

**8TH PAN ARAB HEMATOLOGY ASSOCIATION
CONGRESS**

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PROF. DR. ROSLINE HASSAN

**PUSAT PENGAJIAN SAINS PERUBATAN
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JANUARY

**Pan Arab Conference for Bleeding Disorders
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Riyadh, Kingdom of Saudi Arabia
30 January – 1 February 2019**

And

**Middle East & North Africa Hematology Congress
8Th Pan Arab Hematology Association Congress
17Th Annual Meeting Of Saudi Society Of Hematology
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1-4 February 2019**

A-038: Excellent outcome of nodular lymphocyte predominant Hodgkin lymphoma in the Eastern Province of Saudi Arabia: A real-world case series of 49 consecutive patients treated at a referral center from 2006 to 2017

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Nodular lymphocyte predominant Hodgkin lymphoma (NLPHL) is a rare HL-subtype and its optimal treatment is controversial. In this study we sought to evaluate and explore the contributing factors on the long-term outcome for patients with NLPHL. From 1/2006 to 12/2017, 49 consecutive NLPHL-patients treated in our institution. Their median age was 29 (16-56) years. At diagnosis 42 (86%) patients had typical histology, 4 (8%) variant, and 3 (6%) transformed type. Thirty-one (63%) were staged as I/II, 18 (37%) as III/IV while approximately 10% of patients presented with B-symptoms, extranodal disease or splenic involvement. Bulky disease (≥ 5 cm) had 12%, and bone marrow involvement 4% of patients. The German Hodgkin Study Group (GHSG) risk-score was intermediate in 26 (53%) and high in 12 (24%) patients. Only radiotherapy [\pm Rituximab (RT)] was given in 8 (16%), chemotherapy [\pm Rituximab, (CT)] in 21 (43%), combined modality [\pm Rituximab, (CMT)] in 13 (27%), Rituximab monotherapy in 3, (6%), and active surveillance (AS) in 4 (8%). For the 45 treated patients the overall response rate was 91% (complete responses: 69%) and 98% in the non-transformed histology cases at diagnosis. In a median F/U of 3 years all patients are alive; the 3- and 5-years progression-free survival (PFS) estimates of 80% and 75% while the current PFS is 98%. Two patients experienced transformation at relapse/progression and remain disease-free for 24 and 35months following auto-SCT. The 5-years cumulative risk of transformation (excluding the transformed cases at diagnosis) was 6%. In univariate analysis the: high GHLG risk-score, bulky disease, splenic involvement, transformed histology at diagnosis, and non-RT treatment, identified as unfavorable factors for prolonged PFS ($p < 0.02$), however in the multivariate analysis only the GHLG-score and non-RT approach retained their significance. None factor had any impact on overall survival. In our study, the overall outcome in NLPHL was excellent. Large prospective trials are warranted to determine the optimal treatment approach for NLPHL-patients.

Keywords: Hodgkin, lymphocyte, lymphoma

A-039: Expression level of pro-apoptotic genes determine disease severity of HbE/ beta thalassemia

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Introduction: Beta thalassemia syndromes are inherited disorders that occur as a result of abnormal synthesis of β -globin. As a result, the life span of erythrocytes is shortened. Imbalance of pro-apoptotic and anti-apoptotic genes could result in imbalance of cell survival. BAX and BAK1 are pro-apoptotic genes induced Cyt c release and caspase activation that will lead to cell apoptosis. Ineffective erythropoiesis has been studied in thalassemia, however the underlying apoptotic mechanism is unclear. **Objectives:** To determine the expression of pro-apoptotic genes namely in HbE/B thalassemia with different clinical severity. **Methods:** HbE/Beta thalassemia were classified into different clinical severity based on scoring system adapted from Sripichai, Makarasara *et al.* (2008). Two ml of blood was collected. Reticulocyte were isolated using Ficoll-Paque followed by filtration using cellulose column to remove the remaining WBCs. Reticulocyte RNA then was extracted by Trizol isolation reagent. RT2 profiler PCR array kit from Qiagen was used to evaluate the expression of genes. The pro-apoptotic genes analysis such as Cytochrome C (Cyt c) and the related BAX and BAK1 genes were done using Qiagen Data analysis center online software. **Results:** These three genes were upregulated in severe form of HbE/Beta thalassemia patients. BAX, BAK1 and Cyt c gene expression showed ranged of 2-2.7-fold upregulated. While in mild type, they were downregulated by 0.31. **Conclusion:** This preliminary result showed increased pro-apoptotic genes expression in reticulocytes have a role to the underlying mechanism of ineffective erythropoiesis and determine disease severity of HbE/Beta thalassemia. Further evaluation and validation using more samples is needed.

