Died	Karnofsky 40	Died	
event free survival (EFS) GRFS Current status	Died	Karnofsky 40		CRP-C reactive prote
Event free survival (EFS) GRFS Current status ATG-Anti-thymocyte globulin; AZA-aza	Died athioprine; BAR-baricitinib; B	Karnofsky 40 U-busulfan; CAM-campath;	CKD-chronic kidney disease; (	
event free survival (EFS) GRFS Current status	Died athioprine; BAR-baricitinib; B	Karnofsky 40 U-busulfan; CAM-campath;	CKD-chronic kidney disease; (	
Event free survival (EFS) GRFS Current status ATG-Anti-thymocyte globulin; AZA-aza	Died athioprine; BAR-baricitinib; B yclophosphomide; EBV-Epste	Karnofsky 40 U-busulfan; CAM-campath; in-Barr virus; DVT-deep vein	CKD-chronic kidney disease; ( thromosis; FLU-fludarabine;	GFRS-GvHD (grade
Event free survival (EFS) GRFS Current status ATG-Anti-thymocyte globulin; AZA-aza cortcosteroids; CSA-ciclosporin; CYC-co chronic GvHD requiring systemic thera	Died athioprine; BAR-baricitinib; B yclophosphomide; EBV-Epste apy) and relapse free survival,	Karnofsky 40 U-busulfan; CAM-campath; in-Barr virus; DVT-deep vein ; GVHD- graft versus host dis	CKD-chronic kidney disease; ( thromosis; FLU-fludarabine; sease; HCQ-hydroxychloroquir	GFRS-GvHD (grade ne; HCT-CI-Hematop
Event free survival (EFS) GRFS Current status ATG-Anti-thymocyte globulin; AZA-azi cortcosteroids; CSA-ciclosporin; CYC-cr chronic GvHD requiring systemic thera cell transplantation-specific comorbid	Died athioprine; BAR-baricitinib; B yclophosphomide; EBV-Epstei apy) and relapse free survival, lity index; HLH-hemophagocyt	Karnofsky 40 U-busulfan; CAM-campath; in-Barr virus; DVT-deep vein ; GvHD- graft versus host dii ic lymphohistiocytosis; HTS-	CKD-chronic kidney disease; ( thromosis; FLU-fludarabine; sease; HCQ-hydroxychloroquir High-throughput sequencing;	GFRS-GvHD (grade ne; HCT-CI-Hematop MDS-myelodysplas
Event free survival (EFS) SRFS Current status TG-Anti-thymocyte globulin; AZA-azz cortcosteroids; CSA-ciclosporin; CYC-cr fironic GvHD requiring systemic there cell transplantation-specific comorbid yndrome; MEL-melphalan; MGUS-mu	Died athioprine; BAR-baricitinib; B yclophosphomide; EBV-Epstei apy) and relapse free survival, lity index; HLH-hemophagocyt onoclonal gammopathy of un	Karnofsky 40 U-busulfan; CAM-campath; in-Barr virus; DVT-deep vein ; GvHD- graft versus host dii ic lymphohistiocytosis; HTS- determined significance; M	CKD-chronic kidney disease; ( thromosis; FLU-fludarabine; sease; HCQ-hydroxychloroquir High-throughput sequencing; M-multiple myeloma; MMF-r	GFRS-GvHD (grade ne; HCT-CI-Hematop MDS-myelodysplas mycophenolate mofe
Event free survival (EFS) GRFS Current status ATG-Anti-thymocyte globulin; AZA-azi cortcosteroids; CSA-ciclosporin; CYC-cr chronic GvHD requiring systemic thera cell transplantation-specific comorbid	Died athioprine; BAR-baricitinib; B yclophosphomide; EBV-Epstei apy) and relapse free survival, lity index; HLH-hemophagocyt onoclonal gammopathy of un	Karnofsky 40 U-busulfan; CAM-campath; in-Barr virus; DVT-deep vein ; GvHD- graft versus host dii ic lymphohistiocytosis; HTS- determined significance; M	CKD-chronic kidney disease; ( thromosis; FLU-fludarabine; sease; HCQ-hydroxychloroquir High-throughput sequencing; M-multiple myeloma; MMF-r	GFRS-GvHD (grade ne; HCT-CI-Hematop MDS-myelodysplas mycophenolate mofe

