The Prognostic Significance of Various 13q14 Deletions in Chronic Lymphocytic Leukemia

Peter Ouillette², Roxane Collins², Sajid Shakhan², Jinghui Li², Cheng Li¹, Kerby Shedden³, and Sami N. Malek²

Abstract

Purpose: To further our understanding of the biology and prognostic significance of various chromosomal 13q14 deletions in chronic lymphocytic leukemia (CLL).

Experimental Design: We analyzed data from SNP 6.0 arrays to define the anatomy of various 13q14 deletions in a cohort of 255 CLL patients and have correlated two subsets of 13q14 deletions (type I exclusive of RB1 and type II inclusive of RB1) with patient survival. Furthermore, we measured the expression of the 13q14-resident microRNAs by quantitative PCR (Q-PCR) in 242 CLL patients and subsequently assessed their prognostic significance. We sequenced all coding exons of RB1 in patients with monoallelic RB1 deletion and have sequenced the 13q14-resident miR locus in all patients.

Results: Large 13q14 (type II) deletions were detected in approximately 20% of all CLL patients and were associated with shortened survival. A strong association between 13q14 type II deletions and elevated genomic complexity, as measured through CLL-FISH or SNP 6.0 array profiling, was identified, suggesting that these lesions may contribute to CLL disease evolution through genomic destabilization. Sequence and copy number analysis of the RB1 gene identified a small CLL subset that is RB1 null. Finally, neither the expression levels of the 13q14-resident microRNAs nor the degree of 13q14 deletion, as measured through SNP 6.0 array-based copy number analysis, had significant prognostic importance.

Conclusions: Our data suggest that the clinical course of CLL is accelerated in patients with large (type II) 13q14 deletions that span the RB1 gene, therefore justifying routine identification of 13q14 subtypes in CLL management. Clin Cancer Res; 17(21); 6778–90. ©2011 AACR.

Introduction

Chronic lymphocytic leukemia (CLL) has a varied clinical course, and genomic aberrations are recognized as important to the diverse biological and clinical phenotypes of CLL (1–4). The most frequent chromosomal abnormality in CLL is commonly referred to as del13q14, which is detectable by FISH or single-nucleotide polymorphism (SNP) arrays in approximately 50% of all CLL (5–15). Although generally considered to be associated with shortened survival, a strong association between 13q14 type II deletions and elevated genomic complexity, as measured through CLL-FISH or SNP 6.0 array profiling, was identified, suggesting that these lesions may contribute to CLL disease evolution through genomic destabilization. Sequence and copy number analysis of the RB1 gene identified a small CLL subset that is RB1 null. Finally, neither the expression levels of the 13q14-resident microRNAs nor the degree of 13q14 deletion, as measured through SNP 6.0 array-based copy number analysis, had significant prognostic importance.

Conclusions: Our data suggest that the clinical course of CLL is accelerated in patients with large (type II) 13q14 deletions that span the RB1 gene, therefore justifying routine identification of 13q14 subtypes in CLL management. Clin Cancer Res; 17(21); 6778–90. ©2011 AACR.

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Translational Relevance

Genomic aberrations have important effects on chronic lymphocytic leukemia (CLL) biology and clinical outcome. Recently, a refined description of the sub- stantial anatomic heterogeneity of the most common CLL-associated chromosomal deletion, del13q14, has emerged, and it is increasingly recognized that 13q14 deletions cannot be reduced to a singular pathophysiologic mechanism. Furthermore, knowledge is still evolving about possible differential prognostic effects imparted on CLL by various 13q14 subtypes. In this report, we provide evidence that large 13q14 deletions that are inclusive of the retinoblastoma gene (RB1) are prognostically adverse and that these deletions are frequently associated with unstable CLL genomes. This analysis advances our understanding of the clinical relevance of the most common chromosomal deletion type in CLL and informs future refinements in diagnostic approaches to CLL management.

Materials and Methods

Patients

Between January 2005 and September 2009, a total of 266 patients evaluated at the University of Michigan Comprehensive Cancer Center were enrolled onto this study. The trial was approved by the University of Michigan Institutional Review Board (IRBMED #2004-0962) and written informed consent was obtained from all patients prior to enrollment. Data from 255 of 266 patients were included in this report (5 patients enrolled on the study were excluded because of a diagnosis that was not CLL, and 6 patients had insufficient cryopreserved cells available for the analyses described).

Regardless of whether the subjects were originally diagnosed at our institution or another, we used the same CLL diagnostic criteria, based on the National Cancer Institute-Working Group Guidelines for CLL (24). Eligible patients needed to have an absolute lymphocytosis (>5,000 mature lymphocytes per μL), and lymphocytes needed to express CD19, CD23, slg (weak), and CD5 in the absence of other pan-T-cell markers.

