Humoral Immune Responses against the Immature Laminin Receptor Protein Show Prognostic Significance in Patients with Chronic Lymphocytic Leukemia

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Humoral Immune Responses against the Immature Laminin Receptor Protein Show Prognostic Significance in Patients with Chronic Lymphocytic Leukemia\textsuperscript{1,2}

Birte Friedrichs,\textsuperscript{3} Sandra Siegel,\textsuperscript{3} Marita Kloess, \textsuperscript{†} Adel Barsoum,\textsuperscript{¶} Joseph Coggin, Jr.,\textsuperscript{¶} James Rohrer,\textsuperscript{¶} Ilja Jakob,\textsuperscript{*} Markus Tiemann, \textsuperscript{†} Klaus Heidorn, \textsuperscript{†} Christoph Schulte, \textsuperscript{†} Dieter Kabelitz, \textsuperscript{§} Jörg Steinmann, \textsuperscript{§} Norbert Schmitz, \textsuperscript{*} and Matthias Zeis\textsuperscript{4*}

Chronic lymphocytic leukemia (CLL)\textsuperscript{3} remains an incurable disease involving clonal mature B lymphocytes and is associated with a heterogeneous clinical course in terms of prognosis and necessity of treatment (1). Some patients remain almost asymptomatic and have a nearly unaltered life expectancy, while others show rapidly progressive disease with early need for intensive treatment (2). A variety of prognostic markers, including CD38, ZAP70, and distinct cytogenetic abnormalities, have been described that, alone or in combination, are being used to define treatment strategies according to the patient’s individual risk profile (3–8). The mutational status of the Ig H chain genes (\textit{V}_{\text{H}}\text{ status}) is considered to have the strongest prognostic value, with unmutated Ig H chain (\textit{IgV}_{\text{H}}) genes being associated with a more rapidly progressive course of disease and shorter overall survival as compared with cases with mutated \textit{IgV}_{\text{H}} genes (9, 10).

There is growing evidence that interactions between the host immune system and the tumor may have an impact on clinical outcome (11–13). Ansell et al. demonstrated that the presence of high Th cell numbers in diffuse large B cell lymphoma was associated with a better prognosis (14). Although CTLs directed against tumor Ags directly mediate killing of tumor cells, the role of humoral immune responses controlling malignant disease is less understood. In patients with follicular lymphoma, Weng et al. found humoral immune responses after Id vaccination to be associated with prolonged progression-free survival (15).

The target Ag in this study, the tumor-associated oncofetal Ag/immature laminin receptor (OFA/iLR) is widely expressed in many types of human tumors, including hematological malignancies, while it is absent in normal adult differentiated tissues (16–22). Functional properties of OFA/iLR have not completely been elucidated although it is confirmed to be the precursor molecule of the nonimmunogenic mature 67-kDa protein that plays a role in cell adhesion-associated processes by laminin binding (23, 24). The strong overexpression of OFA/iLR on the cell surface of CLL cells made it a valuable candidate to investigate the role of tumor-specific Ab immunity in CLL patients (22).

The immunogenicity of OFA/iLR has previously been shown in two other human tumor systems, namely breast cancer and renal cell carcinoma. In breast cancer patients, Rohrer et al. established several OFA/iLR-specific CD4\textsuperscript{+} and cytotoxic as well as regulatory CD8\textsuperscript{+} T cell clones (19). In renal cell carcinoma, Höltl et al. showed that patients receiving dendritic cells with lysate of OFA/iLR...
iLR-expressing tumor cells developed enhanced immune responses against OFA/iLR (25).

In this study, we measured humoral anti-OFA/iLR reactivity in untreated patients with CLL and in patients after allogeneic transplantation of blood stem cells. We further determined the specificity and functionality of anti-OFA/iLR Abs and finally investigated progression-free survival in CLL patients in relation to the presence of tumor-specific humoral immune responses.

Materials and Methods

Patients

Sera and PBMC were obtained from a total of 67 patients with untreated CLL, 11 patients with CLL who had undergone allogeneic stem cell transplantation, and 50 healthy donors serving as negative controls. Diagnosis of CLL was based on morphologic and immunophenotypic features according to the classification of the World Health Organization (WHO) (26). Sample collection took place from 2003 to 2006. Written informed consent was provided according to the Declaration of Helsinki. The study was approved by the review board of the local ethics committee.

