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Wendy Cuccuini 1 2 , Josette Briere 1 3 4 , Nicolas Mounier 5 , Hans-Ullrich Voelker 6 , Andreas Rosenwald 6 , Christer Sundstrom 7 , Sergio Cogliatti 8 , Edouard Hirchaud 9 , Loic Ysebaert 10 , Dominique Bron 11 , Jean Soulier 1 2 , Philippe Gaulard 12 13 , Remi Houlgatte 14 , Christian Gisselbrecht 15 , Catherine Thieblemont 1 3 16 *

1 Centre de Biologie et de Pathologie Hôpital Sud Renée Sabran , Centre Hospitalier Lyon-Sud , Chemin du Grand Revoyet 69495 Pierre-Bénite, FR

2 Service d'Hématologie Biologique Hôpital Saint-Louis , Assistance publique - Hôpitaux de Paris (AP-HP) , 1, avenue Claude-Vellefaux 75010 Paris, FR

3 Gvh et Gvl : Physiopathologie Chez l'Homme et Chez l'Animal, Incidence et Role Therapeutique INSERM : U728 , Hôpital Saint-Louis , Assistance publique - Hôpitaux de Paris (AP-HP) , 1, avenue Claude-Vellefaux 75010 Paris, FR

4 Service d'Anatomo-Pathologie Hôpital Saint-Louis , Assistance Publique - Hôpitaux de Paris (AP-HP) , Université Paris VII - Paris Diderot , 1 avenue Claude Vellefaux 75475 Paris cedex 10, FR

5 Service d'Onco-Hématologie CHU Nice , Hôpital l'Archet , 57, Avenue de la Californie 06200 Nice, FR

6 Institute of Pathology University of Wuerzburg (for Deutsche Studiengruppe Hochmaligne Non-Hodgkin-Lymphome [DSHNHL]) , Sanderring 2, 97070 Würzburg, DE

7 Pathology Uppsala University Hospital , S:t Olofsgatan 10B, 753 12 Uppsala, SE

8 Institute of Pathology St Gallen Hospital (for Schweizerische Arbeitgeminschaft für Klinische Krebsforchnung [SAKK]) , Rorschacher Strasse 95, 9007 St. Gallen, CH

9 Physiopathologie et Pharmacologie Cellulaires et Moléculaires INSERM : U533 , IFR26 , Faculté de Médecine (dpt Physiologie) - Université de Nantes , 1, Rue Gaston Veil 44035 Nantes Cedex 01, FR

10 Service d'Hématologie CHU Toulouse , Hôpital Purpan , Place du Docteur Baylac - TSA 40031 - 31059 Toulouse cedex 9, FR

11 Service Hématologie Institut Jules Bordet , Boulevard de Waterloo 121, 1000 Bruxelles, BE

12 Institut Mondor de Recherche Biomédicale INSERM : U955 , Université Paris XII - Paris Est Créteil Val-de-Marne , IFR10 , 8 rue du Général Sarrail 94010 Créteil, FR

13 Service d'anatomie et cytologie pathologiques [Mondor] Assistance publique - Hôpitaux de Paris (AP-HP) , Hôpital Henri Mondor , Université Paris XII - Paris Est Créteil Val-de-Marne , 51 Av Maréchal de Lattre de Tassigny 94000 Créteil, FR

14 Nutrition-Génétique et Exposition aux Risques Environnementaux INSERM : U954 , Faculté de Médecine - Université Henri Poincaré - Nancy I , Bâtiment C - 2ème étage - 9 avenue de la Forêt de Haye - B.P. 184 - 54505 Vandoeuvre-Les-Nancy Cedex, FR

15 GELA : Groupe d'Etude des Lymphomes de l'Adulte C.H. Lyon-Sud , Chemin du Grand-Revoyet 69310 Pierre-Benite, FR

16 Service d'Onco-Hématologie Hôpital Saint-Louis , Assistance publique - Hôpitaux de Paris (AP-HP) , 1, avenue Claude Vellefaux 75010 Paris, FR

* Correspondence should be addressed to: Catherine Thieblemont <catherine.thieblemont@sls.aphp.fr >

