EUROPEAN HEMATOLOGY ASSOCIATION

haematologica

Journal of the European Hematology Association

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Haematologica 2015 [Epub ahead of print]

Citation: Luminari S, Galimberti S, Versari A, Biasoli I, Anastasia A, Rusconi C, Ferrari A, Petrini M, Manni M, and Federico M. Positron emission tomography response and minimal residual disease impact on progression-free survival in patients with follicular lymphoma. A subset analysis from the FOLL05 trial of the Fondazione Italiana Linfomi. Haematologica. 2015; 100:xxx
doi:10.3324/haematol.2015.132811

Positron emission tomography response and minimal residual disease impact on progression-free survival in patients with follicular lymphoma. A subset analysis from the FOLL05 trial of the Fondazione Italiana Linfomi.

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No conflicts of interest need to be disclosed.

Running title: PET and molecular response in patients with FL

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Follicular lymphoma (FL) is the most common indolent B-cell lymphoma in western countries. Overall, 70% of the patients achieve complete remission after first treatment.[1] However, it is characterized by a pattern of relapsing and remitting disease. The outcome of patients with FL has clearly improved,[2] but heterogeneity in patients' survival still remains, making the quest for reliable prognostic factors a relevant issue.

Response assessment of patients with FL can be performed with CT scan and [^{18}F]fluorodeoxyglucose – Positron Emission Tomography (FDG-PET) scan. FDG-PET has been confirmed to have the highest accuracy and was shown to be independent of CT scan and to be a stronger predictor of outcome.[3] Recently, PET has been acknowledged as a recommended procedure for FL staging and response assessment.[4] Moreover, the assessment of MRD by qualitative and quantitative polymerase chain reaction (PCR) for Bcl2/IgH has been evaluated as a prognostic tool in FL.[5] Nevertheless the impact of both end of treatment (EOT) PET and MRD in prognostic assessment remains to be determined.

The aim of the present study was to analyze the prognostic role of combined PET and BCL2/IGH analysis, performed at the EOT, in a subset study of the phase III trial FOLL05 (NCT00774826), in which patients with FL were randomized to R-CVP (rituximab plus cyclophosphamide, vincristine and prednisone), R-CHOP (rituximab plus cyclophosphamide, doxorubicin, vincristine and prednisone) or R-FM (rituximab plus fludarabine and mitoxantrone).[6] This study was conducted in compliance with the Declaration of Helsinki, was approved by the appropriate research ethics committee, and required each patient to provide written informed consent.

In order to be considered for the current study, patients were required to have been enrolled in the FOLL05 trial that included previously untreated high tumor burden Ann Arbor stage II to IV FL grade 1,2,3a.[6] Of note, the FOLL05 study included MRD evaluation at the EOT among planned study procedures.[5] Also, for the purpose of this study patients should also have available data on EOT PET, performed up to three months after the last dose of induction rituximab (+/- chemotherapy) and assessed for the BCL2/IGH at diagnosis and at the EOT within 2 months from last dose. Data on clinical presentation, treatment, response and follow-up were retrieved from the existing and published dataset of the randomized protocol.

PET was centrally reviewed by three independent nuclear medicine physicians applying the Deauville scale. Positive scans (PET+) were defined by residual FDG uptake ≥ score 4 (i.e. uptake moderately > liver uptake). Final result was assigned by agreement between at least two of three reviewers.

Regarding MRD analysis, patients underwent bone marrow (BM) aspirate for qualitative and quantitative assessment of the BCL2/IGH fusion gene. DNAs from the patients were assessed for the BCL2/IGH at diagnosis, and if positive, at the EOT. All qualitative molecular analyses were centralized at the molecular laboratory of the Division of Hematology of the Pisa University, Italy. DNA was extracted from BM mononuclear cells by the Wizard Genomic DNA Purification Kit (Promega). To amplify BCL2/IGH rearrangement, nested qualitative PCR reactions were performed.[7] The sensitivity of the qualitative PCR assays was confirmed by testing serial dilutions of DNA derived from the BCL2/IGH-positive DOHH-2 cell line, achieving a limiting dilution of $1:10^{-5}$. A second reaction for mcr breakpoint was also performed as already reported.[8]

The primary endpoint was progression-free survival (PFS), that was calculated as the time from the date of treatment start until the date of lymphoma progression, relapse, death from any cause or last follow-up visit. Standard descriptive analyses were carried out. For a crude association analysis, categorical data were analyzed using the chi-square or Fisher's exact test (two-sided). Cohen's kappa statistic was used to verify agreement between PET and MRD results. The level of agreement was defined by Koch Landis scale. Survival curves were estimated using the Kaplan–Meier method and compared using the log-rank test. Univariate Cox regression analyses were conducted to verify the prognostic role of final PET and MRD regarding PFS. Two-tailed *P* values <0.05 were considered statistically significant. Statistical analysis was carried out with SPSS software (ver 18.0,Chicago, IL).