The prognostic parameters were performed at time of diagnosis or shortly thereafter. If analysis of somatic hypermutations or fluorescence in situ hybridization (FISH) had not been performed at diagnosis, they were performed at the same time of the immune studies. For all patients except four, information on IgV_{H} gene mutational status and FISH analysis for genetic abnormalities was available. Patient characteristics are summarized in Table I. Healthy donor samples were obtained from blood donors of the institutional department of transfusion medicine (\(n = 50\), male/female ratio 3:1, mean age 55 years).

CLL cells and nonmalignant subsets

Peripheral blood was drawn from healthy donors or CLL patients, and PBMC were obtained by Ficoll density gradient centrifugation and cryopreserved in liquid nitrogen. Isolation of CD19 and PBMC were obtained by Ficoll density gradient centrifugation. Peripheral blood was drawn from healthy donors or CLL patients, CLL cells and nonmalignant subsets (female ratio 3:1, mean age 55 years).

A set of 42 synthetic peptides (OFA1–42) with a length of 17–20 aa overlapping by 5 aa and representing the entire sequence of OFA/iLR was used. Sera were stored at \(-20^\circ C\) until use.

OFA Ab and peptides

Mouse anti-OFA/iLR mAb was used as previously described (21). A set of 42 synthetic peptides (OFA_{1–42}) with a length of 17–20 aa overlapping by 5 aa and representing the entire sequence of OFA/iLR were obtained from Peptides & Elephants. Peptides were provided with >70% purity.

Flow cytometry for CD38, ZAP70, and OFA/iLR expression

Staining of OFA/iLR on CLL cells and nonmalignant subsets (\(n = 3\) for each subset) was performed as previously described (21). FITC-labeled goat anti-mouse Ig (Dako) was used as a secondary reagent. Assessment of intracellular ZAP70 and cell-surface expression of CD38 was conducted as described earlier using the following Ab conjugates: anti-ZAP70 (clone 1E7.2, Caltag Laboratories), anti-CD19-PerCP/Cy5.5 (clone SJ25C1, Beckman Coulter/Immunotech), and anti-CD38-PE (clone HB-7, Caltag Laboratories), or respective isotype control (7, 27). At least 10,000 cells were acquired for all FACS analysis in the CellQuest program on a BD FACScan flow cytometer (BD Biosciences).

Cytogenetic analysis

Based on conventional cytogenetic studies and data from comparative genomic hybridization, a comprehensive set of FISH DNA probes (Abbott Diagnostics) was developed to diagnose the most frequent genomic aberrations in CLL. Our probe set allowed screening for the following partial deletions, partial trisomies, and translocations: del(6q23), del(11q22), tr112, del(13q14), and del(17p13), as previously described (27).

\textit{IgV}_{H} mutational analysis

The sequences were compared with published germline V_{H}, D, and J_{H} genes using DNAPlot software and IMGT database (IMGT, the international ImMunoGeneTics database, http://imgt.cines.fr). Mutational status was calculated as percentage deviation from the closest matching germline V_{H} segment. As previously decided, a cutoff of \(\geq 98\%\) germline homology defined the group with unmutated IgV_{H} (28).

Western blot analysis for OFA/iLR expression and for Abs to recombinant OFA/iLR protein

Standard Western blot analysis for OFA/iLR expression was performed as described previously using the monoclonal anti-OFA/iLR Ab at a concentration of 0.75 \(\mu\)g/ml (21).

\textit{ELISA for Abs to recombinant OFA/iLR protein}

For the analysis of specific anti-OFA/iLRP Abs, a standard ELISA was performed as described elsewhere (29). Purified human OFA/iLR (6 \(\mu\)g/ml) and HIV p24 (1 \(\mu\)g/ml) (Aalto Bio Reagents) were bound to ELISA plates (Greiner Bio-One). Sera were used in a dilution of 1/50. OD was read at 450 nm. Responses against HIV p24 (all patients negative) were used as a negative control and nonspecific reactivity was subtracted from each OFA/iLR OD value. Epitope mapping was performed using 42 overlapping OFA/iLR peptides. For IgG subtype analysis peroxidase-conjugated mouse anti-human IgG1, IgG2, IgG3, or IgG4 were used (all from Zymed Laboratories). All analyses were performed in duplicate.
Complement-mediated cytotoxicity and Ab-dependent cellular cytotoxicity (ADCC)