		Cohort 2	
	Cohort 1	Georgin-	Cohor
	Ferrada et a	Lavialle et al	Present
	(n=83)	(n=116)	(n=44
Demographics			
Age of disease onset, median (range)	66 (41-80)	67 (62.5-73)	57 (22-72
Male sex n (%)	83 (100)	111 (95.7)	25 (58.1)
Clinical Diagnosis			
Relapsing polychondritis n (%)	43 (52)	N/A	0 (0)
Undifferentiated Fever Syndrome n (%)		N/A	0 (0)
Sweets syndrome	18 (22)	N/A	0 (0)
MDS	26 (31)	58 (50)	34 (77)
CMML	0 (0)	0 (0)	10 (23)
Clinical Manifestations n (%)			
Fever	69 (83)	75 (64.6)	0 (0)
Skin involvement	68 (82)	97 (83.6)	6 (14)
Arthritis	48 (58)	33 (28.4)	3 (7)
Pulmonary infiltrates	47 (57)	47 (40.5)	0 (0)
Ear chondritis	45 (54)	37 (31.9)	0 (0)
Unprovoked deep vein thromosis (DVT)	34 (41)	41 (35.3)	0 (0)
Nose chondritis	30 (36)	18 (15.5)	0 (0)
Periorbital edema	25 (30)	10 (8.6)	0 (0)
Hearing loss	24 (29)	N/A	3 (7)
Ocular inflammation	20 (24)	43 (37)	0 (0)
Pulmonary embolism	11 (13)	N/A	0 (0)
Pleural effusion	11 (13)	11 (9.5)	3 (7)
Orchitis	10 (12)	N/A	0 (0)
Airway chondritis	1 (2)	0 (0)	0 (0)
Hematologic Manifestations			
Macrocytic anemia n (%)	81 (97)	N/A	14 (32)
Thrombocytopenia n (%)	40 (83)	N/A	34 (77)
R-IPSS Score* n (%) (MDS patients only	)		
Very low risk	9 (39)	N/A	1 (3)
Low risk	12 (52)	N/A	4 (12)
Intermediate risk	0 (0)	N/A	6 (18)
High risk	2 (4)	N/A	16 (47)
Very high risk	0 (0)	N/A	7 (21)
MDS-associated mutations	7/17 (41)	N/A	19/24 (7
Cohorts 1 and 2, VEXAS patients decribe	d in Ferrada et	all, and Georgir	n-Lavialle e
respectively. Cohort 3 patients from this	s study who we	re transplanted	for

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### Author contributions

SS, AK and JP, conceived and design the study; AA, DM, AMSR, SE, HE, CC, CJAD, MB, VB collected data; JA, AA and SS performed data analysis; SS wrote first draft of manuscript; All authors read, edited and approved manuscript. SS provided funding the study.

# **Conflict of interest**

Authors have no conflict of interest to declare

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# Patient 1 (P1)

P1 was a 51-year-old, previously fit and very active male who developed a severe multisystem inflammatory illness 18 months prior to allogeneic haematopoietic stem cell transplantation (HSCT). The disease was characterized by recurrent sterile fevers with elevated inflammatory markers (CRP, ESR), in several instances culminating in multiorgan dysfunction that necessitated ICU management. Accompanying features included fleeting pulmonary infiltrates, neutrophilic dermatosis and pathergy. He also developed profound weight loss, sarcopenia, transfusion-dependent macrocytic normochromic anaemia and intermittent thrombocytopenia (70-90  $\times$  109/I). During the illness he was diagnosed with an incidental transitional renal cell carcinoma requiring nephrectomy and resulting in chronic kidney disease. He had short-lived but ultimately unsustained responses to various immunomodulatory therapies including high-dose prednisolone, anakinra, tocilizumab and baricitinib.