A total of 41 patients had available data on both PET and BCL2/IGH at the EOT. The median age was 54 years (39-71). Baseline characteristics of the study population did not differ from that of the FOLL05 study (Table 1). The distribution of cases according to EOT PET and MRD is shown in Table 2. PET/MRD concordance was 76%, with Kappa=0.249, suggesting that PET and MRD when done at the end of induction therapy are not strongly correlated.

With a median follow up of 53 months (from 13 to 77 months) 5 year PFS was 62% (95% CI 45 to 75). By univariate analysis, EOT PET+ was associated to a poorer PFS (HR 3.61, 95%CI 1.15-11.4, P=.028), while the EOT positive molecular status had a trend towards a shorter PFS (HR 2.54, 95%CI 0.96-6.72, P=.060) (Figure 1).

In a stratified analysis combining the information of PET and MRD, the 3-y-PFS were 78%, 50% and 27% in PET/MRD -/-, PET/MRD -/+ and PET+ groups,

respectively (p=0.015 for all groups, and p=0.067 between PET/MRD -/- and PET/MRD -/+). We also stratified the patients in 2 groups (PET-/MRD- vs PET+ or MRD+), and the achievement of both PET and MRD negativity was associated to a better outcome (HR 3.42, 95%CI 1.31-8.95, P=.012), with 5-yr PFS of 75% (95% CI 54 to 87%) and 35% (95% CI 11 to 60%) for PET/MDR -/- and PET+, respectively (Figure 2).

To the best of our knowledge, this is the first report combining the information of PET and MRD at the end of the induction treatment in FL patients. Although this is a small subset of a large trial, the present results can provide some insights for future prospective trials.

The results showed that PET and MRD are not strongly correlated with each other and they can be used as complementary techniques at the end of therapy. PET is more accurate for nodal disease, but has important limitations in bone marrow analysis because BM involvement in FL is usually diffuse and with low volume. In contrast, MRD analysis describes disease at BM level and it can reach a very high sensitivity, up to 10^{-5}.

The small study sample represents a major limitation of this study and is due to its retrospective nature and to the established inclusion criteria; MRD analysis was a planned procedure in the FOLL05 trial, but a molecular marker was only available in about 60% of patients.[5] When FOLL05 was designed, PET was not acknowledged as a recommended procedure for staging and response assessment in FL, and so it was not included among the planned study procedures; however, it was performed at physician discretion in substantial proportion of cases.[9] In addition while FDG avidity is almost universally present in FL, with current PCR techniques using both major and minor breakpoint sites

for BCL2/IGH MRD analysis, as done in the present study, only around 50-60% of patients can be studied. This rate can be improved with better methods and technologies (VDJ region analysis or rarer breakpoint regions of BCL2/IGH chromosomal translocation). Although conducted on a small set of patients the strength of this study is the use of blinded central review of FDG-PET scans, the use of Deauville criteria and of dedicated central lab for MRD analysis.

In the last years, the concept that tumor cells release circulating free DNA (cfDNA) into the blood by cells undergoing apoptosis or necrosis enabled the use of whole exome sequencing ("next generation sequencing technologies" – NGS) to detect observed tumor mutations in blood.[10] Recently this technology was validated in DLBCL and allowed the same group to launch a prospective study in the aim of serial sequencing cfDNA during DLBCL treatment and follow-up.[11] This new tool named "liquid biopsy" and the use of peripheral blood might further improve MRD studies in FL.

In conclusion, although conducted on a small series of patients, this study shows that combining both EOT FDG-PET and MRD analysis in patients with FL may improve our ability to predict the risk of progression and provides the rationale to design response adapted trials in FL to tailor post induction therapy to the real risk of relapse. Based on these results, the Fondazione Italiana Linfomi (FIL) planned the FOLL12 trial to investigate the efficacy of a response-adapted strategy, using EOT PET and MRD study in patients with FL (ClinicalTrials.gov Identifier: NCT02063685). In the study all patients receive 6 cycles of R-CHOP or R-bendamustine followed by 2 additional doses of rituximab. All responsive patients in the standard arm are treated with standard 2 year maintenance with rituximab. Responding patients in the experimental

arm receive post-induction therapy based on PET and MRD results: PET- patients do not receive maintenance but are treated with pre-emptive treatment with rituximab if MRD+; PET+ positive patients receive as consolidation a (90)Y ibritumomab tiuxetan dose prior to conventional rituximab maintenance.