Time to first therapy (TTFT) and overall survival were based on the date of trial enrollment (the date of specimen procurement) or alternatively the diagnosis date, respectively (25). CLL treatment was defined as cytotoxic chemotherapy and/or monoclonal antibody therapy for CLL. Clinical information, including Rai stage and all treatments given, was collected for all patients. Patient samples were characterized for selected CLL-associated chromosomal aberrations as a routine clinical test at the Mayo Clinic (Rochester, MN) by FISH. All biomarker assessments were conducted on specimens procured at trial enrollment.

Cell isolation

Flow cytometric sorting of CLL specimens. Cryopreserved peripheral blood mononuclear cells from CLL blood specimens were prepared for fluorescence-activated cell sorting (FACS) into CD19+ and CD3+ cells, as previously described (25).

Preparation of sample DNA

DNA used for SNP 6.0 profiling was extracted from fluorescence-activated cell-sorted CD19+ and CD3+ cells as described (25). For some cases (N = 11), paired buccal DNA was used instead of CD3+ cell–derived DNA.

Array data analysis

The DNA was prepared for hybridization to SNP 6.0 arrays according to the manufacturers’ recommendations. Affymetrix CEL files for each cell sample were analyzed with Genotyping Console software for initial quality control, followed by the use of the Affymetrix "Birdseed" algorithm to generate tab-delimited SNP call files in text format. Call rates for the entire group of CD19+ samples included in this report were between 95.06% and 99.63%, with a mean call rate of 98.53%. Corresponding call rates for CD3+ or buccal DNA were between 93.14% and 99.66%, with a mean call rate of 98.49%.

Sample copy number heatmap displays were obtained from CEL files through use of the freely available software dChip (26), adapted to run on a 64-bit computer environment. For genomic copy number analysis, we visually inspected parallel heatmap copy number images of CD19+ and paired CD3+/buccal DNA samples generated through dChipSNP and using the median smoothening functionality. Only those copy number changes detected in CD19+ DNA that were not found at the same position in paired CD3+/buccal DNA were called somatic. This approach followed our previously externally referenced (FISH) SNP 6.0 genomic lesion calling method in acute myelogenous leukemia that resulted in 100% concordance between SNP 6.0 profiling and FISH results (for a total of 56 lesions analyzed; ref. 27). Furthermore, data on sensitivity and specificity of acquired copy number (aCNA) calling calculated on the basis of data for del17p, del11q, and del13q14 derived from the clinical CLL-FISH panel are summarized in the Supplementary Methods and Results section. Using this approach, the 3 shortest identified aCNAs were 0.024, 0.042, and 0.052 Mb in length and were defined by 18, 27, and 19 consecutive SNP positions, respectively, and the vast majority of aCNAs were defined by more than 100 consecutive SNP positions. In total, we detected 474 subchromosomal losses (size range: 0.024–108.73 Mb) and 62 subchromosomal gains (size range: 0.114–94.626 Mb; ratio of losses to gains of 7.11).

The method used to nominate aCNAs by a statistical algorithm (27) is summarized in Supplementary Methods.

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Exon resequencing of p53, RB1, and the 13q14-resident miRNA genomic locus

Primers to amplify and sequence exons 2 to 10 of human p53 and all coding exons of RB1 and adjacent intronic sequences, including splice junctions, were designed by the primer 3 program (http://frodo.wi.mit.edu/primer3/) and sequence information was generated as described (28). Mutations were confirmed using paired patient CD3+ buccal DNA as templates. The primers to amplify and sequence the 13q14-resident miRNA locus were as follows: F: TTC-TAAGCTCTGTTCAAAATCTG, R: TTGTTGTTCATTACCTATGACTG, and SEQ: TAAACAGTTATCAATAAC.

Determination of ZAP70 and IgVH status

Determination of ZAP70 and IgVH status was carried out as described (25).

Measurement of expression of 13q14-resident microRNAs 15a and 16-1 using normalized quantitative PCR

RNA was prepared from 2 × 10^6 to 4 × 10^6 fluorescence-activated cell-sorted CD19+ cells with the TRizol reagent and resuspended in 100 μL diethyl pyrocarbonate (DEPC)-treated water. cDNA for microRNA reverse transcriptase quantitative PCR (Q-PCR) was made from approximately 5 ng of RNA by the TaqMan MicroRNA Reverse Transcription Kit (Applied Biosystems) and RNA-specific primers. Primers and TaqMan-based probes were purchased from Applied Biosystems (primers-on-demand). Primer/probe mixtures included were as follows: miR16-1 (TM 391), miR15a (RT 389), RNU43 (TM 1095), and RNU49 (TM 1005). Duplicate amplification reactions for microRNAs included primers/probes, TaqMan 2× Universal PCR Master Mix, No AmpErase UNG, and 1.35 μL of cDNA in a 20-μL reaction volume. Reactions were done on an ABI 7900HT machine. Normalization of relative copy number estimates for RNA species of interest was done with the C_t values for the RNU43 or RNU49 as reference (C, mean gene of interest – C_t, mean RNU43 or RNU49). Comparisons between CLL subgroups were carried out though subtraction of means of normalized C_t values. Similar efficacies of amplification of cDNA using primers for miR15, miR16-1, and RNU49 had previously been verified with 2-fold serial dilutions of cDNA made from cell line–derived RNA over a range of eight 2-fold serial dilutions (18).

