

LYMPHOID NEOPLASIA

The mutational landscape of Burkitt-like lymphoma with 11q aberration is distinct from that of Burkitt lymphoma

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KEY POINTS

- Burkitt-like lymphoma with 11q aberration harbors a mutational landscape distinct from sporadic BL.
- Biallelic inactivation indicates a pathogenic role of the INO80 complex-associated *NFRKB* gene in mnBLL,11q.

The new recently described provisional lymphoma category Burkitt-like lymphoma with 11q aberration comprises cases similar to Burkitt lymphoma (BL) on morphological, immunophenotypic and gene-expression levels but lacking the IG-MYC translocation. They are characterized by a peculiar imbalance pattern on chromosome 11, but the landscape of mutations is not yet described. Thus, we investigated 15 MYC-negative Burkitt-like lymphoma with 11q aberration (mnBLL,11q) cases by copy-number analysis and whole-exome sequencing. We refined the regions of 11q imbalance and identified the INO80 complex-associated gene *NFRKB* as a positional candidate in 11q24.3. Next to recurrent gains in 12q13.11-q24.32 and 7q34-qter as well as losses in 13q32.3-q34, we identified 47 genes recurrently affected by protein-changing mutations (each ≥ 3 of 15 cases). Strikingly, we did not detect recurrent mutations in genes of the ID3-TCF3 axis or the SWI/SNF complex that are frequently altered in BL, or in genes frequently mutated in germinal center-derived

B-cell lymphomas like *KMT2D* or *CREBBP*. An exception is *GNA13*, which was mutated in 7 of 15 cases. We conclude that the genomic landscape of mnBLL,11q, differs from that of BL both at the chromosomal and mutational levels. Our findings implicate that mnBLL,11q, is a lymphoma category distinct from BL at the molecular level. (*Blood*. 2019;133(9):962-966)

Introduction

Recently, a subgroup of germinal center-derived B-cell (GCB) lymphomas has been described that resembles Burkitt lymphoma (BL) with regard to morphology, immunophenotype, and gene-expression profile but it lacks the IG-MYC translocation typical for BL.¹⁻⁵ Instead, these cases are cytogenetically characterized by a peculiar pattern of an 11q aberration consisting of a gain in 11q23.2-23.3 followed by a telomeric loss in 11q24.1-qter. According to the revised 4th edition of the *WHO Classification of Tumours of Haematopoietic and Lymphoid Tissue*, these lymphomas have been described as a new provisional entity called “Burkitt-like lymphoma with 11q aberration” (abbreviated herein as “mnBLL,11q”).⁶ In

addition to the 11q aberration, mnBLL,11q, shows various secondary imbalances and harbors a more complex karyotype than BL.²

Recently, the mutational landscape of IG-MYC-translocated BL has been thoroughly investigated⁷⁻¹⁰ and *MYC*, *ID3*, *TP53*, *SMARCA4*, and *GNA13*, for example, have been identified as recurrently mutated genes. In contrast, mutational analyses of mnBLL,11q, have mainly focused on single genes, showing, for example, lack of *ID3* mutations in 14 mnBLL,11q, cases.² This, together with the lack of IG-MYC translocations and the different imbalance patterns, suggests that mnBLL,11q, shows a genetic makeup quite different from IG-MYC-translocated BL.

To more comprehensively delineate the profile of copy-number alterations (CNAs), single-nucleotide variants (SNVs) as well as small insertions and deletions (indels) of mnBLL,11q, we performed array-based imbalance mapping and whole-exome sequencing (WES) in 15 mnBLL,11q.

Study design

In this retrospective analysis, tumor samples of 15 patients were included that had been diagnosed as BL, atypical BL/BL-like or other aggressive B-cell lymphomas, and lacking an IG-MYC translocation. In all cases, the diagnosis of mnBLL,11q, had been considered (refer to supplemental Methods [available on the *Blood* Web site] for detailed description) and an 11q aberration pattern was detected by fluorescence in situ hybridization and imbalance profiling applying the OncoScan CNV FFPE assay (12 cases). For 3 of these cases, the clinical, immunophenotypical, and copy-number data have been published previously.^{1,2,5} DNA extracted from formalin-fixed paraffin-embedded tissue of all 15 patients was subjected to WES. Refer to supplemental Methods for details.

Results and discussion

We analyzed tumor samples of 15 patients retrospectively diagnosed with mnBLL,11q. The median age at diagnosis was 15.5 years (range, 4-52 years) and the male-to-female ratio was 2.75:1. An underlying immunodeficiency was clinically reported in 2 of the cases, both of which had no evidence for an Epstein-Barr virus infection. The characteristics of the cohort are summarized in supplemental Table 1.