Abstract

Approximately 5–10% of diffuse large B-cell lymphomas (DLBCL) harbor a 8q24/*MYC* rearrangement (*MYC* $^{+}$). We determined the prognostic significance of *MYC* rearrangement in patients with relapsed/refractory DLBCL prospectively treated by R-ICE or R-DHAP followed by high-dose therapy and autologous stem cell transplantation. Twenty-eight (17%) of the 161 patients analyzed presented a *MYC* $^{+}$ rearrangement, targeted as either simple hit (25%) or complex hits (n=75%) including *MYC/BCL2, MYC/BCL6,* and *MYC/BCL2/BCL6*. Results were statistically highly concordant in matched primary and relapsed biopsies (n=45). Compared to the *MYC* $^{-}$ DLBCL patients, the *MYC* $^{+}$ DLBCL patients presented with a more elevated lactico-deshydrogenase level (p=.0006) and a more advanced age-adjusted international pronostic index (p=.0039). The 4-year PFS and OS were significantly lower in the *MYC* $^{+}$ DLBCL patients than those in the *MYC* $^{-}$ DLBCL patients, with rates of 18% vs. 42% (p=.0322), and of 29% vs. 62% (p=.0113), respectively. Type of treatment, R-DHAP or R-ICE had no impact on survivals, with 4-year PFS rates of 17% vs. 19% and 4-year OS rates of 26% vs. 31%. In conclusion, *MYC* rearrangement is an early event in DLBCL. *MYC* $^{+}$ DLBCL patients have a significant inferior prognosis than *MYC* $^{-}$ DLBCL patients. Their outcome was not influenced by the proposed salvage therapy.

MESH Keywords Adult ; Aged ; Antibodies, Monoclonal, Murine-Derived ; administration & dosage ; adverse effects ; Antineoplastic Combined Chemotherapy Protocols ; administration & dosage ; adverse effects ; Carmustine ; administration & dosage ; adverse effects ; Chemotherapy, Adjuvant ; Cisplatin ; administration & dosage ; adverse effects ; Combined Modality Therapy ; Cytarabine ; administration & dosage ; adverse effects ; Dexamethasone ; administration & dosage ; adverse effects ; Etoposide ;

INTRODUCTION

Diffuse large B-cell lymphomas (DLBCLs) are recognized as a heterogeneous group of aggressive lymphomas, with numerous clinical, morphological, immunohistochemical and molecular subtypes, as demonstrated by the last World Health Organisation (WHO) classification, which defines no less than 13 subentities[1]. Among the DLBCLs, between 4% to 14% harbor a *MYC* rearrangement (*MYC* DLBCL) as evaluated by fluorescence in situ hybridization (FISH)[2,6]. These cases differ from the defined "borderline" cases, which are considered unclassifiable B-cell lymphomas having features that are intermediate between DLBCL and Burkitt lymphomas [7,8] and presenting with a mixture of medium-to-large-sized cells, a high proliferation rate and an 8q24/*MYC* translocation in 35 to 50% of cases[7,8]. In contrast to the Burkitt lymphomas, *MYC* aberrations in DLBCL are usually associated with multiple cytogenetic abnormalities and other genetic lesions, such as concurrent *BCL2* and/or *BCL6* translocations, so-called "double-hit" or "triple-hit" lymphomas[5,9–13].