Statistical methods

TTF or overall survival was defined as the time (in months) between CLL diagnosis or CLL trial enrollment and the date (in months) of first treatment or the patient’s death. For patients still untreated or alive, the month of censoring was November 2010. Univariate and bivariate analyses were based on Kaplan–Meier estimates of survivor functions. Median survival times were estimated directly from the survivor function estimates. Significance levels for groupwise comparisons in the univariate and bivariate analyses were based on the log-rank test. Assessment of the relationship between outcomes and various dichotomization thresholds and using univariate proportional hazards regression to estimate the corresponding HR.

Results

Patient characteristics

Characteristics of the 132 CLL patients with typical 13q14 deletions as detected through SNP 6.0 profiling (identified within a prospectively enrolled and profiled cohort of 255 CLL patients) analyzed in this study are summarized in Table 1, stratified by 13q14 subtype and treatment status. Data for 123 patients with CLL without typical 13q14 deletions are also summarized (Table 1). Of the 132 patients with CLL with typical 13q14 deletions, 100 (76%) were untreated (U) and 32 (24%) relapsed (T) at the time of study enrollment. Within the group of previously untreated patients, the distribution of important biomarkers across type I or II 13q14 lesions was well balanced: Rai stage 0, 45%/41%; Rai stages 1 or 2, 51%/53%; IgVH unmutated, 32%/29%; ZAP70 positive, 30%/26%; p53 exons 2 to 10 mutated, 11%/6%; del17p present, 7%/3%; and del11q present, 6%/12%. The median time from diagnosis to enrollment and from enrollment to data analysis for previously untreated patients is detailed in Table 1. All outcome analyses described later are based on SNP 6.0 array analysis and biomarker measurements that were conducted on patient samples procured at study enrollment, thus avoiding confounding effects of longitudinal biomarker instability. Outcome was calculated using either the CLL trial enrollment date or the diagnosis date as the reference dates, as indicated, to minimize the effect of lead time biases.

The pathologic anatomy of acquired subchromosomal genomic copy number changes spanning 13q14 in CLL as defined through SNP 6.0 array copy number profiling

We cataloged all aCNAs on chromosome 13 in our CLL cohort using visual inspection of simultaneous displays of dChipSNP-based copy number estimates (heatmaps) for CD19+ cells and paired CD3+ buccal DNA (Fig. 1). Overall, 51.7% (132 of 255) of CLL carried a classical 13q14 deletion as detected through SNP 6.0 arrays that included the genomic region recognized in the clinically used CLL-FISH panel (range of lesion sizes of 0.198–73.775 Mb; see Supplementary Table S1). In addition, rare atypical 13q deletions were identified. As previously described by lower-resolution SNP array platforms (Affymetrix SNP50K XbaI arrays), 13q14 deletions displayed substantial anatomic heterogeneity (18). Nonetheless, multiple distinct break clusters located close to the 13q14-resident miR 15a/16-1 loci and, alternatively, close to and inclusive of all or parts of the RB1 locus were identified. A telomeric cluster of breaks was located at approximately 50.2 to 50.7 Mb physical position, comprising the vast majority of the breaks of short 13q14 deletions. Of the short and relatively uniform 13q14...
Table 1. Patient characteristics

