

## EXPRESSION OF *MDR1*, *LRP*, *BCRP* AND *BCL-2* GENES AT DIAGNOSIS OF CHILDHOOD ALL: COMPARISON WITH MRD STATUS AFTER INDUCTION THERAPY

U.U. Fedasenka\*, T.V. Shman, V.P. Savitski, M.V. Belevceva

Belarusian Research Center for Pediatric Oncology and Hematology, 223053 Minsk, Belarus

**Aim:** to investigate properties of leukemic cells by sorting out children diagnosed with ALL with different response to chemotherapy based on MRD level. **Methods:** We used a minimal residual disease (MRD) data on day 36 obtained with 3-colour flow cytometry as a reference. In view of MRD results, we used real-time PCR to assess expression levels of multidrug resistance associated genes *MDR1*, *LRP* and *BCRP*, antiapoptotic gene *Bcl-2* in initial samples from children diagnosed with ALL. P-gp expression and function in initial samples were analyzed by flow cytometry. **Results:** Briefly, medians of relative expression levels of *MDR1* gene were roughly comparable and in MRD<sup>+</sup> group came to 22.8 (0.02–26.6; n = 9) vs 24.8 (3.9–41.4; n = 10) in MRD<sup>-</sup> group. *Bcl-2* gene showed tendency to higher expression levels in MRD<sup>+</sup> group with median at 5992.9 (521.0–10362.0; n = 9) compared to 3183.6 (1947.9–6581.0; n = 10) in MRD<sup>-</sup> group. *LRP* gene relative expression levels were similar in both groups and came to 1934.9 (1500.7–3490.4; n = 9) and 1408.5 (665.5–2917.1; n = 10) in MRD<sup>+</sup> and MRD<sup>-</sup> groups, respectively. The median of *BCRP* expression levels in MRD<sup>+</sup> group was considerably lower than that in MRD<sup>-</sup> group, namely 76000.0 (48196.2–169230.8; n = 9) and 227967.2 (16683.7–422222.2; n = 10), respectively, but statistical analysis showed no significant difference for this parameter. **Conclusion:** We investigated expression of multidrug resistance genes *MDR1*, *LRP* and *BCRP* and antiapoptotic gene *Bcl-2* in leukemic cells at diagnosis, and MRD level at the end of induction therapy, and could not find obvious relations between these parameters.

**Key Words:** ALL, MRD, Bcl-2, MDR1, LRP, BCRP.

Biological properties of the leukemic cells that survive chemotherapy have attracted attention of scientists for many years but still remain obscure. Although chemotherapy has markedly evolved and current risk adapted protocols succeed for majority of children diagnosed with acute lymphoblastic leukemia, approximately 25% of patients develop a relapse. A relapse is also an adverse prognostic factor and requires a high risk adapted treatment and consequently lead to longer hospitalization and increased drug toxicity [1].

Currently, multidrug resistance is often associated with an efflux of cytotoxic compounds by transmembrane proteins. Most of them belong to ATP-binding cassette superfamily transporters (ABC transporters) [2, 3]. Role of *MDR1* gene and its product P-glycoprotein in acute leukemia has been studied extensively by many investigators. Some of the relevant publications confirmed an association between complete remission rates, overall and relapse-free survival and *MDR1* gene or Pgp expression and/or function in acute leukemia [4–10]. Other studies failed to confirm these results [11–14]. Another ABC-transporter: breast cancer resistance protein (BCRP) and the corresponding gene also may play a role in acute leukemia but larger studies are needed to confirm this [10,

13, 15, 16]. Major vault protein or lung resistance protein (LRP) is often associated with multidrug resistance [11, 17, 18]. This protein is a part of the vault complex, a eukaryotic barrel shaped organelle with a recently described structure but still unknown cell function. Current data on partial colocalization of vaults with cytoskeletal elements, secretory organelles and nucleus suggests its function as a transporter [19–23]. Several studies have already demonstrated a negative role of LRP expression in prognosis of acute leukemia [11, 17, 18, 24–26]. In contrast, other investigators did not point towards a prognostic significance of LRP [12, 27–29].

Surviving during chemotherapy also depends on ability of cells to undergo apoptosis. Antiapoptotic gene/protein Bcl-2 is known to be associated with response and remission rate in acute leukemia, although there were publications with controversial data [30, 31].