The clinical importance of the presence of an *MYC* aberration in DLBCL has been recently suggested in series of patients analyzed in first-line therapy. Patients with *MYC* DLBCL have been reported in one series[6]to present a disease similar to DLBCL but without an *MYC* aberration (*MYC* DLBCL) showing no differences in median age, LDH (Lactico-deshydrogenase), IPI (International Prognostic Index) or performance status. The only difference noted was a higher proliferative rate, as determined by Ki67 staining in excess of 80%, in patients harboring a *MYC* aberrations[6]. In other series, patients with *MYC* DLBCL present with a more aggressive disease including particular clinical features such as poor performance status and bone marrow involvement[5], or more advanced stage, higher IPI, and a higher age-adjusted IPI[2]. With respect to survival, all series agree in reporting that these patients with *MYC* DLBCL have poorer outcomes than patients with *MYC* $^{-}$ DLBCL[5,6], regardless of the treatment regimen included, such as cyclophosphamide, doxorubicin, vincristine, prednisone (CHOP), and CHOP plus etoposide (CHOEP)[4,5]. The presence of *MYC* aberrations retains its negative prognostic significance even in patients treated with rituximab and anthracycline-based immuno-chemotherapy[2,3,6]. However, one recent study reported that a regimen based on DA-EPOCH-R (Dose-adjusted etoposide, vincristine, and doxorubicine for 96 hours with bolus of cyclophosphamide and oral prednisone, plus Rituximab) in first-line may improve the outcome of these patients[14]. Importantly, the prognostic impact of the presence of *MYC* aberrations appears to be independent from other factors such as IPI, and bone marrow involvement[6]. Furthermore, the negative impact of *MYC* aberrations supersedes the favorable prognosis of GC DLBCL, with a significantly worse event-free and overall survivals compared with either the non-GC phenotype or *MYC* $^{-}$ DLBCL[4,6].

The purpose of this study was to screen for *MYC* aberrations in a selected population of patients with relapsed/refractory DLBCLs to determine the frequency of this occurrence and whether there were any defining phenotypic or clinical features in the *MYC* $^{+}$ group and to assess the prognostic impact of *MYC* aberrations in these relapsed/refractory DLBCL patients treated prospectively with R-DHAP (rituximab, dexamethasone, aracytine, cisplatin) vs. R-ICE (rituximab, ifosfamide, etoposide, carboplatin) that was followed by high-dose therapy plus autologous stem cell transplantation (HDT/ASCT).

MATERIALS AND METHODS

The patients studied in the present biological analyses were a subset of the 477 patients analyzed in the CORAL study[15], which enrolled patients aged 18 to 65 years old who presented a relapsed/refractory CD20+ DLBCL to compare the efficacy of R-ICE and R-DHAP followed by HDT/ASCT (part 1) and to test maintenance with or without rituximab (part 2). The study was registered under European Union Drug Regulating Authorities Clinical Trials (EudraCT) No.2004-002103-32 and ClinicalTrials.gov NCT 00137995 and was conducted in accordance with Good Clinical Practice rules. All patients gave written informed consent to participate and to provide tissue material for biological studies.

Fluorescent in situ hybridization (FISH) analysis

Histological material was available for a total of 161 patients at diagnosis (n=121 cases) and/or at relapse (n=87 cases) for FISH analysis. FISH analysis was performed on TMA or full slides of paraffin-embedded 2–3-μm tissue sections using the break-apart probes for *c-MYC*/8q24 (Abbott, France and Germany). Further analyses were conducted using break-apart probes for *BCL2*/18q21 and *BCL6* /3q27 (Abbott, France and Germany). Samples were analyzed with an AxioImager.M1 epifluorescence microscope (Carl Zeiss, Germany). Images were captured with a 63X or 100X oil objective and analyzed with the Isis software (MetaSystems, Germany). The hybridization signal scoring was performed according to Haralambieva et al.[16], with a normal cutoff value of 10%.

Morphology, immunohistochemistry and Cell of origin (COO) algorithms

A panel of five hematopathologists (JB, PG, HUV, CS, SC) conducted a central review to confirm the diagnosis of CD20+ DLBCL[1,17]. None of the 161 cases were intermediate cases between DLBCL and Burkitt lymphoma: all were diagnosed as DLBCL. The same panel of hematopathologists centrally evaluated the immunostainings and the FISH results. Immunostainings against CD10 (clone 56C6, dilution 1/50; Novocastra, Newcastle, United Kingdom), BLC2 (bcl-2 124; Dako, Glostrup, Denmark), IRF4/MUM1 (clone Mum1p, dilution 1/20; Dako A/S), BCL6 (clone P1F6, dilution 1/10; Dako A/S, Glostrup, Denmark), and FOXP1 (clone JC12, dilution 1/50; A.H. Banham, Oxford, United Kingdom) were performed using 3-µm sections either from either full slides or from tissue microarrays (TMAs) containing two or three representative 0.6-mm cores of routinely FFPE (formaldehyde fixed-paraffin embedded) tissue from each cases. The results of each immunostaining trial were considered positive when greater than 30% of the lymphoma cells were stained. The tissue quality was morphologically evaluated on H-E staining. All evaluable cases were given a secondary classification according to the COO algorithms previously described by Hans et al.[18], Muris et al.[19], and Nyman et al.[20].