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Table 1. Comparison of baseline characteristics of study population and FOLL05 patients

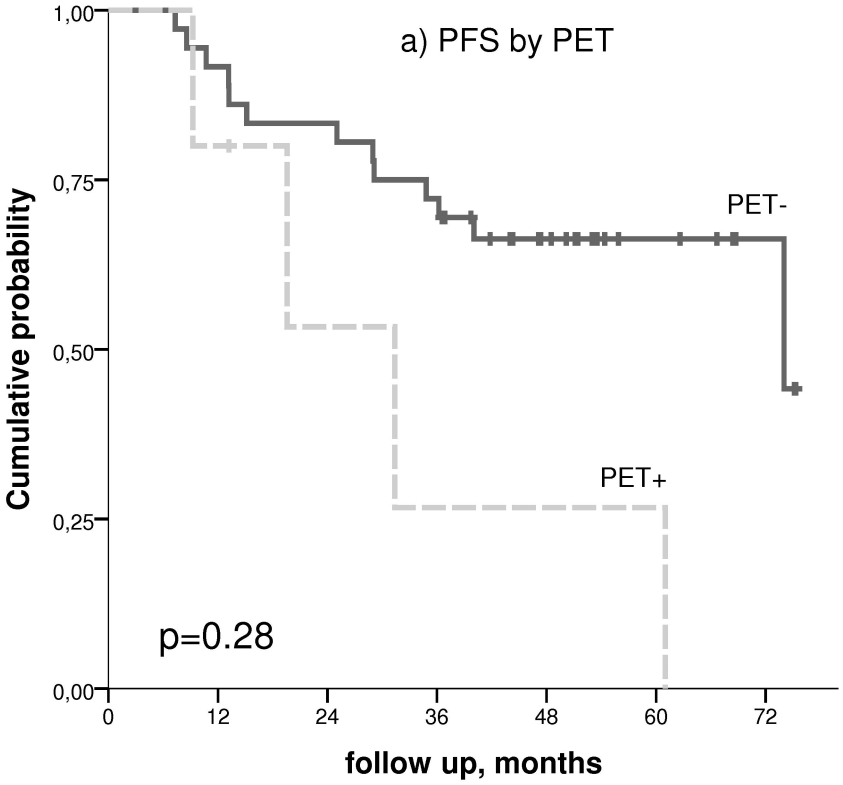
	Present study N=41		Remaining patients from FOLL05 N=463		*p*
	n	%	n	%	
Age > 60	11	27	156	34	0.39
Male sex	19	46	245	53	0.42
Ann Arbor stage III-IV	38	93	423	91	1.0
Bulky disease (> 6 cm)	16	39	118	25	0.07
BM involvement	23	56	251	54	0.47
FLIPI 3-5	16	39	172	37	0.59
First treatment R-CVP R-CHOP R-FM	 12 13 16	 29 32 39	 156 152 155	 34 33 33	 0.7

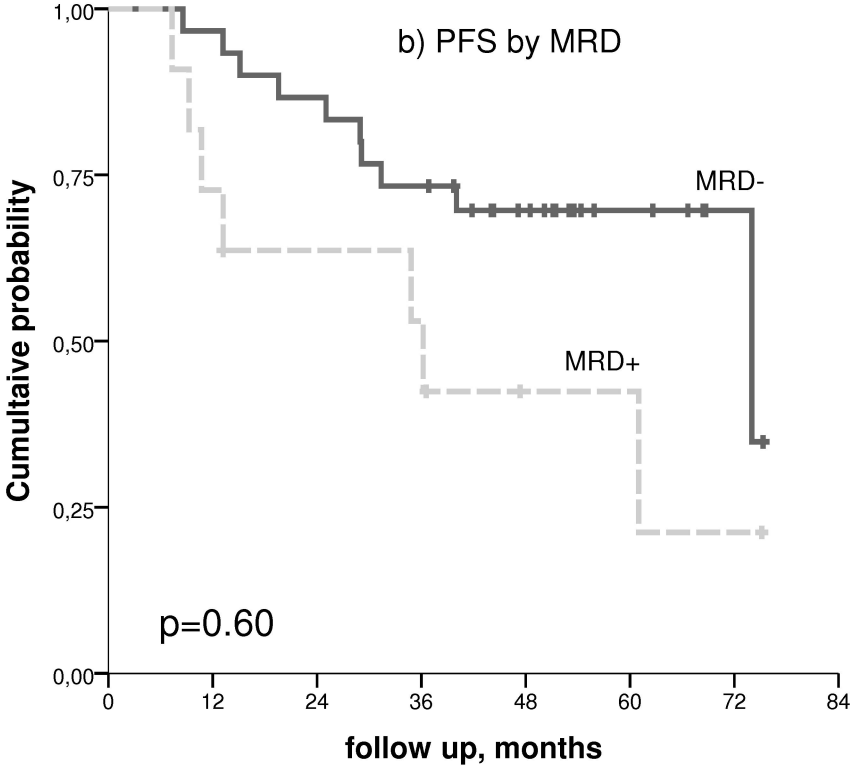
Table 2. Distribution of patients according to PET response and MRD at the end of treatment