Specific cell lysis with Ab and complement was measured using a 2-h $^{51}$Cr-release assay as previously described by Bellucci et al. (30). For complement-dependent cytotoxicity, a 1/4 dilution of rabbit complement (Calbiochem) was chosen. For ADCC, PBMC from healthy donors were used as effector cells at an E:T ratio of 10:1. OFA/iLR-expressing CLL cells (autologous or allogeneic), cells from patients with CLL in Richter transformation that were negative for OFA/iLR expression, and CD19$^{+}$/H11001 purified B cells from healthy donors were used as target cells and incubated with different dilutions of patient serum. All CLL samples used as targets were analyzed by FACS for CD19$^{+}$/H11001 surface expression and contained $>90\%$ CD19$^{+}$ cells, either for high leukemic burden or after CD19$^{+}$/H11001 isolation using MACS as described above.

Statistical methods

To establish cut-off points for OFA/iLR OD values that distinguished between negative and positive cases, we used different approaches including the mean plus two SDs of the healthy donor samples and the receiver operator characteristic curve (31, 32). Using these approaches, the suggested cut-off points lie between 0.06 and 0.13 OD. As for the exploratory nature of the study and to avoid false-positives, an OD of 0.11 for IgG and 0.13 for IgM were chosen as initial cut-off values for determination of positive Ab reactivity for OFA/iLR and were subsequently applied to healthy donors and CLL patients. Student’s $t$ test was used to determine differences in anti-OFA/iLR Abs between healthy donors and CLL patients. Following Dohner et al.’s hierarchical classification, high-risk cytogenetics was defined as the presence of del17p and/or del11q (3). As six of seven patients with tri12 concomitantly had a del1q, the remaining patient with isolated tri12 was also included in the group of high-risk cytogenetics. Survival data were obtained from clinical records. Progression-free survival (PFS) was defined as the time from diagnosis to either disease progression or death from any cause (events) or last follow-up (censored) and was estimated using the method of Kaplan and Meier. In a univariate analysis we compared the Kaplan-Meier curves by the log-rank test and additionally by the Breslow test, which gives more emphasis to early events and is preferred in situations when the proportional hazard assumption may be violated by the data (33). Since CLL is an incurable disease, all patients will eventually experience disease progression, and early differences in events are important. Multivariate Cox regression models, adjusted for established risk factors, were fitted to evaluate the impact of the humoral immune response as a novel prognostic factor on PFS. Relative risks and the corresponding 95% CIs were calculated. $p$ values $\leq 0.05$ were considered to be significant.
Expression of OFA/iLR in patients with CLL and normal B cells

Expression of OFA/iLR protein on CLL cells and B lymphocytes purified from the blood of healthy individuals was determined by flow cytometry and Western blot analysis using the previously described monoclonal OFA/iLR-specific Ab (21). OFA/iLR expression was detectable in all of the 67 samples of CLL patients, although the range of OFA/iLR expression levels was relatively broad (10–98%, mean 63.3%). As described earlier, no OFA/iLR expression was detectable in all of the 67 samples of CLL patients, whereas the range of OFA/iLR expression levels was relatively broad (10–98%, mean 63.3%). As described earlier, no OFA/iLR expression was detectable in all of the 67 samples of CLL patients, whereas the range of OFA/iLR expression levels was relatively broad (10–98%, mean 63.3%).

FIGURE 2. Titers of IgG and IgM anti-OFA/iLR Abs in untreated CLL patients, healthy donors, and CLL patients after allogeneic transplantation. A and B. Results from anti-OFA/iLR ELISA are shown for healthy donors (HD) (■), untreated CLL patients (CLL) (□), mutated CLL patients (▲), and unmutated CLL patients (○) for (A) IgG and (B) IgM, respectively. Black horizontal bars indicate cut-off values for IgG (0.11) and IgM (0.12). Ab response is displayed as OD. C, OD levels from an ELISA analysis for four CLL patients after allogeneic transplantation. Time point −1 represents pretransplant donor sera.