<table>
<thead>
<tr>
<th>Patient characteristics at enrollment</th>
<th>13q-I treatment naïve, no. (%)</th>
<th>13q-I relapsed, no. (%)</th>
<th>13q-II treatment naïve, no. (%)</th>
<th>13q-II relapsed, no. (%)</th>
<th>Non-13q treatment naïve, no. (%)</th>
<th>Non-13q relapsed, no. (%)</th>
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<td>Sample size N = 255 patients†</td>
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<td>14 (5)</td>
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<td>60</td>
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<td>48–82</td>
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<td></td>
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<td>Female</td>
<td>23 (32)</td>
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<td>13 (38)</td>
<td>5 (25)</td>
<td>36 (37)</td>
<td>6 (24)</td>
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<td>21 (62)</td>
<td>15 (75)</td>
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<td>18 (53)</td>
<td>9 (45)</td>
<td>45 (46)</td>
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<td>4 (4)</td>
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<td>10 (29)</td>
<td>11 (55)</td>
<td>50 (51)</td>
<td>19 (76)</td>
</tr>
<tr>
<td>Mutated (&lt;98% homology to germline)</td>
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<td>10 (71)</td>
<td>22 (65)</td>
<td>7 (35)</td>
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<td>5 (20)</td>
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<td>11 (11)</td>
<td>2 (8)</td>
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<td>13 (93)</td>
<td>32 (94)</td>
<td>19 (95)</td>
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<tr>
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<td>3 (21)</td>
<td>4 (12)</td>
<td>8 (40)</td>
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<td>13 (93)</td>
<td>32 (94)</td>
<td>19 (95)</td>
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<td>ZAP 70 expression</td>
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<tr>
<td>Negative (≥20%)</td>
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<td>5 (36)</td>
<td>25 (74)</td>
<td>8 (40)</td>
<td>45 (46)</td>
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<tr>
<td>Positive (≥20%)</td>
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<td>32 (94)</td>
<td>16 (80)</td>
<td>84 (86)</td>
<td>20 (80)</td>
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<td>2 (6)</td>
<td>4 (20)</td>
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</table>

(Continued on the following page)
deletions, 54% (71 of 132) were between 0.678 and 1.944 Mb in length and only 2 lesions were identified that were shorter (CLL145 and CLL97, with lesion lengths of 0.198 and 0.425 Mb, respectively; refs. 29–31).

Using a previously proposed classification schema for typical 13q14 deletions into types I and II (exclusive and inclusive of \(RB1\), respectively), we detected 85 type I lesions and 54 type II lesions (including 7 CLL cases in which both lesion types were identified, existing on separate chromosomes) in this cohort. Furthermore, the frequency of 13q14 type I and type II lesions in the entire CLL cohort (\(N = 255\)) was 33% and 21%, respectively.

Acquired uniparental disomy (aUPD) at 13q was identified in 7 CLL cases as previously described (18). In all these cases, the LOH region was very large (Supplementary Table S2). Six of these 7 cases also contained a region of copy loss

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**Table 1. Patient characteristics (Cont’d)**

<table>
<thead>
<tr>
<th>Patient characteristics at enrollment</th>
<th>13q-I treatment naïve, no. (%)</th>
<th>13q-I relapsed, no. (%)</th>
<th>13q-II treatment naïve, no. (%)</th>
<th>13q-II relapsed, no. (%)</th>
<th>Non-13q treatment naïve, no. (%)</th>
<th>Non-13q relapsed, no. (%)</th>
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</thead>
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<td>1</td>
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<td>1–5</td>
<td>NA</td>
<td>1–5</td>
<td>NA</td>
<td>1–7</td>
</tr>
</tbody>
</table>

*Seven patients had both 13q-I and 13q-II lesions.*

*Multiple FISH abnormalities per patient were individually counted.*

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**Figure 1.** Genomic copy number heatmap display of chromosome 13q of 255 CLL cases ranked by the position of centromeric 13q14 deletion break points: Copy number heatmap displays for paired DNA samples based on SNP 6.0 array profiling were generated with dChipSNP. Left, CD3+ or buccal DNA; right, CLL CD19+ DNA. Blue indicates copy loss, and red indicates copy gain. Each column represents one patient.
at 13q14 (typical 13q14 deletions by FISH), whereas 1 case was associated with a homozygous miR16-1-5p mutation (see later).

A subset of CLL cases displays very low miR16-1/15a cluster expression

The 13q14-resident microRNAs miR16-1 and miR15a, located at 49,521 Mb physical position, are contributors to the biology of these lesions in CLL cells (18, 32–34). In our cohort of 132 CLL cases with typical 13q14 deletions, we identified 4 cases (CLL # 78, 113, 120, and 214; see Supplementary Fig. S1) with breaks occurring in proximity (within 12 kb) to the miR locus and with unresolved miR gene status, whereas 134 lesions unequivocally resulted in the removal of one and occasionally (~10%) both copies of these miRs (see later; ref. 16).

We proceeded with an analysis of the expression of miR16-1-5p and miR15a-5p in 238 of 255 CLL cases with available intact RNA by extending normalized Q-PCR–based measurements to cases not previously reported (18). Measurements were normalized to the expression of 2 unrelated microRNAs, RNU43 and RNU49, through simple subtraction of the means of C\textsubscript{t} values [ΔC\textsubscript{t} mean = C\textsubscript{tm} miR15a or 16 – C\textsubscript{tm} RNU43 or 49; the R\textsuperscript{2} correlation for miR measurements using either RNU43 or RNU49 was 0.867 (miR16.1 data) and 0.84 (miR15a data), respectively]. This resulted in largely negative ΔC\textsubscript{t} values for miR16-1 and positive values for miR15a; this is due to lower C\textsubscript{t} values (higher expression) for miR16-1 relative to the reference microRNAs (Supplementary Table S1).