Microarray procedures and analyses

A subset of 37 patients was selected with both the *MYC* FISH analysis and the GEP (gene expression profiling) analysis realized. A total of 47 samples (20 primary biopsies, 17 relapse biopsies and 5 matched cases) were then included. The microarray procedures are previously described[17]. Briefly, total RNA quantity and initial quality were estimated with a NanoDrop® ND-1000 spectrophotometer, and RNA quality was further assessed by electrophoresis (Agilent 2100 Bioanalyzer: Agilent Technologies, Mississauga, ON). The Agilent Whole Human Genome microarray (G4112F) and a gene-voting method were used to determine the COO based on the genes' discriminating GCB/ABC signatures previously reported by Alizadeh et al.[21]to define a GCB/ABC predictor similar to that described our previous work[17]. The samples were then classified based on this predictor. The microarray data were submitted to the Gene Expression Omnibus (GEO) (GSE26812).

Statistical analysis

As previously reported[17], no statistical variations in each biological parameter analyzed by IHC obtained at diagnosis and at relapse were detected among the matched pairs (data not shown). This finding allowed us to analyze all data in a similar manner, irrespective of whether they were generated from diagnostic or relapse biopsies. All survival analyses were performed on an intention-to-treat basis. Patient characteristics and complete remission rates were compared by the chi-squared and Fisher exact tests. Progression-free survival (PFS) was defined as the time from study entry until disease progression or death. Overall survival (OS) was defined as the time from the start of treatment until death. Survival functions were estimated using the Kaplan-Meier method and compared with the log-rank test[22]. Differences between the results of comparative tests were considered significant at a 2-sided $P < 0.05$. Because the CORAL trial was not stratified by biological data, we controlled for the effects of prognostic factors on outcome due to sampling fluctuations in the treatment groups with a multivariate analysis of survival in a Cox model[23]. All statistical analyses were performed using SAS 9.13 (SAS Institute, Cary, NC) and S-Plus 6.2 (MathSoft, Cambridge, MA) software

RESULTS

Overall, 161 of the 477 patients included in the CORAL trial were included based on a successful FISH analysis at defining the presence or absence of an *MYC* rearrangement using paraffin-embedded-tissue (TMA or full slides). One hundred and twenty-one cases were collected at diagnosis (primary biopsy), and 84 cases were collected at relapse (relapse biopsy), including 45 matched cases with the biopsies obtained at both diagnosis and relapse.

In total, 28 of the 161 (17%) cases disclosed an *MYC* rearrangement. Twenty-one of the *MYC* $^{+}$ cases (75%) had one or more concurrent translocations, implicating either *BCL2* in t(14;18), or *BCL6* in t(3;14), so-called “double-hits”, or *BCL2* in t14;18) and *BCL6* in t(3;14), so-called “triple-hits”. The *MYC* rearrangements were mostly translocations (Table 1). In 2 cases, we observed multiple copies of *MYC*. Considering the 45 matched cases, the results for the primary and secondary biopsies were similar in 87% of the cases (Wilcoxon's paired ranked test p=.99). At diagnosis, 6 (6/45, 13%) cases were *MYC* $^{+}$ cases, and 39 (39/45, 87%) were *MYC* $^{-}$ cases. At relapse 8 (8/45, 18%) cases were *MYC* $^{+}$ cases, and 37 (39/45, 82%) were *MYC* $^{-}$ cases.

Clinical Characteristics

MYC $^{+}$ DLBCL patients were predominantly male (71%) with a median age of 55 years (range: 44–65 years). Compared with *MYC* $^{-}$ DLBCL patients, the *MYC* $^{+}$ DLBCL patients presented with more advanced disease, showing a high aaIPI in 54% of the patients (p=.0039), and an elevated LDH level in 77% of them (p=.0006) (Table 2). There was no difference in the frequency of extranodal site involvement. The number of patients with early relapse, defined as relapse less than 12 months from the end of first-line treatment, was identical in both groups (*MYC* $^{+}$ cases, 61% vs. *MYC* $^{-}$ cases, 50%, p=.3196).