Extensive investigations were undertaken to exclude an infectious or autoimmune cause for the illness including bronchoscopy and bone marrow culture. Computed tomography (CT) scan revealed mild progressive splenomegaly alongside intermittent interstitial pulmonary infiltrates and positron emission tomography (PET) with 2-deoxy-2-[fluorine-18]fluoro-Dglucose (18F-FDG) revealed progressive prominent uptake in the bone marrow and spleen. Bone marrow biopsy showed reduced erythropoiesis and striking erythroid and myeloid precursor vacuolation. Targeted sequencing identified no mutations associated with myeloid malignancy, and chromosome analysis showed a normal male karyotype. Sanger sequencing of *UBA1* identified the Met41Val missense variant at a variant allele fraction of ~0.5. Owing to the treatment resistant and rapidly progressive nature of his disease referral for HSCT was made following recommendation in the National Primary immunodeficiency bone marrow transplant multidisciplinary team meeting.

As there were no matched unrelated donors, the patient received a reduced intensity (Flu/Cy 2Gy TBI), haplo-identical bone marrow transplant with post-transplant cyclophosphamide and ciclosporin/MMF graft versus host disease prophylaxis. The conditioning was well tolerated but fever and diarrhoea developed from the day after donor cells were infused (Day +1). Despite broad spectrum antibiotics the patient required intensive care support for electrolyte derangement and metabolic acidosis from Day +4. Klebsiella and salmonella species were grown from blood cultures, antimicrobial therapy appropriately adjusted and

indwelling lines changed. Following an asystolic cardiac arrest on Day +7, despite maximal intensive support including inotropes, renal and ventilatory support, the patient succumbed to multiorgan failure on Day +11, prior to engraftment.

#### Patient 2 (P2)

P2 is a previously fit and well male, aged 64yrs, presented with retro-orbital pain and swelling and a peri-orbital erythematous rash, which responded initially to iv corticosteroids and antibiotics. Systemic symptoms developed, including fatigue, fevers, night sweats and weight loss, accompanied by an intermittent nodular erythematous rash, worse on forearms and neck. Inflammatory markers were raised, skin biopsy was consistent with erythema nodosum and positron emission tomography (PET) with 2-deoxy-2-[fluorine-18]fluoro-D-glucose (18F-FDG) was non-diagnostic. Bone marrow examination showed hypercellularity with hyperplastic, left-shifted granulopoiesis, reduced megakaryocytes with micromegakaryocytes, disorganised erythropoiesis and trilineage dysplastic features. Targeted sequencing identified no mutations associated with myeloid malignancy, and chromosome analysis showed a normal male karyotype.

The patient's symptoms stabilised on prednisolone (minimum dose 15mg daily), methotrexate (25mg weekly) and hydroxychloroquine (200mg daily). 8 months after presentation the patient was diagnosed with bilateral pulmonary emboli and received long-term anticoagulation with Rivaroxaban. 2.5yrs after initial presentation, genetic sequencing from a saliva sample revealed UBA1 p.Met41Val somatic mosaicism and repeat bone marrow aspirate, now in the context of a macrocytic anaemia, showed evidence of vacuolation in erythroid and granulocytic precursors.

With ongoing requirement for immunosuppression, increasing anaemia and thrombocytopenia and gradual clinical decline, the patient was considered for bone marrow transplantation, discussed at the National Adult Primary Immunodeficiency Bone Marrow Transplant MDT.