In our study we attempted to investigate properties of leukemic cells by sorting out patients with different response to chemotherapy. We used a minimal residual disease (MRD) data on day 36 obtained with 3-colour flow cytometry for ALL patients as a reference. In view of MRD results, we assessed expression levels of multidrug resistance associated genes *MDR1*, *LRP* and *BCRP*, antiapoptotic gene *Bcl-2* and P-glycoprotein expression and function in initial samples from children diagnosed with ALL.

### METHODS

**Patients.** 19 children diagnosed with primary B-lineage ALL were enrolled into the study. The patients age ranged from 1,9 to 18 years with median age at 5,5 years. The study was approved by the Ethical committee of the Research Center, samples were obtained under consideration of all legal requirements.

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\*Correspondence:

Fax: 375 (0)17 265 42 22

E-mail: januarys\_v@yahoo.com

**Abbreviations used:** ABC – adenosine tri-phosphate-binding cassette; ALL – acute lymphoblastic leukemia; AML – acute myeloid leukemia; Bcl-2 – B-cell chronic lymphocytic leukemia/lymphoma 2; BCRP – breast cancer resistance protein; cDNA – complementary deoxyribonucleic acid; Cy5 – cyanine; FACS – fluorescent activated cell sorter; FITC – fluorescein isothiocyanate; MAb – monoclonal antibody; MDR – multidrug resistance; MRD – minimal residual disease; LRP – lung resistance protein; PCR – polymerase chain reaction; PE – phycoerytherin; PI – propidium iodide; P-gp – permeability protein.

**Minimal residual disease detection.** 3-colour flow cytometry was used for MRD detection. Aliquots of bone marrow samples were incubated with monoclonal antibodies (MAb, Becton Dickinson) for 20 min at room temperature in dark. After that, erythrocytes were lysed by FACS Lysing Solution and samples were washed twice in Cell Wash buffer and fixed in paraformaldehyde. The patterns of antigens expression was analyzed with flow cytometer FACScan (Becton Dickinson) using CellQuestPro software. The following combinations of MAb were used: CD20/CD10/CD19, CD58/CD10/CD19, CD10/CD34/CD19, CD10/CD11a/CD19 and CD45RA/CD10/CD19 conjugated with FITC, PE, PE-Cy5. At least  $3 \times 10^5$  leukocytes were analyzed for each MAb combination. MRD positivity was defined as 0,01% of leukemic cells in a total count of leukocytes in a bone marrow sample [32].

**Cell cycle analysis.** Leukemic cells of all used samples were isolated from bone marrow by gradient density centrifugation. To study cell cycle distribution leukemic cells were fixed in 70% ethanol. Then cells were washed and treated with RNase and PI solution [33]. DNA content was evaluated using flow cytometry and ModFit program (Verity Software House).

**P-gp expression and function.** P-gp expression was evaluated with FITC-labeled 17F9 Mab (BD). P-gp function was tested by accumulation of JC-1 (Molecular Probes) with and without cyclosporine A [34]. P-gp expression and function were analyzed by flow cytometer.

**Real-time PCR.** Cells were isolated as described in cell cycle analysis paragraph. Total RNA from leukemic cells was extracted using Gen Elute Mammalian Total RNA Miniprep Kit (Sigma-Aldrich, St Louis, MO, USA). According to manufacturer's protocol after first step (cell lysing) samples were stored at  $-70^\circ$ . When needed, samples were thawed and RNA was extracted. Quantity and quality of obtained total RNA were defined with spectrophotometer Gene Quant RNA/DNA Calculator (GE Healthcare). Reaction of reverse transcription was carried out immediately after RNA extraction using Advantage RT-for-PCR Kit (BD) according to the manufacturer's protocol.

We evaluated expression levels of experimental genes using real-time PCR (iCycler, BioRad). For calculating relative expression levels standard curves method was used. Each standard curve was generated from four 10-fold dilutions of cDNA obtained from IM-9 cell line. cDNA synthesized from one extraction of RNA from IM-9 cell line was used for creating standard curves for analyzed genes and as a calibrator (a sample used as the basis for comparative expression results). Each reaction plate contained standard curves for a target gene and a control gene. Normal gene GUS was used as a control gene [35]. cDNA from IM-9 cell line was used for creating the standard curves because it expresses the control and all the target genes. For all experimental samples, target quantity was determined by interpolating from the standard curve and then dividing by the target quantity of the calibrator. The calibrator, then, becomes the 1X

sample, and all other quantities are expressed as an n-fold difference relative to the calibrator [36]. To avoid using numbers smaller than 1 (when there is less target RNA in the test sample than in the calibrator), all arbitrary units of gene expression levels in our study represent the fold-difference multiplied by 1000.

