Abstract Highlights

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These abstracts highlight some of the cutting-edge research presented at the European Hematology Association (EHA) 2026 Congress. Covering topics ranging from liquid biopsy and cardiovascular risk to pregnancy complications and rare inherited blood disorders, the findings showcase emerging advances that could influence future diagnosis, risk stratification, and patient management across haematology.

ctDNA Detects Lymphoma Years Before Diagnosis

CIRCULATING tumour DNA (ctDNA) can identify lymphoma-associated mutations years before the clinical diagnosis of diffuse large B cell lymphoma and classic Hodgkin lymphoma, according to research presented at EHA2026.[1]

The interval between the earliest molecular events that drive lymphoma development and the onset of symptoms remains poorly understood. Diffuse large B cell lymphoma and classic Hodgkin lymphoma both arise from germinal centre B cells and are characterised by recurrent genetic alterations that accumulate during disease evolution.

Previous observations from population studies have suggested that tumour-derived mutations may be detectable in blood before clinical diagnosis. Veltmaat et al.[1] therefore investigated whether analysis of ctDNA in pre-diagnostic plasma samples could capture these early oncogenic changes and improve understanding of lymphoma development over time.

The study analysed pre-diagnostic plasma samples from 46 individuals in the Dutch Lifelines biobank who later developed lymphoma, including 33 patients with diffuse large B cell lymphoma and 13 patients with classic Hodgkin lymphoma. Matched tumour tissue and white blood cell samples were available for 41 cases.

Using targeted sequencing of 115 genes and selected super-enhancer regions of 14 genes, investigators assessed both single- and multi-nucleotide variants, a distinctive mutational pattern generated through aberrant somatic hypermutation that frequently affects genes involved in B cell regulation.

Overall, pre-diagnostic ctDNA was detected in 67% of cases, with evidence of tumour-derived mutations identified in 31 of the 46 patients included in the analysis. The median interval between blood sampling and lymphoma diagnosis was 21 months.

Among patients with diffuse large B cell lymphoma, single-nucleotide variants were detected in 39% of cases, while multi-nucleotide variants were identified in 61%. In classic Hodgkin lymphoma, multi-nucleotide variants were detected in 69% of patients.

Importantly, ctDNA could be identified many years before diagnosis. The earliest detectable signal occurred 106 months before diagnosis in diffuse large B cell lymphoma and 55 months before diagnosis in classic Hodgkin lymphoma.

In patients with classic Hodgkin lymphoma, ctDNA levels showed a strong correlation with serum thymus and activation regulated chemokine concentrations, a recognised biomarker of disease activity ($r=0.86$; $p<0.001$).

> **Pre-diagnostic ctDNA was detected in 67% of cases, with evidence of tumour-derived mutations identified in 31 of the 46 patients included in the analysis**

Samples with detectable ctDNA were collected significantly closer to diagnosis than ctDNA-negative samples, and ctDNA concentrations increased as the time to diagnosis shortened. Tumour growth rates appeared similar between diffuse large B cell lymphoma and classic Hodgkin lymphoma.

The investigators concluded that ctDNA analysis, particularly approaches based on multi-nucleotide variants, offers a highly sensitive method for identifying early molecular changes associated with lymphoma development and may support future liquid biopsy strategies for earlier diagnosis in patients suspected of lymphoma.

New Atlas Reveals Pregnancy Sickle Cell Disease Vascular Changes

LONGITUDINAL profiling has provided new insights into the biological changes occurring during pregnancy in people with sickle cell disease (SCD), an inherited blood disorder that can cause abnormal red blood cell shape and contribute to vascular complications. The study, presented at the EHA2026, mapped changes across blood and placental pathways linked to inflammation, coagulation, and immune activity.[2]

Pregnancy in SCD is considered high-risk, with maternal morbidity and mortality rates reported as up to 20-fold higher than the general population. Previous evidence has linked SCD itself with endothelial injury, inflammation, and hypercoagulability, and these processes are amplified in pregnancy, potentially contributing to adverse pregnancy outcomes. The wider vascular-inflammatory landscape in pregnant persons with SCD (PP-SCD) remains incompletely characterised.

Researchers aimed to create a proteo-transcriptomic atlas of pregnancy in SCD and identify potential biomarkers and functional pathways that distinguish PP-SCD from healthy pregnancy and non-pregnant SCD.