The patient received a reduced intensity, Flu/Mel/Alemtuzumab conditioned transplant with a 10/10 matched unrelated donor. Conditioning was well tolerated and a good graft achieved with engraftment of neutrophils and platelets on post-transplant days 12 and 13 respectively and 100% donor chimerism in myeloid and T cell compartments at three months. However, the patient had a stormy clinical course over the 9 months following transplant with

inflammatory encephalitis and haemophagocytic lymphohistiocytosis (HLH) treated with corticosteroids, anakinra and the JAK inhibitor baracitinib, Epstein Barr Virus (EBV) reactivation treated with rituximab, severe peripheral muscle wasting, severe chronic skin graft versus host disease treated with ciclosporin, corticosteroids and extracorporeal photophoresis, recurrent bacterial chest and urinary infections and hypogammaglobulinaemia (requiring immunoglobulin replacement therapy), with a current Karnofsky performance score of 40.

#### Patient 3 (P3)

P3 initially presented at the age of 52 with fevers, weight loss, widespread nodular skin rash, bilateral hilar and mediastinal lymphadenopathy and pulmonary infiltrates. He was initially diagnosed with systemic sarcoidosis and treated with corticosteroids, to which he had a good response. Over the next 2 years he remained dependent on corticosteroids for control of his symptoms and failed to respond to multiple traditional synthetic DMARDs. His diagnosis was revised to undifferentiated systemic autoinflammatory disorder and he was treated with anakinra, but shortly after the treatment was initiated, he developed extensive injection site reactions necessitating anakinra discontinuation. Subsequently, he was switched to tocilizumab. He had a partial response and remained dependent on a small dose of prednisolone (5-10mg daily) for symptomatic control. His treatment was complicated by severe pulmonary infections requiring hospital admission. Consequently, tocilizumab was changed to baricitinib, but he remained reliant on prednisolone. Later it was established that he had developed secondary adrenal insufficiency. He was diagnosed with VEXAS 7 years after the initial onset of symptoms. Shortly afterward the diagnosis was established his anaemia progressed and he became transfusion dependent. The indications for his transplant were ongoing, poorly controlled inflammatory illness and progressive bone marrow failure. HSCT was performed 2 years after the diagnosis of VEXAS at the age of 61. His initial recovery after HSCT was relatively straightforward. He had no symptoms of graft versus host disease (GvHD), but shortly after being discharged home, he developed progressive leg weakness and double incontinence, and extensive screening investigations were negative. He was diagnosed with post-transplant myelitis, postulated to relate to a toxic cause, possibly a rare effect of conditioning treatment with fludarabine. Although his day 100 follow-up tests showed almost CD3 and CD15 donor chimerism with no evidence of the original UBA1 mutation on peripheral blood and bone marrow testing, his haematological graft function was sub-optimal, particularly in the red cell series and he remained red blood cell transfusion dependent. His post-transplant bone marrow was hypocellular and the 9-month CD3 chimerism declined slightly to 91%, CD15 99%. His inflammatory illness remained in complete remission, however he deteriorated progressively from a neurological standpoint, with progressive cord signal abnormalities on MRI spine, complete paraplegia and loss of vision. He did not respond to further attempts at immunomodulation and immunosuppression with steroid pulses and intravenous immunoglobulin, and following multidisciplinary advanced care planning

discussions with his family expressed the wish to be managed at home with palliative care. He passed away from an infective episode 11 months following his transplant.

#### Patient 4 (P4)

P4 initially presented when 59 years old with fleeting pain in multiple joints, followed by abrupt onset of redness and swelling in his left ear with elevated inflammatory markers and anaemia. Pinna cartilage biopsy confirmed non-specific mild perichondrial chronic inflammation but no features of acute chondritis and the diagnosis of relapsing polychondritis was made. There was an initial excellent clinical response to oral prednisolone although there was symptom recurrence at lower doses. Disease modifying drugs were under consideration, however two years after initial diagnosis he represented with symptoms of progressive anaemia with Hb 49, an MCV of 127 with normal haematinics. Bone marrow biopsy showed modest dyserythropoiesis, megaloblastoid morphology and an increase in granulopoiesis but all with full maturation. There were no ringed sideroblasts, micromegakaryocytes or blasts seen. Cytogenetics and NGS myeloid screen were normal. As there was no response to EPO, and the patient required ongoing two weekly packed cell transfusions, three years after initial presentation the patient received a Flu/Bu/ATG 9/10 DP permissive mismatched MUD. The patient tolerated treatment well, with minimal limited liver and skin GVHD, and had no further recurrence of polychondritis. He is now more than three years post-transplant and remains 100% donor with no active GVHD on 10mg ciclosporin bd.