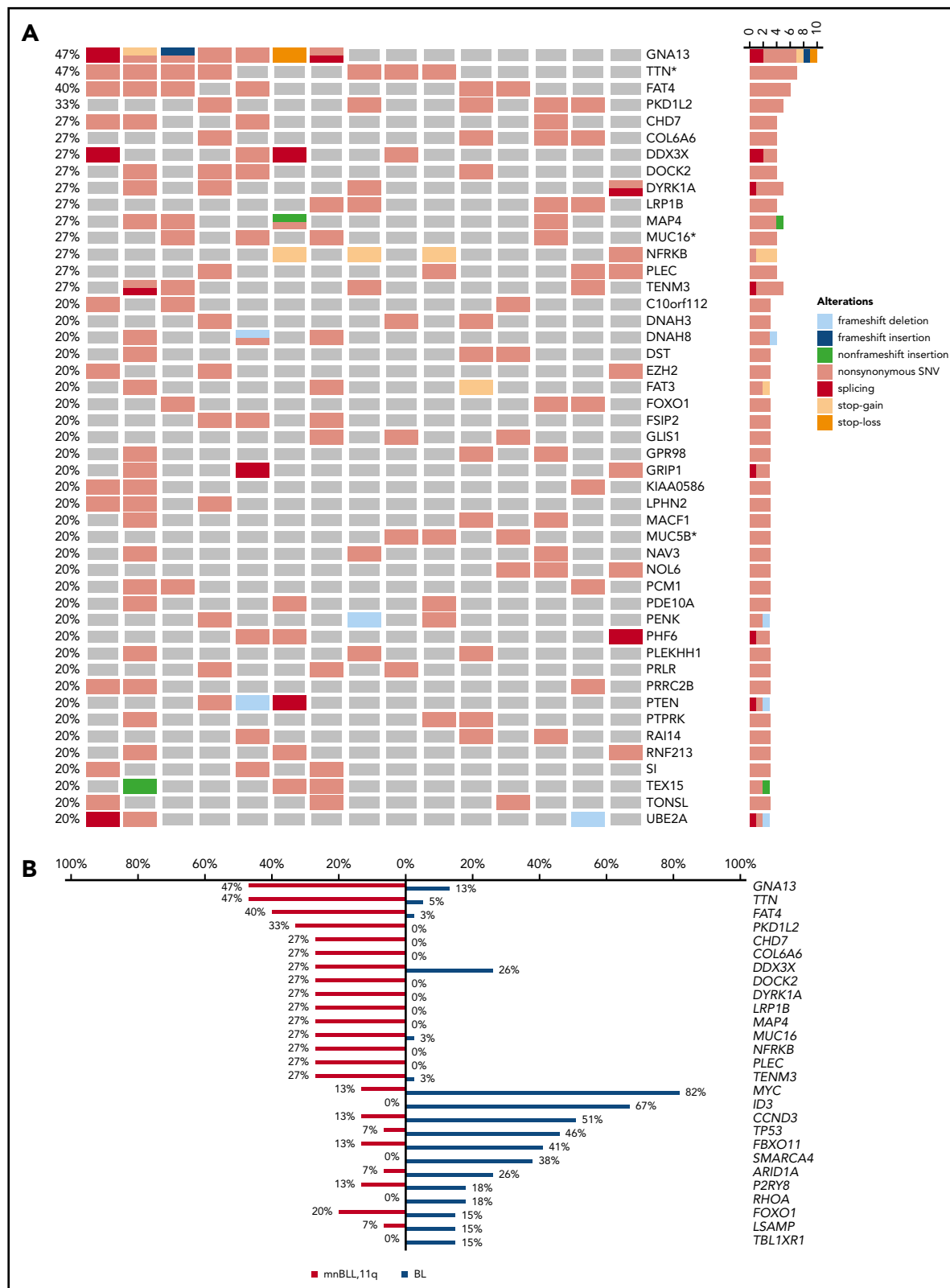
As a part of the retrospective workup, we analyzed the CNAs in 12 cases not reported before (excluding the 3 cases reported in Salaverria et al²). The median number of CNAs in these 12 cases (gains, losses, and copy-number neutral losses of heterozygosity) was 6.5 (range, 3-38), not significantly differing from the findings reported by Salaverria et al using a different array platform (median, 12.2; range, 2-28).² Considering the 12 novel CNA profiles and those of the 3 cases previously reported,² the typical pattern of chromosome 11q gain/loss was observed in 13 of 15 mnBLL,11q, cases (supplemental Figure 1; supplemental Table 2). In the remaining 2 cases, in agreement with fluorescence in situ hybridization studies (supplemental Table 1), only a telomeric loss in 11q24.1-qter was detected without concomitant gain in 11q23. We consider such alterations, which have also recently been reported in 1 mnBLL,11q, case,² as a variant 11q aberration. This might point to a more pronounced pathogenic role of the genes in the deleted rather than in the gained region. Besides the changes on chromosome 11, other recurrent imbalances included (partial) trisomy 12 (7 of 15 cases, minimally gained region in 12q13.11-q24.32), and gain in 7q34-qter and loss in 13q32.3-q34 (both 3 of 15 cases) (supplemental Figure 1).