Subsequently, we ranked all CLL cases according to mean SNP 6.0 array-based chromosomal copy number estimates for an approximately 0.669 Mb chromosomal region between rs9535414 (immediately centromeric to the miR16-1/15a locus) and rs706593 (~650 kb telomeric to the miR16-1/15a locus) encompassing 216 consecutive copy number measurements. Next, we plotted mean ΔC\textsubscript{t} values for miR15a and miR16-1 versus 13q14 genomic copy number measurements for all CLL cases (grouped by 13q14 deletion status) and calculated mean normalized

![Image of Figure 2](https://www.aacrjournals.org/)

Figure 2. A–D, normalized expression of miR15a and miR16-1 versus SNP 6.0 array-based copy number estimates for typical 13q14 deletions. A–D, mean ΔC\textsubscript{t} values (miR15a or miR16-1 – housekeeping microRNAs) as single dots (y-axis) versus SNP 6.0 profiling-based copy number estimates for 13q14 deletions (x-axis) grouped by 13q14 deletion status. Red numbers indicate mean ΔC\textsubscript{t} values for CLL groups with copy number less than 1 or 1 or more and 13q14 deletions or non-del13q status. Black dots indicate CLL cases with unresolved miR gene status. Red dots indicate CLL cases with del13q. Blue dots indicate cases without del13q.
expression values for miR16-1 and miR15a for the CLL cases with more extensive chromosomal loss (copy number estimates <1) and for the CLL cases with less extensive loss (copy number estimates ≥1) or no loss (cases without 13q14 deletions). Data are summarized in Fig. 2A–D, with mean miR expression levels indicated with red numbers.

Mean normalized expression values of both miR16-1 and miR15a were substantially lower (miR15a ~8-fold and miR16-1 ~4-fold, respectively) in the CLL subgroup with more extensive del13q14 deletions (copy number estimates <1) as opposed to the group with no del13q14. For CLL cases with monoallelic 13q14 deletions and associated copy number estimates of 1 or more (the majority of such cases had copy number estimates of ~1.2) as compared with cases without 13q14 deletions, there was evidence for a gene dosage effect for miR15a expression (~1.3- to 1.9-fold lower) but no such effect for miR16-1 expression.

This combined data suggests that approximately 12% to 15% of CLL cases have very low miR16-1/15a levels and that the majority of CLL cases (~85%) display an overlapping range of expression of these miRs, with mild relative reductions in miR15 expression in mononucleically deleted 13q14 cases.

Assessment of elevated HRs for short overall survival based on analysis of thresholded centromeric or telomeric 13q14 lesion breakpoints

Given various published observations on CLL 13q14 deletion sizes, associated gene deletions, and clinical parameters, including our proposal for 13q14 subclassification into types I and II based on RB1 gene status, we modeled HRs for shortened survival for dichotomized 13q14 groups defined by distinct physical chromosomal break positions. Specifically, various dichotomized 13q14 groups were defined by sliding the separation/break points across all physical positions actually identified in the 13q14 deletions in this cohort (based on the physical positions of either telomeric or centromeric breaks; Supplementary Table S1). Using such an approach, we determined that the location of centromeric breakpoints strongly influenced the risk for short overall survival in CLL, whereas the telomeric breakpoints had little effect (Supplementary Fig. S2).

Specifically, the HR for short overall survival increased as the centromeric separation break for the two 13q14 groups moved closer to the telomere, with the highest HRs identified for breaks at approximately 48 to 48.5 Mb physical position, followed by a sharp drop in risk. The RB1, with well-documented effects on cell-cycle control and chromosomal instability in cancer cells, is located at 47.776 to 47.954 Mb physical position and is very close to the cohort dichotomization breakpoints that are associated with peak HRs for short overall survival. The centromeric separation breakpoints for the two 13q14 groups were 48.9 Mb and 48.5 Mb, respectively.

We also considered a classification schema centered on RB1 (see also RB1 mutation and expression data later). Additional genes located telomeric to RB1 and in the area (48–48.5 Mb physical position) demarcated by the highest HRs for short overall survival included LPAR6, P2RY5, RCRTR2, and CSYSLTR2, but none of these genes have well-established roles in biological processes that are known to affect cancer cells. Finally, only 4 actual 13q14-associated chromosomal breakpoints occurred between 48 and 48.5 Mb physical positions, creating modest uncertainty about the actual physical positions associated with peak HRs as estimated by our approach.