IHC and cell of origin

MYC $^{+}$ DLBCL cases expressed significantly more CD10 than *MYC* $^{-}$ DLBCL cases (60% vs. 34%, respectively p=.0137) as shown in Table 3. Immunohistochemical expression of BCL6, MUM/IRF4, and FOXP1 in *MYC* $^{+}$ tumor cells were observed in 77%, 33%, 81% of the cases, respectively without significant differences compared with the *MYC* tumor cells.

The COO phenotype assignments by IHC based on Hans's algorithm, Muris's algorithm, and Nyman's algorithm, were available for 152 cases. Based on Hans's algorithm, *MYC* $^{+}$ DLBCL cases were classified as GC in 63% of the cases, whereas 46% were classified as GC in the MYC^{-} DLBCL cases. Thirty-seven cases were assigned by GEP. Based on the GEP predictor for the GCB/ABC genotype, 3 *MYC* $^{+}$ DLBCL cases exhibited a GCB profile.

Impact on response and survival of MYC rearrangements in patients with relapsed/refractory DLBCL

At salvage therapy, 83 patients were treated with R-DHAP and 78 were treated with R-ICE. After the induction treatment (R-ICE or R-DHAP), the overall response rate (ORR) was lower in the cohort of patients with *MYC* $^{+}$ DLBCL than in the cohort of patients with *MYC* $^{-}$ DLBCL (50% vs. 69%, respectively, p=.0519); see Table 2.

The complete response rate (CR) after induction treatment (R-ICE or R-DHAP) was significantly lower in patients with *MYC* $^{+}$ DLBCL than in those with *MYC* $^{-}$ DLBCL (25% vs. 45%, p=.0497). After the induction treatment, fewer *MYC* $^{+}$ DLBCL patients underwent HDT/ASCT than those *MYC* $^{-}$ DLBCL patients (43% vs. 60%, p=.0928).

The 4-year PFS and OS were significantly lower in the *MYC* $^{+}$ DLBCL patients than in the *MYC* $^{-}$ DLBCL patients (Figure 1), with rates of 18% vs. 42% (p=.0322), and 29% vs. 62% (p=.0113), respectively. The same result was observed for the *MYC* $^{+}$ DLBCL patients who underwent the HDT/ASCT. These *MYC* $^{+}$ DLBCL patients treated with HDT/ASCT had a 4-year PFS and OS rates of 14% and 23 %, respectively.

No difference was observed when we compared the group of cases with *MYC* rearrangements consisting of single chromosomal aberrations and the group of cases with *MYC* rearrangements presenting as complex aberrations with dual and triple translocations. The 4-year PFS (16% vs. 17%, p=.8700) and OS (25% vs. 33%, p=.7677) rates were similar in the single-hit and in the complex-hit groups.

Impact of R-ICE and R-DHAP treatment

The type of treatment (R-ICE or R-DHAP) did not influence the outcomes of the *MYC* $^{+}$ DLBCL patients. The corresponding ORR and CR rates were 50% and 25% in the *MYC* $^{+}$ DLBCL patients, respectively, with no differences observed after R-ICE (ORR = 40%, CR 23%) or R-DHAP (ORR= 62%, CR = 26%) (ORR p=.1607; CR, p=.8268) (Table 4). In patients with *MYC* $^{-}$ DLBCL, the CR rates were 35 % and 54% with R-ICE and with R-DHAP respectively (p=.0250).

With respect to survival, R-ICE and R-DHAP yielded similar results in the cohort of patients with *MYC* $^{+}$ DLBCL. The 3-year PFS was at 19% in the R-ICE arm and 17% in the R-DHAP arm (Figure 2). The respective 3-year OS rates were 26% and 31% (Figure 2). In the cohort of patients with MYC^{-} DLBCL, the 3-year PFS and OS rates were 31% and 51% in the RICE arm and 53% and 71% in the RDHAP arm, respectively.