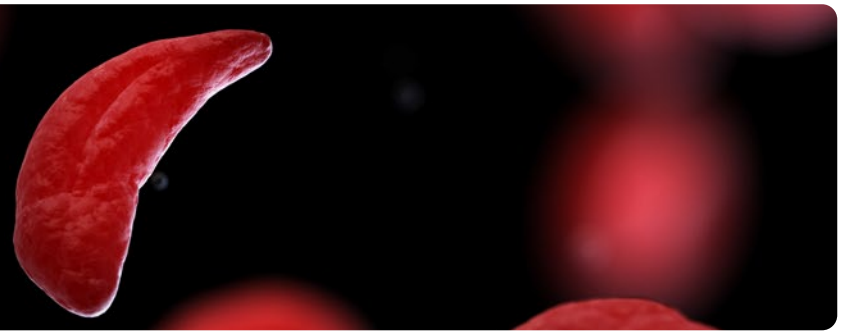
The team analysed serial plasma samples collected during each trimester and postpartum from six PP-SCD, alongside eight non-pregnant SCD controls and pregnant people with normal haemoglobin. Plasma proteins were assessed using a large-scale protein analysis platform, with complement findings validated separately. Placental single-cell RNA sequencing was also performed.

Compared with the pregnant people with normal haemoglobin group, pregnancy in SCD was associated with 595 differentially abundant plasma proteins in early pregnancy and 114 in late pregnancy, including proteins involved in endothelial activation and coagulation pathways, complement activity, hypoxia, angiogenesis, and innate immune signalling. The study identified a dynamic vascular-inflammatory signature across pregnancy in SCD.

Further analyses showed changes in endothelial and complement markers over gestation, including evidence of complement activation and pregnancy-related amplification of coagulation and inflammation pathways beyond those seen in non-pregnant SCD. Placental analysis found preserved overall cellular composition in uncomplicated pregnancies, but identified signs of endothelial hyperactivation and immune cell activation.

The study authors noted that the findings are based on a small cohort and require further validation. The integrated blood and placental atlas could support future efforts to improve risk stratification and explore biomarkers that may help guide management of SCD pregnancies.

> **Maternal morbidity and mortality rates reported as up to 20-fold higher than the general population**



Atherosclerotic Cardiovascular Disease Affects One in Six Adults with β-Thalassemia

ATHEROSCLEROTIC cardiovascular disease (ASCVD) affects a substantial proportion of adults living with β-thalassemia and appears to be driven by traditional cardiovascular risk factors rather than disease-specific features, according to research presented at EHA2026.[3]

Advances in treatment have dramatically improved survival for patients with β-thalassemia, shifting attention towards age-related comorbidities. While heart disease remains the leading cause of death in this population, the burden of ASCVD has not previously been well characterised.

> **Traditional cardiovascular risk factors were strongly associated with ASCVD**

Researchers analysed clinical, laboratory, and imaging data from 235 adults with β-thalassemia receiving care at a tertiary centre in Milan, Italy. The cohort included patients who were both transfusion-dependent and non-transfusion-dependent, with a median age of 49 years.

Overall, 15.7% of patients had evidence of ASCVD. Most cases involved atherosclerotic plaques in the carotid, aortic, or femoral arteries, while only a small number of patients had experienced a previous myocardial infarction or ischaemic brain lesion. As expected, ASCVD prevalence increased with age.

Traditional cardiovascular risk factors were strongly associated with ASCVD. Alcohol consumption, a history of smoking, glucose intolerance, diabetes, and increasing blood pressure were all linked to a significantly greater likelihood of developing atherosclerotic disease.

By contrast, no associations were observed between ASCVD and haemoglobin levels, iron overload, ferritin concentrations, transfusion dependence, or markers of ineffective erythropoiesis. Lipid profiles were also unusual, with most patients demonstrating cholesterol levels within or below the normal range, regardless of ASCVD status. Similarly, endothelial activation markers did not differ between patients with and without vascular disease.

The investigators concluded that conventional cardiovascular risk factors remain important determinants of ASCVD in ageing patients with β-thalassemia. However, the atypical lipid profile seen in this population suggests that existing cardiovascular risk assessment tools may be inadequate, highlighting the need to develop thalassemia-specific approaches to cardiovascular risk prediction and prevention.