Results of univariate outcome analyses of SNP 6.0 array-detectable 13q14 deletions and overall survival in CLL

We initially determined the prognostic value of SNP 6.0 array-defined 13q14 type I and type II deletions on overall survival in the CLL cohort (UT + T; N = 132) using univariate analysis and either the CLL sample procurement/trial enrollment date or the CLL diagnosis date as the reference date. For both analyses, overall survival was significantly shorter for CLL patients with 13q14 type II abnormalities, as opposed to patients with 13q14 type I abnormalities (Kaplan–Meier plots for these analyses are displayed in Fig. 3A and C). These findings were true in the analyses in which CLL cases that carried both 13q14 deletion types (N = 7) were included and hierarchically assigned to type II status (shown) or, alternatively, were excluded from analysis. Next, we analyzed the prognostic value of SNP 6.0 array-defined 13q14 type I and type II deletions on overall survival in the untreated subset of patients (UT; N = 100) and again noted shortened survival of CLL patients with 13q14 type II, as opposed to type I lesions (Kaplan–Meier plots for these analyses are displayed in Fig. 3B and D).

Finally, given that the nature of 13q14 deletion may also influence initial CLL disease progression, we analyzed TTFT estimates for the 2 13q14 types but found no strong effects.

Deletion 13q14 type II lesions are associated with a higher incidence of coexisting CLL-FISH–detectable chromosomal abnormalities than 13q14 type I lesions

Next, we determined the frequency of 13q14 deletions of type I and II lesions that are associated with coexisting genomic lesions as detected through (i) CLL-FISH-25 or (ii) SNP 6.0 array profiling (see later). We defined 13q14 deletions of either type I or II lesions as “FISH-complex” if they were associated with one or more additional abnormalities in the clinically used CLL-FISH panel [and if these abnormalities were detected in ≥25% of nuclei analyzed (FISH-25); this is to remove low percentage lesions of unclear clinical or biological significance]. Using these criteria, the following frequencies were measured: 13q14-I (N = 85): sole abnormality (74 of 85 = 87%), FISH-complex (11 of 85 = 13%); 13q14-II (N = 54): sole abnormality (38 of 54 = 70%), FISH-complex [16 of 54 = 30%; (P = 0.03, the Fisher exact test); CLL cases with both type I and II lesions (N = 7) were counted as 13q14-I and 13q14-II].
Outcome analysis for del13q14 subtypes and associated CLL-FISH lesions

We proceeded with an outcome analysis of the relative contributions of 13q14 subtypes by category (I vs. II) versus associated CLL-FISH-25-based genomic complexity. Initially, we focused on bivariate analyses in which 13q14 lesion types were further separated into sole lesions or lesions coexisting with any other CLL-FISH-25 lesion (CLL cases that carried both 13q14 lesion types were included and hierarchically assigned to type II status). Data are summarized in Fig. 3E–H. From these analyses, the following conclusions can be supported: (i) sole 13q14 lesions of either type were associated with a relatively better prognosis than either type existing in the presence of additional FISH findings; (ii) trends for shorter overall survival for 13q14 type II deletions with CLL-FISH complexity versus 13q14 type I deletions with CLL-FISH complexity were observed; (iii) trends for shorter overall survival for sole 13q14 type II versus sole 13q14 type I lesions were observed, albeit more pronounced in CLL cases that were relapsed at the time of analysis (UT + T plots); and (iv) 13q14 type II deletions with CLL-FISH complexity were substantially enriched in relapsed CLL patients (frequency 45%).

Deletion of 13q14 type II lesions is associated with a higher incidence of coexisting SNP 6.0 array-detectable acquired subchromosomal copy number aberrations than 13q14 type I lesions

Next, we determined the frequencies of either 13q14 lesion type that were associated with 2 or more additional SNP 6.0 array-based subchromosomal aCNAs (total aCNA complexity ≥3). The following frequencies were measured: (i) 13q14-I (N = 85), sole abnormality (45 of 85 = 53%) and 13q14-I plus 2 or more aCNA (16 of 85 = 19%); (ii) 13q14-II (N = 54), sole abnormality (20 of 54 = 37%) and 13q14-II plus 2 or more aCNAs (18 of 54 = 33%; P = 0.02, the Fisher exact test; CLL cases with both type I and II lesions were counted as 13q14-I and 13q14-II). For comparison, the frequency of 3 or more SNP 6.0 array-based subchromosomal aCNAs in our entire CLL cohort of 255 profiled patients was 20% (35, 36).

