Alterations of red blood cell metabolome in overhydrated hereditary stomatocytosis

Dhouha Darghouth,1,7,8 Bérengère Koehl,1,7 Jean François Heilier,6,8 Geoffrey Madalinski,5 Petra Bovee,7 Giel Bosman,7 Jean Delaunay,4,6 Christophe Junot,7 and Paul-Henri Roméo1,8

1Commissariat à l’Energie Atomique, Direction des Sciences et du Vivant, Institut de Radiobiologie Cellulaire et Moléculaire, Laboratoire de Recherche sur la Réparation et la Transcription dans les Cellules, Souches, Fontenay-aux-Roses, France; 2Inserm U967, Fontenay-aux-Roses, France; 3Université Paris-Diderot, Paris, France; 4Université Paris-Sud, Paris, France; 5Laboratoire d’Etude du Métabolisme des Médicaments (LEMM), DSV/iBiTec-S/PI, Bâtiment 136, CEA/Saclay, Gif-sur-Yvette, France; 6Université Catholique de Louvain, Louvain Center for Toxicology and Applied Pharmacology, Brussels, Belgium; 7Department of Biochemistry, Radboud University Nijmegen Medical Centre and Nijmegen Centre for Molecular Life Sciences, Nijmegen, The Netherlands; and 8INSERM U 779, Le Kremlin-Bicêtre, France

ABSTRACT

Overhydrated hereditary stomatocytosis, clinically characterized by hemolytic anemia, is a rare disorder of the erythrocyte membrane permeability to monovalent cations, associated with mutations in the Rh-associated glycoprotein gene. We assessed the red blood cell metabolome of 4 patients with this disorder and showed recurrent metabolic abnormalities associated with this disease but not due to the diminished half-life of their erythrocytes. Glycolysis is exhausted with accumulation of ADP, pyruvate, lactate, and malate. Ascorbate metabolic pathway is altered probably due to a limited entry of dehydroascorbate. Although no major oxidative stress has been reported in patients with overhydrated hereditary stomatocytosis, we found decreased amounts of oxidized glutathione, creatine and ergothioneine, suggesting transporter abnormalities and/or uncharacterized oxidative stress. These results pinpoint major metabolic defects of overhydrated hereditary stomatocytosis erythrocytes and emphasize the relevance of red blood cell metabolomics for a better understanding of the pathophysiological bases of hemolytic anemia associated with erythrocyte abnormalities.

Key words: metabolome, red blood cells, hemolytic anemia.

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Introduction

Overhydrated hereditary stomatocytosis (OHSt), which is clinically characterized by a hemolytic anemia, is a rare disorder of red blood cells (RBCs) associated with increased membrane permeability to monovalent cations and increased activity of the Na+/K+-ATPase.1 OHSt diagnosis is based on a hemolytic anemia associated with a massive right shift of the osmotic gradient, the decrease of osmotic resistance, together with a major increase in the monovalent cation leak. Blood smears show stomatocytes and bowl-shaped RBCs presenting a slit-like area. OHSt is associated with mutations in the gene encoding the Rh-associated glycoprotein (RhAG), a member of the Rh complex.2 RhAG may function as an ammonium transporter and/or a gas channel.3,5 When expressed in Xenopus laevis oocytes, the human wild-type RhAG induces a monovalent cation leak considerably enhanced when mutated RhAG transporters are expressed instead.2 Among membrane abnormalities, OHSt RBCs display a sharp reduction or an absence of stomatin,6 an integral RBC membrane protein. In human RBCs, stomatin acts as a molecular switch that partly converts the glucose transporter 1 (Glut1) into a transporter for L-dehydroascorbic acid (DHA) that is metabolized producing ascorbate. In the absence of stomatin, the DHA transport by Glut1 undergoes a 2-fold decrease while glucose uptake is significantly increased,7 suggesting an enhanced glycolysis in OHSt RBCs. Altogether, these results indicate that the OHSt physiopathology affects several metabolic pathways in RBCs and may disrupt homeostasis of RBC metabolism. We have developed a simple strategy for the extraction and global mass spectrometry-based analyses of...
metabolites from purified human RBCs. Here we use this strategy to distinguish metabolic changes in RBCs from OHS patients in order to fully characterize the metabolic bases of this disease.