Next, we analyzed the mutational profile (SNVs and indels) of mnBLL,11q, using WES. We identified 47 genes showing potentially protein-changing SNVs in ≥ 3 of 15 mnBLL,11q, cases (Figure 1A; supplemental Table 3). Strikingly, the genes recurrently mutated in BL (>15% of BL patients

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Among the most frequently mutated genes in mnBLL,11q, were *GNA13* and *TTN*, mutated in each 7 of 15 cases. *GNA13* mutations, which frequently occur in GCB lymphomas like BL^{7,9} and GCB-DLBCL,¹³ lead to a loss of protein function.¹⁴ In line, 5 of 11 *GNA13* mutations detected in 7 mnBLL,11q, were likely deleterious (frameshift, stop-gain, stop-loss, splice-site), whereas the remaining 6 mutations were nonsynonymous mutations located in functional domains of the protein (supplemental Figure 6A-B). We could verify 9 of 11 *GNA13* mutations by Sanger sequencing. In line, in silico modeling of the *GNA13* mutations confirmed the deleterious nature of the mutations leading to a loss of function or destabilizing the G-protein's function (supplemental Table 3; supplemental Figure 6A-B). Extending the analysis to all genes belonging to the $G\alpha 13$ -signaling pathway, we identified, in 8 of 15 mnBLL,11q, cases, mutations in 1 of the pathway genes (supplemental Figure 6C) with *GNA13* being the most frequently affected (7 of 8 cases). Most of the mutations in the other genes co-occurred with the *GNA13* mutations (3 of 4 cases).

The role of *TTN* mutations in mnBLL,11q, is unclear. It needs to be considered that several other large and/or late replicating genes are contained within the list of recurrently mutated genes in mnBLL,11q, besides *TTN* (Figure 1A). Such genes are mutated in several cancer types (refer to supplemental Results and discussion) but their pathogenic role in tumor development is