Given the known strong association of p53 mutations with elevated genomic complexity in CLL, we determined p53 exon 2 to 10 mutation frequencies in the CLL cases with 13q14 type I or II deletions and 2 or more additional SNP 6.0-based aCNAs: There were 16 cases with 13q14-I plus 2 or more aCNA, of which 7 (44%) were mutated in p53 exons 2 to 10, and there were 18 cases with 13q14-II plus 2 or more aCNA, of which 7 (44%) were mutated in p53 exons 2 to 10.
Results of outcome analyses of 13q14 deletions of type I or II lesions stratified by associated SNP 6.0 array profiling–detectable subchromosomal aCNA loads versus overall survival in CLL

We proceeded with bivariate outcome analysis of 13q14 deletions of type I and II lesions grouped by associated SNP 6.0 array-based subchromosomal aCNA status of 2 or more and 3 or more, respectively (CLL cases that carried both 13q14 lesion types were included and hierarchically assigned to type II status). Kaplan–Meier plots for these analyses are displayed in Fig. 4A–H. From these analyses, the following conclusions are supported: (i) 13q14 lesions of either type with elevated associated aCNA counts were associated with a significantly worse prognosis than either type with no or additional aCNAs below indicated thresholds; and (ii) 13q14 type II deletions were prognostically more adverse than 13q14 type I deletions, as evidenced by an accelerated disease course in cases with low associated complexity (aCNA ≤1 or ≤2, respectively), a finding that was particularly evident in CLL cases that were relapsed at the time of analysis (UT + T plots).

Next, we conducted bivariate outcome analysis of 13q14 deletions of type I and II lesions stratified by associated SNP 6.0 array-based subchromosomal aCNA status of 2 or more and 3 or more, respectively, based on aCNA nominations that had been made by algorithmic aCNA calling methods (see Supplementary Methods). Results were similar to results based on aCNA nominations made through visual heatmap inspection. Kaplan–Meier plots are displayed in Supplementary Fig. S3A–H.

Degree of 13q14 deletions and outcome in CLL

The degree of 13q14 deletions was quantified using the mean of 216 consecutive copy number estimates based on probes located within 13q14 deletions and correlated with the outcome measures TTF and overall survival for the group of 132 CLL patients with 13q14 deletions. The CLL cohort was dichotomized at every actual copy number cutoffs (the latter based on small N) optimally separated the cohort, suggesting that the degree of 13q14 deletion could have negative effects on CLL outcome once larger cohorts are studied (for this cohort, the 95% confidence bands in gray overlapped an HR of 1; ref. 37).

![Figure 4](image-url)
13q14-resident miR15a/16-1 expression and outcome in CLL

The relative expression levels of the 13q14-resident miRs as measured by Q-PCR (see earlier) were tested as a prognostic factor. The CLL cohort was dichotomized at every actual normalized miR expression measurement (actual ΔCt values) and HRs computed. No clear prognostic effects were identified (Supplementary Fig. S5A–H and S6A–H). This was equally true for 13q14-resident miR levels tested as prognostic factors in the entire CLL cohort (N = 255; data not shown).

CLL with 13q14 type II are associated with lower RB1 mRNA expression levels and RB1 frameshift mutations or biallelic RB1 deletions in a minority subset of cases

The RB1 gene coding exons were resequenced in 53 of the CLL with 13q14 type II deletions, resulting in the identification of 2 cases (CLL# 158 and 173) with somatically acquired truncating frameshift mutations. Together with one case of CLL with biallelic RB1 deletion (CLL# 13), this indicates that approximately 5% of CLL with 13q14 type II deletions are RB1 null.

Next, we measured RB1 mRNA expression by normalized Q-PCR in the first 160 consecutively enrolled cases with intact RNA and identified significantly lower RB1 expression in CLL with 13q14 type II deletions as opposed to CLL with 13q14 type I deletions or no 13q14 deletions. Data are summarized in Fig. 5.

Identification of rare somatically acquired mutations in 13q14-resident miR16-3p and miR16-5p in CLL

Sequence analysis of the genomic locus for miR16 and 15a and flanking sequences in the entire CLL cohort identified 2 somatically mutated miR16 cases and no miR15a mutations. CLL # 61 harbored a heterozygous 6 bp deletion spanning miR16-3p, whereas CLL # 70 carried a homozygous 1 nucleotide deletion in miR16-5p in the setting of chromosome 13 aUPD. The vast majority of CLL cases (99%) carried wild-type miR 16 and 15a genes. Data are summarized in Fig. 6.

Discussion

In this study, we used SNP 6.0 arrays to interrogate genomic DNA isolated from fluorescence-activated cell-
sorted CD19\(^+\) cells compared with either paired sorted CD3\(^+\) cells (96%) or paired buccal (4%) DNA from 255 CLL patients for acquired chromosomal copy number changes (aCNA) and LOH with a detailed focus on 13q14 deletions. The novel findings from this study are (i) that 13q14 deletions have varying effects on CLL clinical behavior, with large 13q14 deletions (type II: inclusive of RB1) associated with an inferior prognosis; (ii) that 13q14 type II deletions are frequently associated with additional aCNA (a total aCNA count of \(>/= 3\) was detected in \(~35\%\) of cases; ref. 35); (iii) that approximately 10\% to 15\% of CLL with biallelic 13q14 deletions display markedly reduced miR15a/16-1 levels but that the effect of monoallelic miR loss on miR expression is subtle and only shown for miR15a; (iv) that the relative expression levels of the 13q14-resident miRs do not substantially affect CLL prognosis; (v) that a few CLL cases with 13q14 type II deletions carry RB1 frameshift mutations and therefore are RB1 null; and (vi) that rare CLL cases harbor acquired mutations in miR16.1.