Keywords: Genes, pro-apoptotic, thalassemia

A-040: FLT3 receptor/CD135 expression by flow cytometry in acute myeloid leukemia: Relation to FLT3 gene mutations and mRNA transcripts

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Background: Alterations of the *FLT3* gene are the most frequent molecular aberrations seen at diagnosis of acute myeloid



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مؤسسة عامة - Gen. Org.



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CONGRESS BOOK

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SESSION 8B: THALASSEMIA DISORDERS ORAL ABSTRACTS

MODERATORS: MORTHADA HUSSAIN (IRAQ) - WAHEED TURKOSTANI (KSA)

⌚ 15:20 – 15:35

CLINICAL AND LABORATORY WORKUP OF A PATIENT WITH WHIM SYNDROME

🎤 RABAB ELHAWARY (EGYPT)

⌚ 15:35 – 15:50

ASSOCIATION BETWEEN GENOTYPE AND DISEASE COMPLICATIONS IN EGYPTIAN PATIENTS WITH BETA THALASSEMIA

🎤 TAMER HASSAN (EGYPT)

⌚ 15:50 – 16:05

EXPRESSION LEVEL OF PRO-APOPTOTIC GENES DETERMINE DISEASE SEVERITY OF HBE/BETA THALASSEMIA

🎤 ROSLINE HASSAN (MALAYSIA)



Expression Level of Pro-Apoptotic Genes Determine Disease Severity of HbE/Beta thalassemia

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Introduction

- Hb E/ β -thalassemia is inherited disorders that occur as a result of abnormal synthesis of β -globin
- Co-inheritance of α -globin hemoglobinopathies and increase level of HbF have shown to modulate the presentation of Hb E/ β -thalassemia , but not in all patients, suggesting that other factors may contribute to heterogeneity of the disease.
- Hb E/ β -thalassemia presented with a wide range of disease severity, ranging from essentially asymptomatic to a severe transfusion-dependent state

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Introduction

- In Hb E/ β -thalassemia , mutation of beta globin gene caused imbalance in the globin synthesis either due to reduce (β^+) or absent (β^0) production of the β -globin chain of the adult hemoglobin tetramer
- The severity of the disease is directly related to the imbalance between these globin chains, and precipitation of the excess α -globin chains, leading to oxidative damage of the cell membrane of RBC precursor with result ineffective erythropoiesis
- However the mechanism of this phenomenon still remains unclear



Introduction

- Anemia in Hb E/ β -thalassemia is due to both ineffective erythropoiesis AND reduce RBC lifespan, in some cases the erythroid precursor cells within the bone marrow undergo apoptosis
- Two mechanism of apoptosis namely intrinsic and extrinsic causes.
- Intrinsic apoptosis is initiated by the stress-mediated release of cytochrome c from the mitochondria.



Introduction

- In response to apoptotic stimuli, pro-apoptotic members of the Bcl-2 protein family (Bax and Bak) become activated and act on the mitochondria to induce the release of cytochrome c leads to cell death via the activation of a caspase cascade.
- There is limited study on the expression of these pro-apoptotic genes in relation to disease severity of Hb E/ β -thalassemia patients

Ref: Liam Portt et al, 2011 Anti-apoptosis and cell survival: A review

The 15th Annual Meeting of Southeastern Hematology 2018 & 20th Ann Hematology Association (UAMH)

15th Annual Meeting 2018



OBJECTIVES

To determine the expression of pro-apoptotic genes Cyt c, Bax and Bak1 in relation to clinical severity of HbE/ β thalassemia patients.

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