Hans status, IPI, CtDNA and TMTV, only an elevated IPI (P = 0.02) and high CtDNA load (P = 0.04) remained significant.

Conclusion: Despite a limited follow-up, this institutional study conducted in a large cohort of patients with aggressive B-cell lymphoma treated in real life, emphasizes that high CtDNA load and high TMTV are strong predictors of poor outcome. These characteristics at baseline could help tailoring therapy in these patients.

Keywords: Diagnostic and Prognostic Biomarkers, PET-CT, Liquid biopsy

No conflicts of interest pertinent to the abstract.

091 | CIRCULATING TUMOR DNA LOAD AND TOTAL METABOLIC TUMOR VOLUME IN DIFFUSE LARGE B CELL LYMPHOMA (DLBCL) PATIENTS TREATED BY R-CHOP – FROM REMARC, A LYSA STUDY

E. Bohers[1], M. Delfau-Larue[2], L. Vercellino[3], A. Cottereau[4], M. Viennot[1], P. Viailly[1], G. Salles[5], H. Tilly[6], G. Damaj[7], C. Haioun[8], V. Ribrag[9], F. Morschhauser[10], R. Casasnovas[11], E. Nicolas-Virelizier[12], P. Feugier[13], R. Bouabdallah[14], G. Cartron[15], L. Renaud[16], L. Chartier[17], C. Portugues[17], M. Meignan[18], F. Jardin[1], C. Thieblemont[19]

[1]*Team Genetics and Biomarkers in Lymphoma and Solid Tumors, INSERM U1245, Normandy University, Rouen, France,* [2]*Hematobiology and Immunobiology Department, INSERM U955 Eq9, APHP, University Hospital Henri Mondor, Créteil, France,* [3]*Department of Nuclear Medicine, APHP, Saint-Louis Hospital, Paris, France,* [4]*Department of Nuclear Medicine, APHP, Cochin, Paris, France,* [5]*Memorial Sloan Kettering Cancer Center, Lymphoma Department, New York, New York, USA,* [6]*Department of Hematology, Henri Becquerel Center, Rouen, France,* [7]*Department of Hematology, Caen University Hospital, Caen, France,* [8]*Department of Hematology, Henri Mondor University Hospital, Créteil, France,* [9]*Department of Hematology, Gustave Roussy Institute, Villejuif, France,* [10]*Department of Hematology, Lille University Hospital, Lille, France,* [11]*Department of Hematology, Dijon University Hospital, Dijon, France,* [12]*Department of Hematology, Leon Berard Center, Lyon, France,* [13]*Department of Hematology, Nancy university Hospital, Vandoeuvre-les-Nancy, France,* [14]*Department of Hematology, Paoli Calmette Institute, Marseille, France,* [15]*Department of Hematology, Montpellier University Hospital, Montpellier, France,* [16]*Department of Hematology, Lille University Hospital, Lille, France,* [17]*LYSARC, Lyon Hospital, Pierre-Benite, France,* [18]*Department of Nuclear Medicine, APHP, University Hospital Henri Mondor, Creteil, France,* [19]*Department of Hematology, APHP, Saint-Louis Hospital, Paris, France*

Background: Circulating tumor DNA (ctDNA) quantification has been shown to predict therapeutic benefit in patients (pts) with DLBCL. We recently investigated the prognostic impact of total metabolic tumor volume (TMTV) in DLBCL pts responder to R-CHOP in the REMARC study. In the present ancillary study, we wish to analyze the potential correlation of ctDNA with the outcome and relate these results to functional imaging by PET/CT (TMTV). We also aim to correlate the circulating tumor DNA load with the new score TMTV plus ECOG PS.

Patients and Methods: 794 pts were included in the study either at diagnosis (n = 446) or at the end of R-CHOP (n = 347). At the end of R-CHOP, 650 pts achieved a complete response and were randomized to receive 2 years of lenalidomide or placebo. Tumoral cfDNA measurements were performed using a dedicated 36 genes panel with the QiaSeq® technology. CtDNA concentrations were expressed in haploid genome equivalents per mL of plasma (hGE/mL) and calculated by multiplying the mean variant allele frequency (VAF) by the concentration of total cfDNA (Bohers *et al.* Blood Cancer J 2018).The optimal ctDNA cut-offs for PFS and OS were determined by X-tile analyses and confirmed by a training validation method.

Results: A total of 240 pts were analyzed, including 62 non-responder and non-randomized pts (NR-NRP) and 173 responder and randomized pts (REMARC pts). 5 pts had no interpretable ctDNA analysis and were excluded.

Among the 235 NR-NRP/REMARC cohort, a ctDNA > 3.74 was present in 14% of pts and was predictive for PFS (HR = 1.68, 95%CI 1.02–2.76, p = 0.0397) and OS (HR = 2.15, 95%CI 1.28-3.61, p = 0.0031). The 3y-PFS for pts with a ctDNA > 3.74 was 47.3% (95% CI: 30%-63%) *vs* 71.5% (95% CI: 65%-77%) for pts with a ctDNA ≤ 3.74. The 3y-OS for pts with a ctDNA > 3.74 was 56.4% (95%CI: 38%-71%) *vs* 81.8% (95% CI: 76%-87%) for pts with a ctDNA ≤ 3.74.

Among the 173 R-CHOP responder patients (REMARC cohort), the 12 months-relapse free survival since last cycle of R-CHOP for pts with a ctDNA > 3.74 at diagnosis was 61.1% (95%CI: 35%-79%) *vs* 88.7% (95%CI: 82%-93%) for pts with a ctDNA ≤ 3.74 (p = 0.009). However, a ctDNA > 3.74 was not predictive either for PFS (HR = 1.64, 95%CI: 0.84-3.21, p = 0.14) nor for OS (HR = 1.91 95%CI: 0.93-3.89, p = 0.07). Among the 100 pts with ctDNA and TMTV available, median log ctDNA was found significantly higher in TMTV > 220 (n = 58) *vs* TMTV < 220 (p = 0.002). However, no significant impact of ctDNA (threshold 3.4) and TMTV(threshold 220) was observed on PFS and OS.

Conclusion: Using a routinely targeted sequencing panel for ctDNA measurement, we confirmed the prognostic value of ctDNA concentration to predict outcome in DLBCL patients. For patients responding to R-CHOP, high ctDNA level was significantly associated with high TMTV and early relapse.

The research was funded by: BMS

Keywords: Diagnostic and Prognostic Biomarkers, Aggressive B-cell non-Hodgkin lymphoma

No conflicts of interest pertinent to the abstract.

092 | HIGH RISK AGGRESSIVE B-CELL LYMPHOMA ON THE LIQUID BIOPSY

L. Meriranta[1], A. Alkodsi[1], A. Pasanen[1], M. Lepistö[2], Y. N. Blaker[3], J. Jørgensen[4], P. Mapar[5], M. Björkholm[6], M. Jerkeman[7], H. Holte[3], E. Pitkänen[5], P. Ellonen[8], S. Leppä[1]

[1]*University of Helsinki and Helsinki University Hospital Comprehensive Cancer Centre, Department of Oncology and Applied Tumor Genomics Research Program, Helsinki, Finland,* [2]*University of Helsinki, Institute for*