Results

Expression of OFA/iLR in patients with CLL and normal B cells

Expression of OFA/iLR protein on CLL cells and B lymphocytes purified from the blood of healthy individuals was determined by flow cytometry and Western blot analysis using the previously described monoclonal OFA/iLR-specific Ab (21). OFA/iLR expression was detectable in all of the 67 samples of CLL patients, although the range of OFA/iLR expression levels was relatively broad (10–98%, mean 63.3%). As described earlier, no OFA/iLR expression was detectable in all of the 67 samples of CLL patients, whereas the range of OFA/iLR expression levels was relatively broad (10–98%, mean 63.3%). As described earlier, no OFA/iLR expression was detectable in all of the 67 samples of CLL patients, whereas the range of OFA/iLR expression levels was relatively broad (10–98%, mean 63.3%).

OFA/iLR Abs are present in sera from untreated patients with CLL as well as in patient sera after allogeneic stem cell transplantation

First, specificity of the monoclonal anti-OFA/iLR Ab used for all subsequent ELISA analysis was confirmed by dot blot shown in Fig. 1C. Anti-OFA/iLR Abs specifically detected the recombinant protein but not the nonrelated protein survivin and, conversely, OFA/iLR protein was not recognized by the nonrelated anti-survivin Ab. Given the frequent expression of OFA/iLR on the surface of CLL cells, we next analyzed whether patients developed spontaneous humoral immune responses toward this Ag. The presence of anti-OFA/iLR IgG and IgM Abs was evaluated by means of an ELISA assay using the recombinant OFA/iLR protein as a coating agent. Seventy-six untreated patients with CLL and 50 healthy volunteers were analyzed. In 22 of 67 patients (32.8%), IgG OFA/iLR Abs were detected (Fig. 2A). In 12 of 67 patients (17.9%), IgM OFA/iLR Abs were identified (Fig. 2B), whereas 5 (7.4%) patients had both IgG and IgM Abs detected. Four of 50 healthy donors (8%) had IgG or IgM OD levels above the cut-off point. Untreated patients with advanced stage of disease (Binet C) did not show any detectable levels of IgG or IgM Abs against OFA/iLR (n = 10, data not shown). CLL patients had statistically significant higher levels of anti-OFA/iLR-IgG and -IgM (p = 0.012 and p = 0.049, respectively) while there was no statistically significant difference between the humoral response of mutated and unmutated patients (Fig. 2, A and B).

We also looked for anti-OFA/iLR Ab levels in 11 patients with CLL who had undergone allogeneic stem cell transplantation (allo-SCT). The time from allo-SCT until first analysis of sera varied from 4 to 44 mo (median 14.8 mo). Eight of 11 sera showed detectable IgM and/or IgG anti-OFA/iLR Abs after allo-SCT. Interestingly, six of eight patients who achieved a complete remission after transplantation with complete donor chimerism also showed significant anti-OFA/iLR responses. Characteristics of allografted patients and Ab responses are shown in Table II. For four patients, donor sera were available, which all tested negative for
anti-OFA/iLR Abs. Immune responses against OFA/iLR developed after allo-SCT sustained for several months, but decreased over time without signs of relapse or loss of full donor chimerism (Fig. 2C).

Specific recognition of OFA/iLR epitopes differs between untreated patients and patients after allogeneic SCT

All patient sera with significant anti-OFA Ab levels (IgG, n = 20; IgM, n = 9; IgG + IgM, n = 5) were included in an epitope mapping assay to confirm epitope specificity. A panel of 42 overlapping peptides representing the entire sequence of the OFA/iLR protein was used in an IgG and IgM ELISA. Twenty-three patients recognized at least one distinct epitope of the OFA/iLR sequence. To exclude nonspecific reactivity, only those patients with specific epitope recognition were considered to have reactive sera. Fifteen patients with reactive sera recognized more than one epitope. Fig. 3A shows the distribution of all recognized peptide epitopes from untreated CLL patients in relation to the localization of functional domains of OFA/iLR. The distribution of specific IgG and IgM responses includes association with intracellular as well as extracellular located epitopes. CLL patients after allogeneic stem cell transplantation who mounted Ab responses against OFA/iLR (n = 8) exclusively recognized peptide epitopes from aa 159–290 located toward the extracellular C-terminal end of the OFA/iLR protein sequence. In contrast to the untreated patient group, intracellular domains were not recognized (Fig. 3B).