## **METHODS**

VEXAS patients were identified via two national clinical networks, National Primary immunodeficiency bone marrow transplant group and The HLH Across Speciality Collaboration (https://www.hihasc.org). Clinical data was collected retrospectively. Patients who were transplanted for myelodysplastic syndrome or Chronic myelomonocytic leukaemia indications were identified from a single centre (Leeds Teaching Hospitals NHS Trust). The study was performed in accordance with the local ethical approval for investigation of a suspected haematological disorder (ethical committee approval 16/NE/0105).

Genetic testing was performed by pooled amplicon sequencing of all *UBA1* exons using an adapted method published previously(1). Briefly, primers targeting each exon were designed and tagged with M13 sequences (Supplementary Table 1). Following amplification of each exon individually, all amplicon products from each DNA sample were pooled and purified using a 1:1 ratio of AMPure beads:pooled amplicons. A second round of amplification using 50ng pooled amplicons was then performed to attach indexed sequencing adapters to each sample. Indexed amplicons from all samples were subsequently pooled and an AMPure bead purification performed to create the final sequencing library. 3x 500ng pools were sequenced by GeneWIZ (EZ-Amplicon Seq) to a minimum read depth of 50,000 reads per pool. Resulting fastq files were aligned and variants analysed as previously described(1). Potential variants were validated by PCR and Sanger sequencing of the original DNA samples.

#### References:

1. Poulter J, Consortium UV, Morgan A, Cargo C, Savic S. A High-Throughput Amplicon Screen for Somatic UBA1 Variants in Cytopenic and Giant Cell Arteritis Cohorts. J Clin Immunol. 2022.