Amplifications were carried out in a total volume of 25  $\mu$ l containing cDNA, Platinum Quantitative PCR SuperMix-UDG (Invitrogene, Carlsbad, CA, USA, final concentration of  $MgCl_2$  was raised to 4 mM), 300 nM of forward and reverse primer, and 200 nM of TaqMan probe. The following primers were used (5' to 3'): Bcl-2 forward primer: TTG GCC CCC GTT GCT T, reverse primer: CGG TTG TCG TAC CCC GTT CTC, TaqMan probe: FAM AGC GTG CGC CAT CCT TCC CAG BHQ1; MDR1 forward primer: AGGAAGACA TGA CCA GGT ATG C, reverse primer: CCA ACA TCG TGC ACA TCA AAC, TaqMan probe: FAM CCT GGC AGC TGG AAG ACA AAT ACA CAA BHQ1; LRP forward primer: CAG CTG GCC ATC GAG ATC A, reverse primer: TCC AGT CTC TGA GCC TCA TGC, TaqMan probe: FAM CAA CTC CCA GGA AGC GGC GGC BHQ1; BCRP forward primer: TGG CTG TCA TGG CTT CAG TA, reverse primer: GCC ACG TGA TTC TTC CAC AA, TaqMan probe: FAM AGC AGG GCA TCG AGC TCT CAC CCT G BHQ1.

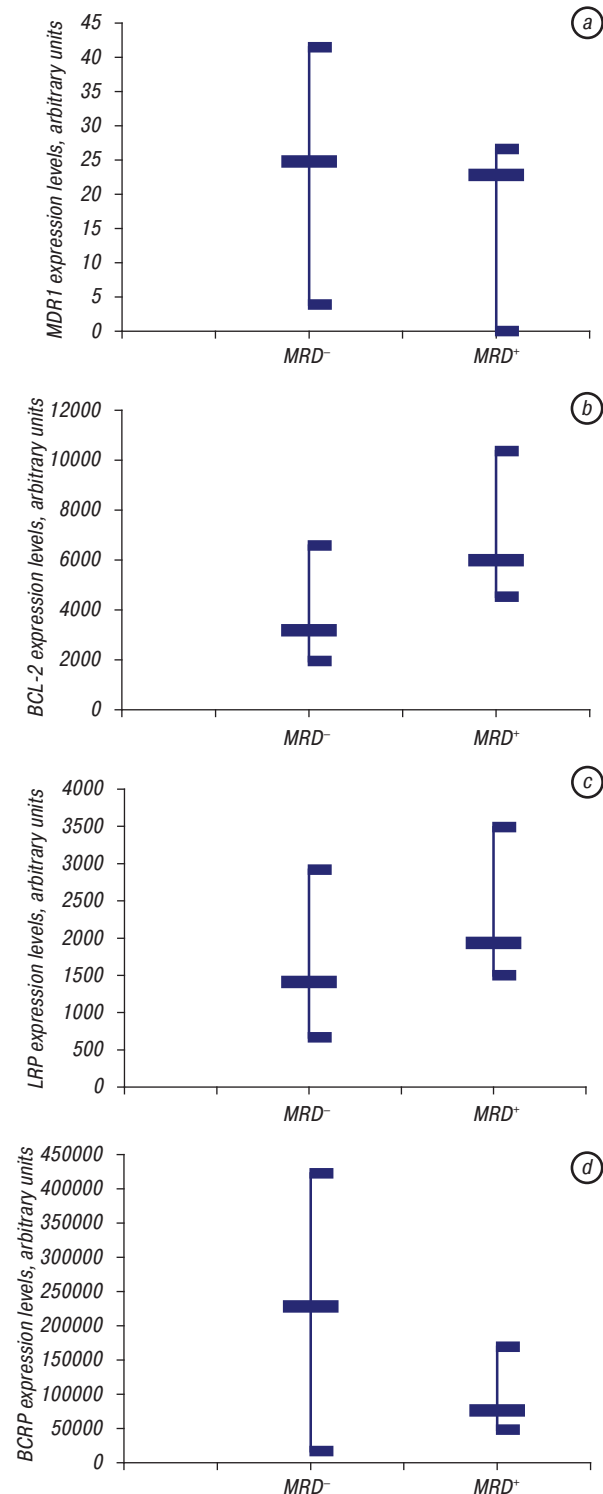
**Statistical analysis.** Results of experiments were presented as the median (lower quartile — upper quartile; valid number of cases tested). We used nonparametric Mann — Whitney U test to compare a certain property between two groups and Spearman Rank order for correlation tests (results presented as R value; P of significance; valid number of pairs tested). All calculations and graphs were computed using software STATISTICA 6.1.