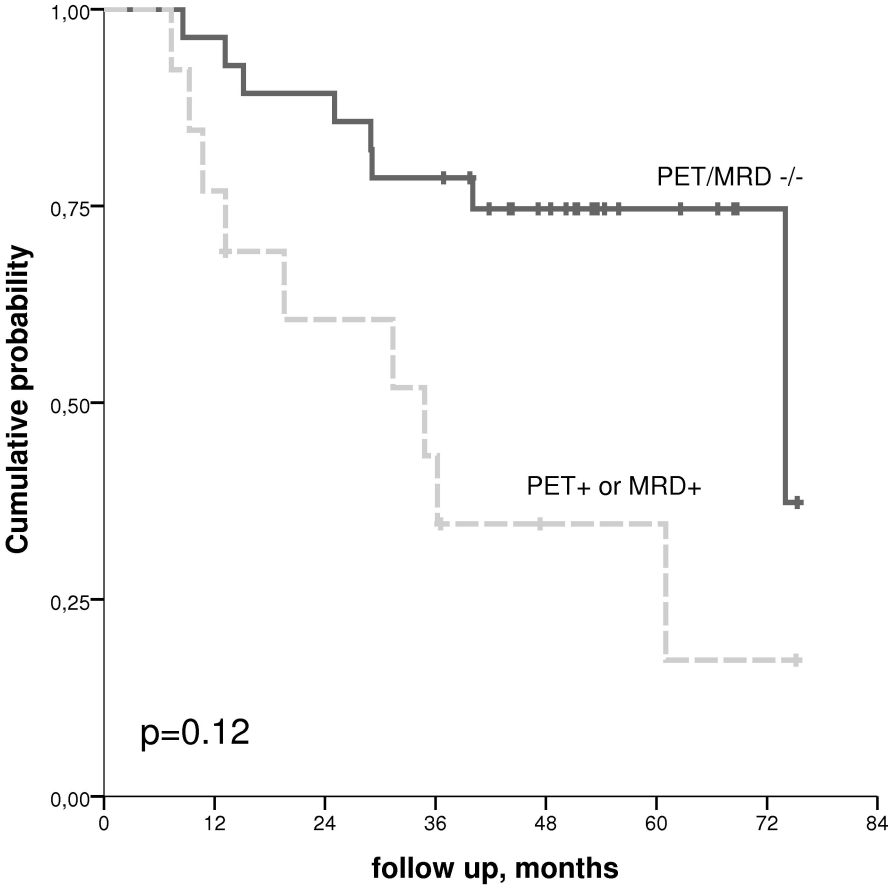
	PET negative	PET positive
MRD negative	28 (68%)	2 (5%)
MRD positive	8 (20%)	3 (7%)

Figures legend

Figure 1 A: PFS by PET; Figure 1 B: PFS by MRD
Figure 2: PFS according to combination of PET and MRD results.


a) PFS by PET
1,00
0,75
0,50
0,25
0,00
Cumulative probability
PET-
PET+
p=0.28
0
12
24
36
48
60
72
follow up, months


b) PFS by MRD
1,00
0,75
0,50
0,25
0,00
Cumultaive probability
MRD-
MRD+
p=0.60
0
12
24
36
48
60
72
84
follow up, months


1,00
0,75
0,50
0,25
0,00
Cumulative probability
PET/MRD -/-
PET+ or MRD+
p=0.12
0
12
24
36
48
60
72
84
follow up, months