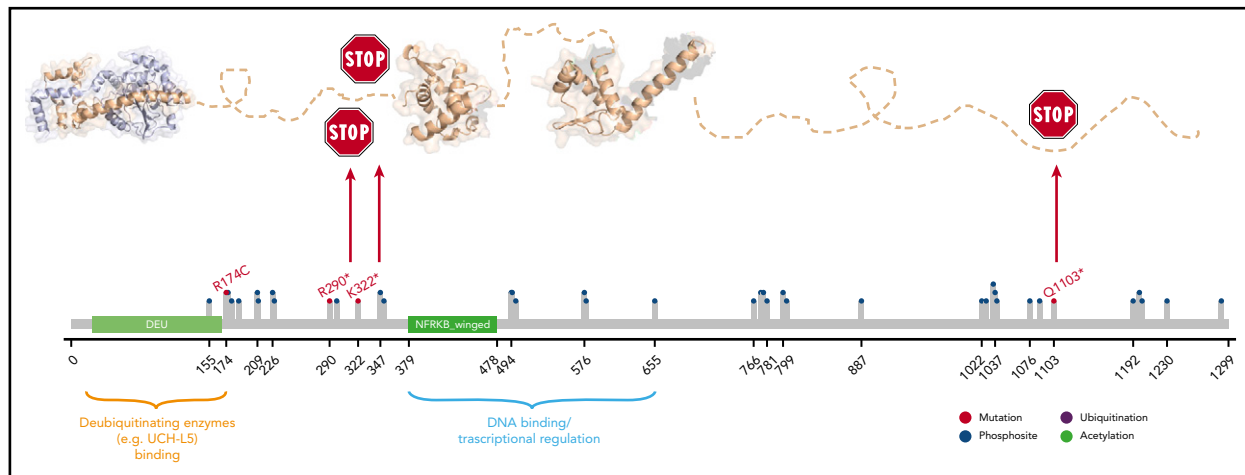


Figure 2. Modeling of *NFRKB* mutations. *NFRKB* mutations (red lollipops) annotated on protein primary sequence with additional information regarding post-translational modifications (PTMs) and domain composition. Three-dimensional structural model showing the deubiquitinating enzyme-binding domain (Protein Data Bank identifier [PDB ID]: 4UF5), the winged domain (PDB ID: 3U21), and the transcriptional regulation domain (by homology; PDB ID: 3BY6). The 2 stop-gain mutations R290* and K322* are predicted to delete the protein region responsible for mediating interactions with transcriptional regulators and/or DNA whereas leaving the N-terminal region deputed to the interaction with deubiquitinating enzymes. The R174C mutation is predicted to perturb adjacent phosphosites, for example, S176, and is located in a motif predicted by the Eukaryotic Linear Motif (ELM; elm.eu.org) to be either the phosphorylation site of GSK3 and MAPK or the docking site for USP7 or the Pin1 WW domain. The C-terminal deletion by Q1103* is predicted to have detrimental consequences, as it is rich in phosphorylation sites (eg, CK1 and GSK3) or recognition sites for FHA and WDR5.

unclear.¹⁵ Modeling of the *TTN* mutations confirmed the mutations to be rather nononcogenic and, hence, constitute most likely passenger variants (supplemental Table 3).

Next, we asked whether genes in the minimal regions of gain and loss were targeted by mutations in addition to imbalances. Three of 45 genes (*PCSK7*, *DSCAML1*, *TMEM25*) mapping to the minimal region of gain were mutated in each only 1 mnBLL,11q, case. With regard to genes located in the minimally deleted region, we confirmed previous findings of recurrent mutations in *ETS1* (2 of 15 cases, including 1 published mutation²) and detected recurrent mutations in *NFRKB* (4 of 15), which were verified by Sanger sequencing (supplemental Table 3). Interestingly, 3 of 4 *NFRKB* mutations were stop-gain mutations and, accordingly, *NFRKB* function is supposed to be biallelically lost in these 3 cases, that is, by deletion of 1 allele and mutation of the other. In silico modeling of the mutations further supported the deleterious character of the mutations (Figure 2; supplemental Table 3; supplemental Results and discussion). In line, *NFRKB* expression was described to be significantly lower in mnBLL,11q, compared with BL based on expression-array analysis ($P < .007$; supplemental Figure 7).² *NFRKB* encodes a nuclear factor related to the κ B-binding protein, belonging to the INO80 chromatin-remodeling complex,¹⁶ which plays a role in transcriptional regulation.¹⁷ Extending the analysis to all genes of the INO80 complex showed mutations in 5 of 15 mnBLL,11q, cases. Given the absence of recurrent mutations in genes of the SWI/SNF chromatin-remodeling complex in mnBLL,11q, it is intriguing to speculate that mutations in the INO80 complex in mnBLL,11q, have a comparable function as the mutations in the SWI/SNF complex in BL.

Finally, besides *NFRKB*, only *MACF1*, *UBE2A*, and *DST*, each mutated in 3 of 15 mnBLL,11q, have been reported to be differentially expressed in comparison with BL.²

Taken together, our data clearly show that besides the chromosomal translocation and imbalance patterns, the mutational profile of mnBLL,11q, is also strikingly different from BL and non-BL. Our findings suggest a role of *GNA13* in the pathogenesis of mnBLL,11q, and identify the INO80 complex-associated gene *NFRKB* as a candidate gene in the deleted region in 11q24.3. Moreover, our findings support the recognition of mnBLL,11q, as an entity distinct from not only *MYC*-positive BL but also from other aggressive GCB lymphomas like DLBCL. Finally, the observations presented, particularly the lack of a BL-specific mutation pattern, combined with lack of an IG-*MYC* fusion, might aid in the differential diagnostic process distinguishing IG-*MYC*-translocated BL from mnBLL,11q.

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Authorship

Contribution: B.B., H.H., L.L., G.O., G.R., E.S.J., R.A.-Y., and W.K. provided tumor samples and clinical data; S.B. and I.N. performed cytogenetic analysis; J.A., H.T., and P.N. performed WES; J.S., K.K., D.H., and M.S. analyzed the WES data; C.W.K. performed expression analysis; F.R. and R.B.R. modeled the functional impact of the mutations; R.W. analyzed the OncoScan data and interpreted the WES data; R.S. designed the study and coordinated the project; R.W., J.S., and R.S. interpreted the data and wrote the manuscript; and all authors read and approved the final manuscript.

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Footnotes

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There is a *Blood* Commentary on this article in this issue.

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