Binding of anti-OFA/iLR Abs can be specifically inhibited

To validate the specificity of the detected anti-OFA/iLR Abs, an inhibition assay was performed in the presence of recombinant OFA/iLR protein, which was formerly used as a coating Ag in the ELISA. As demonstrated in Fig. 4A, reactivity to OFA/iLR of respective patient sera was inhibited by addition of the OFA/iLR protein in a dose-dependent manner. No inhibitory effect was observed when HIV p24 protein or β2-microglobulin was added. Using reactive serum as the source of primary Ab and a FITC-conjugated secondary Ab in a FACS analysis, CD19+ purified malignant B lymphocytes (CLL cells) from an OFA/iLR positive patient were recognized but not OFA/iLR-negative CLL cells (Fig. 4B). Serial dilutions of serum at 1/25, 1/50, and 1/100 showed dose-dependent recognition.

Predominant subclasses of OFA/iLR Abs are IgG1 and IgG3 and implicate a Th1-biased immune response

For further characterization of OFA/iLR-reactive sera, IgG subclass analysis was performed in an ELISA assay. Sera from patients recognizing at least one specific OFA/iLR epitope were subclassified. Sera from healthy donors were also analyzed for control purposes although they were not reactive in the screening of ELISA for OFA/iLR reactivity. Fig. 5A shows values of OD for
IgG1, IgG2, IgG3, and IgG4 Abs. The distribution of subclasses is shown in Fig. 5B, which defines the highest value for each patient as predominant IgG subclass. IgG1 was the predominant subclass in 14 of 18 patients, while IgG3 anti-OFA/iLR Ab was the major IgG subclass for 8 patients. IgG4 was found to be predominant in serum from only one patient. In five patients, high values for both IgG1 and IgG3 Abs were detectable. No correlation was found between the detection of predominant IgG subclass and the mutational status or OFA/iLR expression of CLL cells (data not shown).

**Anti-OFA/iLR Abs induce ADCC and complement activation**

We next determined the functional properties of the reactive sera. The ability of OFA/iLR Abs to lyse OFA/iLR-expressing CLL cells was determined in an ADCC assay and complement-dependent cytotoxicity (CDC) assay. Sera from patients that showed strong responses in the initial screening ELISA as being responsive to one specific OFA/iLR epitope in the epitope mapping were able to induce lysis of autologous OFA/iLR-positive CLL cells (Fig. 6, A and E) in a dose-dependent manner. Furthermore, reactive sera were able to induce lysis of allogeneic, OFA/iLR-expressing CLL (Fig. 6, B and F) cells but not normal CD19\(^+\) B cells (Fig. 6, C and G) or CLL cells from patients with Richter transformation (III) were incubated with OFA/iLR-reactive serum in serial dilutions of 1/25, 1/50, and 1/100 as a source of primary Ab and a rabbit anti-human IgG as a secondary Ab.

**PFS in patients with humoral reactivity to OFA/iLR**

To determine whether the presence of specific anti-OFA/iLR Abs influenced PFS, patients were grouped according to the presence/absence of a humoral immune response, which specifically recognized at least one OFA/iLR epitope, and were then analyzed using Kaplan-Meier plots. The median duration of follow-up was 72 mo. In a univariate analysis, the group of patients with reactive sera (n = 23) showed a significantly lower probability of disease progression compared with patients...
with nonreactive sera (Fig. 7A). Median PFS for patients with reactive sera was 114 mo compared with 66 mo for the nonreactive group (p = 0.029). Patients with unmuted V_H genes had a PFS of 70 mo compared with 96 mo for mutated V_H genes (p = 0.128) (Fig. 7B). A PFS of 36 vs 96 mo was found for patients with presence or absence of high-risk cytogenetics, respectively (p = 0.005) (Fig. 7C). Comparing the reactive and nonreactive groups of patients, the distribution of V_H status did not vary significantly due to the low number of patients. The number of patients with high-risk cytogenetics differed significantly (reactive 8.6% vs nonreactive 40.9%) between the two subgroups. Exact characteristics of the two groups are displayed in Table III. Keeping in mind the possible limitations, we investigated whether the presence of humoral immune responses influenced the time to progression in a multivariate analysis. In the final model with adjustment for V_H mutational status and high-risk cytogenetics, the presence of humoral immune responses against OFA/iLR remained significant and revealed a relative risk of 0.36 (95% CI 0.14–0.94; p = 0.038). Results from the statistical analysis are summarized in Table IV.