## RESULTS AND DISCUSSION

Results of minimal residual disease monitoring at the end of the induction therapy is thought to be a very informative tool for prediction of a relapse [32]. Thus, we confronted data on drug resistance and apoptosis genes expression levels of all initial samples enrolled into the study with the results of MRD detection on day 36 of the same samples. MRD positivity was defined as 0,01% of leukemic cells in a total count of leukocytes in a bone marrow sample. By this criterion, all studied samples were divided into two groups: MRD positive (MRD<sup>+</sup>, n = 9) and MRD negative (MRD<sup>-</sup>, n = 10). In MRD<sup>+</sup> group the count of leukemic cells ranged from 0.03% to 0.3% with median at 0.08%. In MDR<sup>-</sup> group the quantity of leukemic cells ranged from 0.001% to 0.006% with median at 0.003%. Graphical summary of relative expression levels of studied genes in two groups of patients represented on Figure 1.

Medians of relative expression levels of MDR1 gene (Figure, a) were roughly comparable and in MRD<sup>+</sup> group came to 22.8 (0.02–26.6; n = 9) vs 24.8 (3.9–41.4; n = 10) in MRD<sup>-</sup> group. These results suggest that expression of MDR1 gene in bulk population of leukemic blasts at diagnosis does not reflect their multidrug resistance potential. Several similar studies confirmed this hypothesis [12, 14, 37]. P-glycoprotein expression may be an adverse

prognostic factor in adult (but not childhood) ALL [10]. We were able to supplement data on *MDR1* gene expression with P-gp expression and function profiles for most studied samples. However, neither function nor expression of P-gp protein displayed any significant differences in compared MRD<sup>+</sup> and MRD<sup>-</sup> group (data not shown). Probably due to the small group of samples we were also unable to show statistically significant correlation between expression of *MDR1* gene and P-gp expression and function.



**Figure.** Relative expression levels of *MDR1* (a), *BCL-2* (b), *LRP* (c) and *BCRP* (d) genes in groups of ALL patients with negative (MRD<sup>-</sup>) and positive (MRD<sup>+</sup>) minimal residual disease at the end of the induction therapy. Medians, 25 and 75 percentiles are shown

According to many researchers, expression of Bcl-2 protein has generally been associated with an adverse prognosis in CLL and AML [38, 39]. Other studies either did not confirm this or, in contrast, showed an improved EFS in childhood ALL [40–42]. Some authors speculated that such controversy may be a result of post-translational modifications of Bcl-2 [30, 43]. According to our study, *Bcl-2* gene (Figure, b) showed a tendency ( $P=0.1$ ) to higher expression levels in MRD<sup>+</sup> group with median at 5992.9 (4521.0–10362.0;  $n=9$ ) compared with 3183.6 (1947.9–6581.0;  $n=10$ ) in MRD<sup>-</sup> group.

Cellular distribution and a putative transport function of vault complexes suggest their role in drug resistance [44]. Therefore, increased expression level of the major vault protein (or lung resistance protein) encoded by *LRP* gene potentially may serve as a marker of a multidrug resistance phenotype. It was shown that reduced intracellular retention of daunorubicin *in vitro* is associated with higher *in vitro* drug resistance and higher *LRP* levels, rather than Pgp or *MRP* expression [11, 17, 18]. Although, other publications showed no association of *LRP* gene expression levels with response to therapy neither in ALL, nor in AML patients [12, 27, 28]. In our studies *LRP* gene (Figure, c) relative expression levels were similar in both groups and came to 1934.9 (1500.7–3490.4;  $n=9$ ) and 1408.5 (665.5–2917.1;  $n=10$ ) in MRD<sup>+</sup> and MRD<sup>-</sup> group, respectively.