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Primer name	Primer sequence (5' to 3')
UBA1_Ex2-3F	TGTAAAACGACGGCCAGTCCCCTCTTTGCTGTAAAATG
UBA1_Ex2-3R	CAGGAAACAGCTATGACCTCATGGCCCAACACATACC
UBA1_Ex4-5F	TGTAAAACGACGGCCAGTAGAGGATAAGGTTGGGTGGG
UBA1_Ex4-5R	CAGGAAACAGCTATGACCTGAATAAACCAGAGATGGGC
UBA1_Ex6-7F	TGTAAAACGACGGCCAGTACTGCCTGAGTCCTCCACAC
UBA1_Ex6-7R	CAGGAAACAGCTATGACCAGGAAGGACTACTGCAGCC
UBA1_Ex8F	TGTAAAACGACGGCCAGTGGCTGCAGTAGTCCTTCCTG
UBA1_Ex8R	CAGGAAACAGCTATGACCGCCAGAACCCAGGAACATATC
UBA1_Ex9-10F	TGTAAAACGACGGCCAGTCCTTATCTTGCAGGGGTTG
UBA1_Ex9-10R	CAGGAAACAGCTATGACCAGAGGCATGGTGAGCCTG
 UBA1_Ex11-12F	TGTAAAACGACGGCCAGTGTGTCCACACTCCCTGCC
– UBA1_Ex11-12R	CAGGAAACAGCTATGACCAGGGAGGAGGGTTAGAGAGG
– UBA1_Ex13F	TGTAAAACGACGGCCAGTCATCATTGGGGACATTTCTG
UBA1 Ex13R	CAGGAAACAGCTATGACCAGGGGTGATGGCCAGAG
UBA1 Ex14F	TGTAAAACGACGGCCAGTGAGTGAGGGGGTGATGGGTAG
UBA1_Ex14R	CAGGAAACAGCTATGACCAACAAGAGCGAAACTCCG
UBA1_Ex15F	TGTAAAACGACGGCCAGTCCACCCTGGAACTGCAC
UBA1_Ex15R	CAGGAAACAGCTATGACCCGTGACCACCTCACC
UBA1_Ex16F	TGTAAAACGACGGCCAGTCCTCCTGATGTTTCTTTCC
UBA1_Ex16R	CAGGAAACAGCTATGACCTGGCCTCTTTCCCTTC
UBA1_Ex10R	TGTAAAACGACGGCCAGTAATAATGCCTGCGGAAACC
UBA1_Ex17R	CAGGAAACAGCTATGACCGATGCCTTGGCTGGTGG
—	TGTAAAACGACGGCCAGTGTAAGATTGCTCTGGAGCCC
UBA1_Ex18F	
UBA1_Ex18R	CAGGAAACAGCTATGACCTGCAGGCTCCCATTTCAG TGTAAAACGACGGCCAGTCGTGAAGATTGTCAGAGAGGC
UBA1_Ex19-20F	
UBA1_Ex19-20R	CAGGAAACAGCTATGACCGTGGGGGGGGGGGGGGCTGGACTAGG
UBA1_Ex21-22F	TGTAAAACGACGGCCAGTATCTCAGACCTTAGCCTGGG
UBA1_Ex21-22R	
UBA1_Ex23F	TGTAAAACGACGGCCAGTCCCTCTGTAGACCCTGAGGC
UBA1_Ex23R	CAGGAAACAGCTATGACCGGGTATGACGTGAATCAGAACC
UBA1_Ex24-25F	TGTAAAACGACGGCCAGTGGATGGAGACAGATGGGG
UBA1_Ex24-25R	CAGGAAACAGCTATGACCGACAGCTGGATGATGAGGC
UBA1_Ex26F	TGTAAAACGACGGCCAGTCACTGCCCCTACCTACCTG
UBA1_Ex26R	CAGGAAACAGCTATGACCTGGAAGGGGTGTGGAGAG
M13-F_indexA	ACACTCTTTCCCTACACGACGCTCTTCCGATCTGTGAATATTGTAAAACGACGGC
M13-F_indexB	ACACTCTTTCCCTACACGACGCTCTTCCGATCTACAGGCGTTGTAAAACGACGGG
M13-F_indexC	ACACTCTTTCCCTACACGACGCTCTTCCGATCTCATAGAGTTGTAAAACGACGGC
M13-F_indexD	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTGCGAGACTGTAAAACGACGGG
M13-F_indexE	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTCTCTACTTGTAAAACGACGGCC
M13-F_indexF	ACACTCTTTCCCTACACGACGCTCTTCCGATCTCTCGTCTGTAAAACGACGGC
M13-F_indexG	ACACTCTTTCCCTACACGACGCTCTTCCGATCTCCAAGTCTTGTAAAACGACGGC
M13-F_indexH	ACACTCTTTCCCTACACGACGCTCTTCCGATCTTTGGACTCTGTAAAACGACGGC

M13-R_index6	GACTGGAGTTCAGACGTGTGCTCTTCCGATCTTATCGCACCAGGAAACAGCTATGACC ary Table 1 – Primer sequences for amplicon sequencing.
M12 D indox6	
M13-R_index5	GACTGGAGTTCAGACGTGTGCTCTTCCGATCTCGCTATGTCAGGAAACAGCTATGACC
M13-R_index4	GACTGGAGTTCAGACGTGTGCTCTTCCGATCTTACTCATACAGGAAACAGCTATGACC
M13-R_index3	GACTGGAGTTCAGACGTGTGCTCTTCCGATCTCGTCTGCGCAGGAAACAGCTATGACC
M13-R_index2	GACTGGAGTTCAGACGTGTGCTCTTCCGATCTTCGATATCCAGGAAACAGCTATGACC
M13-R_index1	GACTGGAGTTCAGACGTGTGCTCTTCCGATCTCTAGCGCTCAGGAAACAGCTATGACC