Discussion

The role of spontaneous tumor-specific immune responses in controlling CLL is largely unknown. Furthermore, the number of characterized tumor Ags expressed on the cell surface of CLL cells is limited. As an example, the individual B cell receptor and its complementary determining region (CDR3) represent an individual-specific tumor Ag that elicits immune responses in a number of B cell malignancies including CLL. The advantage of a highly selective specificity of the Id is counterbalanced by the enormous technical difficulties to generate Id-derived epitopes (34–37). The OFA/iLR is expressed intra- and extracellularly in various tumor entities (17, 25, 38–40). Recently, our group identified HLA-A*0201-presented T cell epitopes derived from OFA/iLR protein in patients with hematological malignancies including B-CLL (22). The wide expression on CLL cells and its known immunogenicity made OFA/iLR a suitable target structure to determine tumor-specific humoral immunity in CLL patients (19, 21, 41).

In the current study, we were able to detect specific IgG and IgM Abs against OFA/iLR in 23 of 67 untreated patients with CLL, significantly more than those present in healthy donor sera. Moreover, 8 of 11 patients after allogeneic SCT showed significant levels of anti-OFA/iLR Abs. Only few data exist documenting the presence and significance of humoral immune responses against defined tumor Ags. In acute myeloid leukemia and myelodysplastic syndrome, Elisseeva et al. described humoral immune responses against Wilms tumor gene products and suggested a possible correlation between leukemic tumor burden and production of Wilms tumor Abs (42). In the present study, anti-OFA/iLR Abs are detectable both in untreated patients with potentially ongoing antigenic stimulation and in patients after allotransplantation in the absence of malignant B cells. Analysis of serial samples of patients after allo-SCT showed a decline of Ab responses after transplantation in the absence of relapse or loss of chimerism, which might be explained by decreasing tumor burden with concomitantly decreasing OFA/iLR expression.

IgG subclass analysis of the detected anti-OFA/iLR Abs revealed a predominant IgG1 and IgG3 Ab response in both untreated and transplanted patients, which is in agreement with previous data on autologous Ab responses in acute myeloid leukemia and myelodysplastic syndrome. Some experimental evidence exists that this reactivity pattern is associated with a Th1-driven immune response, also necessary for CTL induction (43–45). In agreement with our previous data, the current findings support the rationale for the use of OFA/iLR-derived epitopes to elicit OFA/iLR-specific CTL responses (21). The presence of both IgG and IgM isotypes suggests the involvement of a class switch promoting CD4+ Th cells as evidence of a coordinated immune response against OFA/iLR.

The graft-vs-leukemia (GVL) effect after allogeneic stem cell transplantation can result in complete remission of CLL and indicates the usefulness of immunotherapeutic approaches for this disease (28, 46). Although T cells clearly remain the critical components of the GVL effect, some studies also emphasize the presence of a tumor-specific humoral immune response (29, 47–50). We were able to detect significant levels of Ab titers against OFA/iLR in CLL patients receiving an allotransplant, although further investigation is needed to clarify the functional...
FIGURE 6. OFA/iLR-reactive patient serum mediates specific CDC and ADCC. A–D, Ab-mediated cellular cytotoxicity; healthy donor PBMC were added in an E:T ratio of 1:10. E–H, Complement-dependent cytotoxicity. A and E, OFA/iLR-reactive patient sera (CLL1 and CLL2) mediate lysis of autologous CLL cells via ADCC (A) and CDC (E). B and F, OFA/iLR-reactive sera from untreated patients (CLL3 and CLL4) and patients after allogeneic SCT (allo1 and allo2) lyse OFA/iLR-expressing cells (CLL1 and CLL2). A, B, E, and F, Anti-OFA/iLR Ab was used as a positive control. Healthy donor sera (HD1 and HD2) were used as negative controls. C and G, Negative control with normal B cells as target cells. D and H, Negative control with OFA/iLR-negative CLL cells in Richter transformation as target cells.
The role of these Abs with regard to GVL in CLL. The detected Abs from untreated as well as transplanted patients were capable of recognizing and efficiently killing OFA/iLR-expressing CLL cells while sparing OFA/iLR-negative cells. It remains unclear at this point why the killing of CLL cells is inefficient in vivo. It is possible that deficient killing in vivo may be linked to Fc receptor polymorphisms or NK cell defects, which remains to be investigated.