Impacts of the GCB and non-GCB phenotypes

When we classified the entire cohort of the 161 patients into subgroups based on the GCB vs. non-GCB phenotype using Hans's algorithm, the GCB DLBCL patients treated with R-DHAP had a significantly higher complete remission rate than the non-GCB DLBCL patients (49% vs. 31%, p=.0348), as previously reported[17](Table 4).

Multivariate analysis using a Cox proportional hazard model including the presence or absence of *MYC* aberrations, the type of induction treatment, R-ICE vs. R-DHAP, and the GC vs. non-GC phenotype based on Hans's algorithm confirmed that the only significant factor for both PFS and OS was the presence of a *MYC* aberration, with a relative risk [RR] of 1.8 for PFS (p = .0248), and an RR of 2 for OS (p = .0162).

DISCUSSION

A limited number of studies evaluating the prognostic importance of *MYC* status have been reported to date but all were in the context of first-line treatment based on CHOP or CHOP-like regimens, with or without rituximab[2,4–6,11,13]. This report is the first study to analyze the impact of *MYC* aberration in patients less than 65 years old with relapsed/refractory DLBCL.

Several characteristics of the clinical presentation of the disease and the patients with *MYC*+ DLBCL at relapse are interesting to highlight. First, the median ages *MYC* $^{+}$ DLBCL and *MYC* $^{-}$ DLBCL patients are similar. Second, the times to relapse between the end of first-line treatment and the time of relapse treatment, which correspond to the randomization in the CORAL trial, are similar in both patient cohorts. Third, the clinical presentation of *MYC* $^{+}$ DLBCL seems more aggressive than that of *MYC* $^{-}$ DLBCL, as reported previously in a series of patients undergoing first-line treatment[2,5,6]. *MYC* $^{+}$ DLBCL LDH levels were more often elevated, as were the IPI scores. However, we did not observe more patients with more than one extranodal site, representing 29% of the patients in our series.

All of the prior studies performed in first-line treatment using anthracycline-based regimens with or without rituximab found a strong prognostic impact of *MYC* gene rearrangement. In the context of relapsed/refractory DLBCL, the outcomes of the *MYC* $^{+}$ DLBCL patients were also found to be worse than those of the *MYC* $^{-}$ DLBCL patients. This was true regardless of the type of induction treatments, i.e. R-ICE or R-DHAP. Complete remission rates were low, accounting for approximately 25% of the *MYC* $^{+}$ DLBCL patients. Less than half of these responder *MYC* $^{+}$ DLBCL patients followed the complete course of treatment and received the high-dose treatment with autologous stem cell transplantation, compared with 60% in the *MYC* $^{-}$ DLBCL group.

With the caveat that this study examined a relatively small number of cases, the type of aberrations of *MYC* gene (single-, double- or triple-hit) had no impact on these results. The role of the *MYC* aberration appeared to be the same whether the aberration was extra copies of the gene or a chromosomal translocation implicating *MYC*. We observed no differences when *MYC* aberrations were associated as complex hits with other aberrations including *BCL2* and *BCL6* gene rearrangements.

Taking the opportunity to analyze the tumors at both diagnosis and relapse in the 45 matched cases, *MYC* aberrations were found be present or absent in a similar ways in the biopsies at diagnosis and those at relapse. This suggests that the occurrence of *MYC* aberration is probably an early event in the pathogenesis of this tumor.

Regarding the phenotypes of the cases, an *MYC* aberration was strongly associated with the GCB phenotype, showing significant associations with CD10 expression and a GCB phenotype based on a GEP analysis. The *MYC* $^{+}$ cases were more often classified as GCB based on Hans's algorithm. The outcome of the patients with GCB phenotypes based on Hans's algorithm who were treated with R-DHAP was better than the outcome of the patients with non-GCB phenotype, except when *MYC* gene was rearranged. *MYC* rearrangement was found to counteract the good prognosis associated with the GCB profile and R-DHAP treatment.