Real-World Study Confirms Benefits of Mitapivat in Pyruvate Kinase Deficiency

MITAPIVAT demonstrated high response rates and a favourable safety profile in adults with pyruvate kinase deficiency (PKD) treated in routine clinical practice, according to the first multicentre real-world study from Italy presented at EHA2026.[4]

PKD is a rare inherited haemolytic anaemia characterised by chronic haemolysis, ineffective erythropoiesis, and frequent long-term complications. Although mitapivat is the first disease-modifying therapy approved for PKD, evidence from real-world populations has remained limited.

Researchers retrospectively analysed outcomes in 30 adults treated with mitapivat across nine Italian haematology centres. The cohort included both transfusion-dependent (33%) and non-transfusion-dependent patients, with a median follow-up of 19 months.

Overall, 67% of patients responded to treatment. Among non-transfusion-dependent patients, haemoglobin levels increased significantly from a median of 9.45 g/dL at baseline to 11.1 g/dL after treatment, with a sustained median increase of 2.2 g/dL. In the transfusion-dependent group, 70% experienced a meaningful reduction in transfusion requirements, while 60% achieved complete transfusion independence.

Treatment was also associated with marked improvements in markers of haemolysis, including reductions in reticulocyte count, lactate dehydrogenase, and indirect bilirubin, alongside increased haptoglobin levels. Most responses occurred within the first 3 months of treatment.

Response varied according to genotype, with patients carrying biallelic missense mutations demonstrating the highest response rates. In contrast, baseline pyruvate kinase enzyme activity did not predict treatment response, and previous splenectomy had no significant impact on outcomes.

> **Response varied according to genotype, with patients carrying biallelic missense mutations demonstrating the highest response rates**

The safety profile was consistent with previous clinical trials. Increases in low-density lipoprotein and total cholesterol were observed in around one in five patients but were manageable, and no new safety concerns emerged.

The investigators concluded that mitapivat is highly effective in routine clinical practice, substantially improving anaemia in non-transfusion-dependent patients while enabling many transfusion-dependent patients to achieve transfusion independence. The findings also highlight genotype as an important predictor of treatment response, supporting a more personalised approach to managing PKD.

Higher Mortality Rates in Haematological Malignancies Complicated by Pulmonary Embolism

MORTALITY rates among patients aged 25 years and above with haematological malignancies complicated by pulmonary embolism (PE) increased in the USA between 1999–2023. Interestingly, this coincided with a significant decline in overall mortality rates in patients with haematological malignancies over the same period according to a new study presented at EHA2026.[5]

PE remains a common and potentially fatal complication in patients with cancer, where an increased tendency for blood clotting contributes to a higher risk of venous thromboembolism and related mortality. Previous literature has focused on solid tumours, increasing venous thromboembolism in patients with cancer without the inclusion of haematological malignancies.

Researchers analysed age-adjusted mortality rates in individuals aged 25 years and over with haematological malignancies and haematological malignancies complicated by PE between 1999–2023 in the United States. The analysis also examined differences according to sex, age, region, urban or rural residence, and race using average annual percentage change (AAPC) and annual percentage change (APC).

Over the 24-year study period, haematological malignancies showed a steady decline with an AAPC of -1.75 (95% CI: -1.81–-1.69). The authors suggested that this decline was achieved through improvements in diagnosis, treatment and management of haematological malignancies.

Conversely, mortality among patients with haematological malignancies complicated by PE increased over the study period. Rates rose gradually between 1999–2017 before accelerating markedly from 2017–2023 (APC: 3.02; 95% CI: 0.51–5.58).

Mortality rates for haematological malignancies with PE increased across all dimensions, notably among males, the Western region and individuals aged 75 years or over. Higher mortality rates were also observed in non-metropolitan areas and among non-Hispanic Black individuals.

Overall, this study found disparities in mortality rates between patients with haematological malignancies and those with haematological malignancies complicated by PE.

Going forward, the authors called for future research to develop tailored intervention strategies guided by differences between subgroups to ultimately reduce the mortality rates among patients with PE and to optimise prognosis.

> **This study found disparities in mortality rates between patients with haematological malignancies and those with haematological malignancies complicated by PE**

References

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