This study is characterized by several methodologic strengths including paired (CD19\(^+\) vs. CD3\(^+\)) array analysis for all CLL samples, ultrahigh-purity (sorted) cells as a source of DNA and RNA (for miR expression analysis), and a rigorous and conservative genomic copy number data analysis schema that had previously been externally validated by FISH (27). The analysis of paired samples is of particular importance for the accurate determination of genomic complexity in cancer cell genomes in the setting of ultrahigh-resolution SNP arrays, given that the vast majority of copy number variations (CNV) are less than 1 Mb in length. In all, our approach results in very high specificity and sensitivity for aCNA, thus avoiding problems for the precision of genomic clinical correlative analysis resulting from under- or overcalling of genomic lesions.

As part of the work presented here, we provide refined estimates for optimal physical separation cutoffs for 13q14 deletions into prognostically significant subtypes. From a practical perspective, routine inclusion of a probe for RB1 or genes located within 300 to 500 kb telomeric region to RB1 should reliably identify CLL patients carrying more adverse 13q14 subtypes (17).

Our novel identification of somatically acquired RB1 null states, including somatically acquired RB1 mutations, provides evidence that for a subset of 13q14 deletions, RB1 is a relevant target gene. Furthermore, this conclusion is supported by the well-studied effects of RB1 on cell-cycle control and genomic stability (38). However, given the identification of multiple 13q14 deletion types, it is likely that additional 13q14-resident genes actively influence CLL biology and clinical phenotypes and that the identification of such genes remains an important research objective.

The identification of rare CLL with miR16.1 mutations provides additional evidence for a functional role of this microRNA in CLL pathophysiology. Interestingly, 1 of the 2 miR16.1 mutations occurred in miR16.1-3p, indicating that further studies of this gene product are warranted. Of note, however, monoallelic miR16.1 loss is insufficient to affect miR16.1 expression compared with nondeleted CLL cases, thus providing constraints on models relating to the exact role of this microRNA in 13q14 biology.
This report is based on CLL patients enrolled prospectively at a single center with an outcome focus on overall survival. To minimize the effect of biases introduced through sample collections relative to prior treatments or actual dates of diagnosis, we have analyzed and presented data for the untreated and combined (untreated and relapsed) CLL cohort separately, using either the diagnosis or trial enrollment date as the reference dates. Such an analysis approach seems particularly relevant to biomarkers that change over the course of a patient’s illness or for markers for which such a change is likely but not yet proven through longitudinal analysis (inclusive of the hypothesis that 13q14 type II deletions arise during CLL disease evolution). About the conclusion that 13q14 type II deletions constitute a factor associated with and contributory to more aggressive CLL, we were able to show that these lesions are disproportionally associated with elevated genomic complexity in CLL: a trait associated with aggressive CLL (25). It is, however, important to note that additional studies with substantially larger patient numbers are needed to be able to measure the relative contribution of 13q14 deletion subtypes versus other factors known to affect CLL clinical behavior.

One of the current, still speculative, interpretations of the combined available data on 13q14 deletions in CLL is that short 13q14 deletions affect genes that confer a growth or survival/antiapoptotic advantage on CLL cells, whereas longer 13q14 deletions are part of CLL disease evolution and degeneration into more aggressive subtypes; the latter would be due to increased genomic instability (as also seen with 17p and 11q deletions) and an ensuing potential for outgrowth of more aggressive CLL subclones (35, 39) and likely other as-yet unidentified mechanisms.

References


In summary, our data show that 13q14 deletions in CLL are biologically and prognostically distinct entities and that routine clinical identification of 13q14 type I and II deletions would allow for refined CLL patient risk stratification.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

Authors’ Contributions

P. Ouilliete, J. Li, and S. Malek carried out the laboratory research. R. Collins and S. Malek analyzed clinical data. K. Sheden, S. Shahkan, and C. Li assisted with statistical analysis and software development for data analysis. S. Malek conceived the study and supervised the work. P. Ouilliete, K. Sheden, and S. Malek wrote the manuscript.

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lymphocytic leukemia, and its homologous region on mouse chromo-
The Prognostic Significance of Various 13q14 Deletions in Chronic Lymphocytic Leukemia

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