In conclusion, *MYC* rearrangements were found to be present in 17% of the patients with relapsed/refractory DLBCL, defining a small group of patients with a very bad prognosis independently from the known prognostic risk factors and regardless the type of treatment proposed, even in the case of HDT/ASCT. Moreover, our results suggest that this genetic event is probably an early event in the pathogenesis of the tumor and is associated with a GCB phenotype. Finally, our data together with those of previous studies highlight the fundamental role of *MYC* in the prognosis of DLBCL, particularly GCB-like DLBCL. This finding suggests the importance of performing FISH analysis for MYC rearrangement in highly proliferative DLBCL and emphasizes the need for new treatments for patients with *MYC* $^{+}$ DLBCL.

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Footnotes:

Author contributions W. Cuccuini performed research, analyzed data and contributed to the writing of the paper J Briere designed and performed research, analyzed data, and wrote the paper N Mounier designed and performed research, analyzed data, and wrote the paper Hans-Ullrich Voelker performed research, analyzed data, and contributed to the writing of the paper A. Rosenwald analyzed data and contributed to the writing of the paper C. Sunstrom analyzed data and contributed to the writing of the paper S Coggliati analyzed data and contributed to the writing of the paper E Hirchaud analyzed data and contributed to the writing of the paper L Ysebaert analyzed data and contributed to the writing of the paper D Bron analyzed data and contributed to the writing of the paper J Soulier analyzed data and contributed to the writing of the paper P Gaulard analyzed data and contributed to the writing of the paper R Houlgatte performed research, analyzed data, and wrote the paper C Gisselbrecht analyzed data and contributed to the writing of the paper C. Thieblemont designed research, analyzed data, and wrote the paper

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Figure 1

Progression-free survival and overall survival according to the presence (*MYC*+) or the absence (*MYC*−) of *MYC* aberration

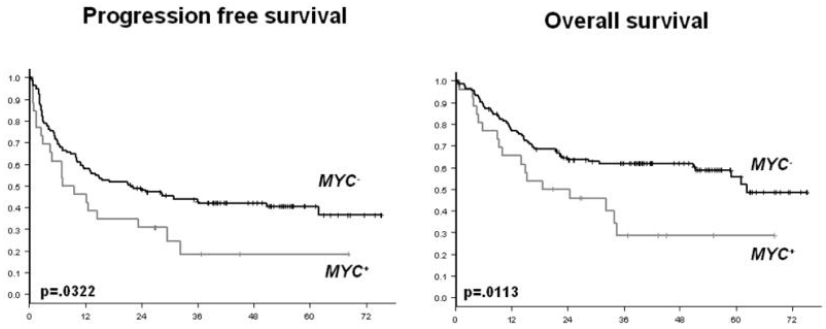

Figure 2

Progression-free survival and overall survival according to the treatment and the presence (*MYC*+) or absence (*MYC*−) of *MYC* aberration

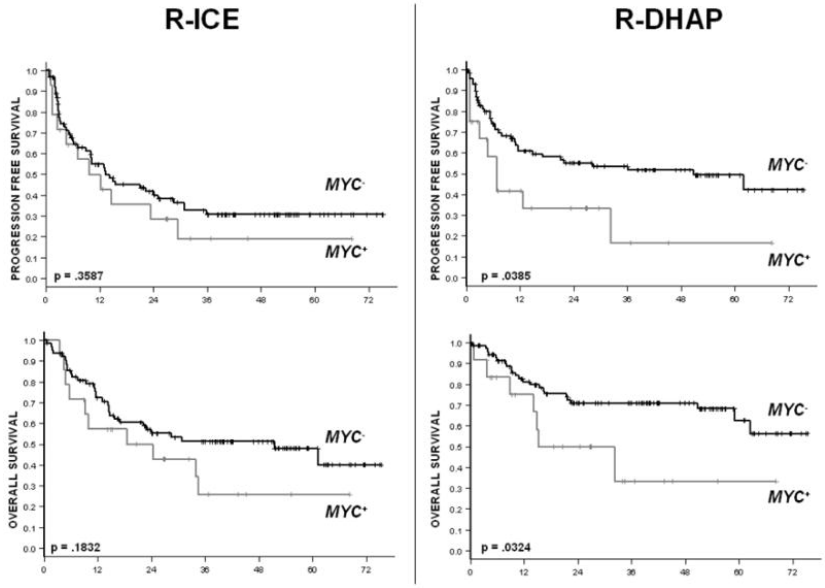

Table 1

Type of *MYC*/8q24 aberration and its association with other rearrangements including *BCL2*/18q21 and *BCL6*/3q27 in the relapsed/refractory DLBCL