**Design and Methods**

Blood samples were collected from 4 French patients (3 males and one female) from three different families carrying the Phe65Ser mutation in RhAG, and 24 healthy adults as controls, including 5 relatives of the patients. Hemoglobin levels of the patients were between 9.9 and 12.7 g/dL with an average of 11.3 g/dL. Reticulocyte count (325 ± 10^9/L, range 269-445 ± 10^9/L; 10.8%, range 7.5-15.8%) and the mean red cell volume of the patients had increased (134 fl, range 122-144 fl). Written informed consent was obtained from all patients and controls in accordance with the Declaration of Helsinki.

Preparation of RBC lysates, metabolite extraction from RBCs, parameters for liquid chromatography coupled to electrospray-LTQ-Orbitrap mass spectrometry, and data processing were performed as previously described. Control RBCs were fractioned according to the age of the RBCs. The percentage of leukocytes in RBC purified samples was determined using an automated cell counter (Abacus Junior Hematology Analyzer, Diatron). For all samples, the percentage of leukocytes was less than 0.01%.

**Results and Discussion**

Red blood cell metabolites from OHS patients and controls were analyzed by LC/MS with detection in both ion modes: negative and positive. Detected biomolecules are amino acids, organic acids, amines, lipids, sugars, hormones, peptides, and proteins. The selectivity of metabolite detection is obtained from the chromatographic retention time and to the accuracy of mass measurements. Processing of the metabolic fingerprints led to 1524 and 785 relevant ions in the negative and positive ion modes, respectively. The hundreds of thousands of signals contained in the data sets make statistical analysis problematic. The resulting data matrices were subjected to multivariate statistical analyses using Principal Component Analysis (PCA), an unsupervised method that can summarize the information content of the original data set and visualize it in a 2-dimensional space.

Eighty-nine metabolites were identified from the metabolic fingerprints. Twenty-nine displayed significantly decreased (Figure 1B) or increased (Figure 1C) concentration variations between controls and OHS patients are shown. Values are ratios of individual levels observed for OHS patients (blue point) and controls (green, mean with 95% CI) to mean levels obtained for healthy subjects. (B-C) A metabolic signature of OHS patients is obtained from LC/MS analysis of RBC extracts. Metabolites exhibiting significant concentration variations between controls and OHS patients are shown. Values are ratios of individual levels observed for OHS patients (blue point) and controls (green, mean with 95% CI) to mean levels obtained for healthy subjects. (B) Metabolites whose levels are decreased in OHS patients. (C) Metabolites whose levels are increased in OHS patients.

![Figure 1](image-url)
tions in OHSt patients compared with controls. No significant metabolite concentration differences were found between RBC extracts from OHSt patients with low (7.5%) and high (15.8%) reticulocyte count (data not shown) indicating that the differences observed were not directly related to the number of reticulocytes present in the analyzed samples. A similar absence of effect of reticulocyte concentration on the RBC metabolome was found in a previous study on sickle cell disease.8

To ensure that this metabolic signature was directly related to OHSt and not to the diminished half-life of OHSt RBCs (data not shown), we compared the metabolomes of young RBCs, i.e. less than 20-day old cells, containing 1.6% reticulocytes, from healthy subjects to those of OHSt patients’ RBCs. To this end, control’s RBCs were fractioned according to their ages9 and the metabolomes of the different fractions were analyzed by LC/MS. Then, for each discriminating metabolite previously identified, we compared the metabolite concentration ratio of OHSt patients’ RBCs on controls’ RBCs with the ratio of young fraction on all fractions in normal RBCs. Metabolites exhibiting comparable concentration ratios were considered to have been impacted by the age of RBCs. This analysis showed that the concentration of metabolites, such as GSH, deoxy-ribose-5-phosphate, aspartate, leucine, spermine or threonate, was related to the youth of OHSt RBCs and not to intrinsic metabolic disorders of OHSt patients’ RBCs (Figure 2A and B).