Interestingly, Ab responses observed in patients after allogeneic transplantation only recognized peptides of the extracellular part toward the C-terminal end of the OFA/iLR sequence while Abs from untreated CLL patients recognized epitopes from the entire sequence. Although it has to be investigated whether this phenomenon is an expression of a specific immune recognition pattern, it provides valuable information for the generation of therapeutic Abs directed against OFA/iLR-expressing tumor cells.

Untreated CLL patients mounting an Ab response against OFA/iLR showed a significantly longer period of time to progression compared with those patients with nonreactive sera, which was also confirmed in a multivariate analysis. Prognostic relevance of humoral immune responses was recently demonstrated for several other malignancies including ovarian cancer and follicular lymphoma (15, 51). Our data presented here suggest that humoral immunity to OFA/iLR is a new indicator of prolonged PFS in untreated CLL patients. Considering the retrospective design of the study, the rather small cohort, and a median follow-up time of only 72 mo, the presence of OFA/iLR Abs must be assessed prospectively along with other markers to confirm the prognostic value seen in this study.

Table III. Characteristics of CLL patients with reactive and nonreactive sera against OFA/iLR

<table>
<thead>
<tr>
<th>Cytogenetics (FISH)</th>
<th>Positive Anti-OFA/iLR Response</th>
<th>Negative Anti-OFA/iLR Response</th>
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<tbody>
<tr>
<td>n = 23</td>
<td>n = 44</td>
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<tr>
<td>Normal</td>
<td>9 39.1</td>
<td>17 38.6</td>
</tr>
<tr>
<td>Deletion 13q14</td>
<td>12 52.2</td>
<td>15 34.1</td>
</tr>
<tr>
<td>Trisomy 12</td>
<td>1 4.3</td>
<td>6 13.6</td>
</tr>
<tr>
<td>Deletion 11q</td>
<td>1 4.3</td>
<td>11 25.0</td>
</tr>
<tr>
<td>Deletion 17p</td>
<td>0 2.3</td>
<td>1</td>
</tr>
<tr>
<td>V_H status</td>
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<td></td>
</tr>
<tr>
<td>Mutated (&gt;98% homology)</td>
<td>15 65.2</td>
<td>19 43.2</td>
</tr>
<tr>
<td>Unmutated (&gt;98% homology)</td>
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<td>22 50.0</td>
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<tr>
<td>Not available</td>
<td>0 3</td>
<td>6.8</td>
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Table IV. Univariate and multivariate statistical analysis of risk factors including anti-OFA/iLR humoral immune response, V_H mutational status, and cytogenetic aberrations

<table>
<thead>
<tr>
<th>Risk Factor</th>
<th>Univariate Analysis</th>
<th>Multivariate Analysis</th>
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<tr>
<td></td>
<td>Median PFS (mo)</td>
<td>Relative Risk</td>
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<tr>
<td></td>
<td>95% CI</td>
<td>p</td>
</tr>
<tr>
<td>Humoral response</td>
<td>0.029</td>
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<tr>
<td>Yes (23)</td>
<td>114 64–164</td>
<td>0.36 0.14–0.94</td>
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<tr>
<td>No (44)</td>
<td>66 40–92</td>
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<tr>
<td>V_H status</td>
<td></td>
<td>0.128</td>
</tr>
<tr>
<td>Unmutated (34)</td>
<td>70 27–113</td>
<td>2.26 0.88–5.77</td>
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<tr>
<td>Mutated (30)</td>
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<td>Unfavorable FISH</td>
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<td>1.88 0.78–4.53</td>
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<td>No (51)</td>
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</table>
In summary, we for the first time describe tumor-specific anti-OFA/iLR Abs in sera of CLL patients with prognostic relevance, which is suggestive of a humoral immune control in CLL. The functionality of these Abs and the recognition of extracellular epitopes of the OFA/iLR sequence have significant implications for the development of immunotherapeutic approaches targeting OFA/iLR<sup>+</sup> tumor cells.

Disclosures

The authors have no financial conflicts of interest.

References