	n	(%)
Total of patients analysed	**161**	**(100)**
Presence of *MYC*/8q24 aberration	**28**	**(17)**
Simple hit : *MYC*/8q24 only	**7**	
Complex hits	**21**	
Double hit		
MYC/8q24 and *BCL2*/18q21	**13**	
MYC/8q24 and *BCL6*/3q27	**4**	
Triple hit		
MYC/8q24 and *BCL2*/18q21and *BCL6*/3q27	**4**	
No rearrangement	**133**	**(83)**

Table 2

Baseline characteristics of patients with either *MYC* $^{+}$ or *MYC* $^{-}$ relapsed/refractory DLBCL

	MYC $^{+}$ DLBCL		*MYC* $^{-}$ DLBCL		p
No. of patients	**n =28**	%	**n =133**	%	
Sex					
Male	20	71	77	59	.1835
Female	8	29	56	41	
Age					
Median	55		54		.1135
Range	44–65		19–65		
PS(ECOG)					
0–1	23	82	122	92	.1128
2–3	5	18	11	8	
Ann Arbor Stage					
I–II	8	29	63	48	.0200
III–IV	20	71	70	52	
Elevated LDH	20	77	53	40	.0006
Extranodal site > 1	8	29	33	25	.1821
aaIIPI					
0–1	12	46	94	71	.0081
2–3	14	54	38	29	
Initial response					
CR-CRU	16	57	81	61	.3669
CRU	2	7	18	14	
PR	5	18	18	14	
Stable disease	2	7	4	3	
Progression	5	18	12	9	
Time to relapse					.3196
< 12 months	17	61	67	50	
≥ 12 months	11	39	66	50	
Prior rituximab treatment	20	71	80	60	.2635
Treatment at relapse					
RICE	15	54	63	53	.5505
RDHAP	13	46	70	47	
Response at induction					
CR/CRU	7	25	60	45	.0497
PR	5	18	20	15	
Overall response (CR/CRU/PR)	14	50	92	69	.0519
Transplant	12	43	80	60	.0928

Table 3

Immunohistochemical staining results, cell of origin classification based on GC/nonGC algorithms, according the presence or the absence of *MYC* aberration

Cases		***MYC* +**		***MYC* −**	
Parameter	**n**	**(%)**	**n**	**(%)**	**p**
Immunohistochemistry					
CD10	27		127		
Positive	16	60	84	66	.0137
Negative	11	40	43	34	
BCL6	26		128		
Positive	20	77	88	69	.4065
Negative	6	23	40	31	
MUM1/IRF4	27		128		
Positive	9	33	62	48	.1523
Negative	18	67	66	52	
FOXP1 (Barrans)	27		128		
Positive	22	81	86	67	1420
Negative	5	19	42	33	
BCL2	27		128		
Positive	22	81	31	76	.5239
Negative	5	19	97	24	
GC/nonGC algorithm publication					
Hans et al.	27		125		
GC	17	63	57	46	.1017
Non GC	10	37	68	54	
Muris et al.	27		126		
Group 1	22	82	80	63	.0719
Group 2	5	19	46	37	
Nyman et al.	23		123		
ABC	5	22	30	24	.7846
Others	18	78	93	76	
Cell of origin based on GEP					
	3		24		
GC	3	100	13	54	-
ABC	0	0	11	46	

GC indicates germinal center; GEP gene expression profiling, and ABC, activated B-cell

Table 4

Complete response considering type of treatment (R-ICE vs R-DHAP) and phenotype characteristics including cell of origin based on Hans's algorythm and MYC aberration

Treatment	Complete response		p (X2)
	R-ICE n=78 (%)	R-DHAP n=83 (%)	
Patients analysed by FISH	29 (37)	35 (42)	.3187
Hans COO			
GC	24 (31)	41 (49)	.0348
Non GC	37 (47)	32 (38)	.2931
***MYC* aberration**			
Presence	20 (26)	19 (23)	.8268
Absence	27 (35)	45 (54)	.0250

GC = Germinal Center