In the glycolytic and pentose phosphate pathways, we detected decreased concentrations of many metabolic intermediates, such as hexose-1,6-bisphosphate, phosphoglycerate, i.e. 2-phospho-glycerate or 3-phosphoglycerate, or deoxy-ribose-5-phosphate (Figures 1B and 3A), while others, like hexose-6-phosphate, glyceraldehyde-3-phosphate, bisphosphoglycerate, phosphoenolpyruvic acid and disphosphoglyceric acid, did not vary (Figure 3A). All final products of glycolysis, i.e. pyruvate, lactate and malate (which can be produced from pyruvate), displayed higher concentrations in OHSt patients’ RBCs (Figures 1C, and 3A) than in controls’ RBCs. As RBCs of the OHSt patients display a very high activity of the Na⁺K⁺-ATPase, thought to compensate for the monovalent cation leakage associated with the mutated RhAG transporter, these results are consistent with the high levels of ATP required for the Na⁺K⁺-ATPase activity,1 ATP production only depending on glycolysis in RBCs. Interestingly, we did not observe any variations in concentration of glycolysis end-products, such as pyruvate or lactate, in sickle cell disease RBCs,5 strongly suggesting that
the alteration in the concentrations of these glycolysis end-products was related to specific alterations of OHSt patients’ RBCs.

Because of the reduction or absence of stomatin in OHSt patients’ RBC membranes, the DHA transport by the Glut1 transporter decreases. Although DHA could not be detected by the method used, the ascorbate concentration underwent a 1.7-fold decrease in OHSt patients’ RBCs together with an increase in the concentrations of threonate and threonolactone; two metabolites originating from ascorbate degradation products (Figures 1B and C, and 3B). The same decrease in threonate concentration was found in young erythrocytes compared to whole RBC population, thus indicating the relative impacts of OHSt and age of RBCs on the increase or decrease of the metabolite concentrations detected. Finally, the variations in the concentration of metabolites that are part of the ascorbate pathway were moderate explaining why, despite the decreased uptake of DHA by OHSt patients’ RBCs, no clinical manifestation of an ascorbate deficit in OHSt patients was reported.

The moderate decrease in reduced glutathione (GSH) concentration found in OHSt patients’ RBCs is in line with decreased RBC GSH concentration in 3 cases of hemolytic anemia11 and is consistent with the decrease in GSH concentration probably being linked to the young age of OHSt patients’ RBCs (Figure 2A). We also found a 12-fold decrease of oxidized glutathione (GSSG) concentration (Figures 1B and 3A and B). This variation might be due to an increased GSSG efflux from RBCs, given that the membrane GSSG efflux transporter MRP1 is ATP-dependent and has a higher affinity for GSSG than for GSH.12 As OHSt RBCs are known to produce more ATP than normal RBCs, the efflux of GSSG through MRP1 might increase.

Only two amino acids (glutamine and tryptophan) showed increased concentrations in OHSt patients’ RBCs (Figures 1C and 3C), whereas the concentrations of glycine, serine, glutamate, alanine, choline, valine, tyrosine, phenylalanine, histidine, asparagine, and lysine remained unchanged. Carnitine and acetyl-carnitine concentrations had increased in OHSt cells (Figures 1C and 3C) which might indicate increased membrane turnover.
A decreased concentration of ergothioneine in OHS patients' RBCs was noted compared to controls, which was also observed in sickle cell disease (SCD) patients. This discrepancy might be due to the increased consumption of ergothioneine by specific transporters (OC1N) in OHS patients. Furthermore, a decreased concentration of creatine was detected in OHS patients, which might be due to the decreased synthesis in the erythrocytes of overhydrated hereditary stomatocytosis (OHSt) patients. This might be related to a decreased permeability to monovalent cations in the red cell membrane of OHS patients, as suggested by Dellaunay et al. (1994). The decreased concentration of ergothioneine in OHS patients' RBCs was also observed in sickle cell disease patients, suggesting that these alterations are linked to OHS. In conclusion, the metabolic signature of OHS patients' RBCs might be useful for the diagnosis of OHS and could be an appropriate and useful method to assess large patient cohorts with frequent rare diseases such as OHS, for which specific metabolite transport and accumulation of plasma and intracellular concentrations of ergothioneine and creatine are decreased. Some of the alterations in metabolism, such as increased GSH or desoxyribose variations, are also found in young normal RBCs and in sickle cell disease RBCs. Conversely, other alterations, such as pyruvate or lactate variations, were found only in the metabolic signature of OHS patients' RBCs, suggesting that these alterations are linked to OHS.