Since its discovery in 1998, the role of expression level of BCRP in AML and ALL have been actively studied with contradictory results [10, 16]. According to some researchers, expression levels of *BCRP* gene in initial and relapsed samples of ALL patients were not different, and there were no association between this gene overexpression and unfavorable prognosis [15]. According to our data, the median of *BCRP* gene (Figure, d) expression levels in MRD<sup>+</sup> group was considerably lower than that in MRD<sup>-</sup> group, namely 76000.0 (48196.2–169230.8;  $n=9$ ) and 227967.2 (16683.7–422222.2;  $n=10$ ), respectively, but statistical analysis showed no significant difference for this parameter.

According to recent publication, higher proliferating activity within initial samples of ALL correlated with an increased drug sensitivity [45]. Similarly, higher complete remission rate in AML was associated with high proliferative activity [46]. Nevertheless, these findings contradict with some earlier publications [47, 48]. Cell cycle distribution tests performed for present investigation showed a tendency ( $P=0.15$ ) to lower percentage of cells in S + G2M phase in MRD<sup>+</sup> group: 10.1 (3.9–12.1;  $n=7$ ) compared with 13.5 (8.2–17.2;  $n=6$ ) in MRD<sup>-</sup> group.

In conclusion, we investigated expression of multidrug resistance and apoptosis related genes in leukemic cells at diagnosis and MRD level at the end of induction therapy and could not find obvious relations between these parameters. Larger study is required to prove these results, although similar investigations showed association between an apoptosis-resistant protein profile, Pgp activity and MRD level in AML [49, 50]. It is also possible, that treatment response

depends on the expression of multidrug resistance and apoptosis associated genes not in total population but in the putative leukemic stem cells population instead [51]. Apparently, identification of intrinsic qualities of chemoresistant cells would lead to a better understanding of mechanisms of drug resistance and may potentially give more opportunities for targeted therapy development.

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## ЭКСПРЕССИЯ ГЕНОВ *MDR1*, *LRP*, *BCRP* И *BCL-2* ПРИ УСТАНОВЛЕНИИ ДИАГНОЗА ОЛЛ У ДЕТЕЙ: СРАВНЕНИЕ С РЕЗУЛЬТАТАМИ МОНИТОРИНГА МИНИМАЛЬНОЙ РЕЗИДУАЛЬНОЙ БОЛЕЗНИ ПОСЛЕ ИНДУКЦИОННОЙ ТЕРАПИИ

**Цель:** изучить свойства лейкозных клеток детей больных ОЛЛ с положительным и отрицательным результатом мониторинга минимальной резидуальной болезни после индукционной терапии. **Методы:** согласно результатам мониторинга минимальной резидуальной болезни (MRD) с помощью трехцветной проточной цитометрии на 36-й день больные были разделены на 2 группы: MRD<sup>-</sup> и MRD<sup>+</sup>. Для изучения уровней экспрессии генов *MDR1*, *LRP*, *BCRP* и *BCL-2* в образцах костного мозга пациентов с диагнозом первичного ОЛЛ использовался метод относительной количественной ПЦР в режиме реального времени. **Результаты:** медианы уровней экспрессии гена *MDR1* в изученных группах пациентов отличались незначительно и составили 22,8 (0,02–26,6; n = 9) в MRD<sup>+</sup> и 24,8 (3,9–41,4; n = 10) в MRD<sup>-</sup> группе. Тенденция к повышенной экспрессии гена *BCL-2* выявлена в группе MRD<sup>+</sup>, где медиана составила 5992,9 (521,0–10362,0; n = 9), по сравнению с 3183,6 (1947,9–6581,0; n = 10) в группе MRD<sup>-</sup>. Относительная экспрессия гена *LRP* в изучаемых группах оказалась сходной, медианы составили 1934,9 (1500,7–3490,4; n = 9) и 1408,5 (665,5–2917,1; n = 10) в MRD<sup>+</sup> и MRD<sup>-</sup> группах соответственно. Медиана уровня экспрессии гена *BCRP* в группе MRD<sup>+</sup> была значительно ниже таковой в группе MRD<sup>-</sup> — 76000,0 (48196,2–169230,8; n = 9) и 227967,2 (16683,7–422222,2; n = 10) соответственно, однако статистических анализ не подтвердил значимость различий. **Выводы:** при изучении уровней экспрессии генов *MDR1*, *LRP*, *BCRP* и *BCL-2* в лейкозных клетках при установлении первичного диагноза ОЛЛ у детей и при мониторинге MRD после индукционной терапии не выявлена связь между данными параметрами.

**Ключевые слова:** ОЛЛ, МРБ, *BCL-2*, *MDR1*, *LRP*, *BCRP*.