Genetic modifiers of fetal hemoglobin affect the course of sickle cell disease in patients treated with hydroxyurea

by Pierre Allard, Nareen Alhaj, Stephan Lobitz, Holger Cario, Andrea Jarisch, Regine Grosse, Lena Oevermann, Dani Hakimeh, Laura Tagliaferri, Elisabeth Kohne, Annette Kopp-Schneider, Andreas E. Kulozik, and Joachim B. Kunz, Collaborative Groups: German Sickle Cell Disease Study Group)

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**Title**
Genetic modifiers of fetal hemoglobin affect the course of sickle cell disease in patients treated with hydroxyurea

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**Running Head**
Modifiers of SCD treated with hydroxyurea

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**Data sharing statement**
The protocol of the SCD registry is available in German language at www.sichelzellkrankheit.info. For original data, please contact joachim.kunz@med.uni-heidelberg.de. As the informed consent does not allow disclosing individual patient data, only aggregated data can be provided upon request.

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Authorship Contributions
PA collected and analyzed data and wrote the manuscript; NA and AK-S performed statistical analyses; SL, HC, AJ, RG, LO, DH, LT, AEK designed the study; EK performed genetic analyses; JBK designed and supervised the study, analyzed data and wrote the manuscript; all investigators of the German Sickle Cell Disease Study Group contributed patient data.

Disclosure of Conflicts of Interest
The authors declare no competing financial interests.

Keywords
Sickle cell disease, fetal hemoglobin, hydroxyurea

Abstract
The course of sickle cell disease (SCD) is modified by polymorphisms boosting fetal hemoglobin (HbF) synthesis. However, it has remained an open question how these polymorphisms affect patients who are treated with the HbF-inducing drug hydroxyurea/hydroxycarbamide. The German SCD registry offers the opportunity to answer this question, because >90% of patients are treated according to national guidelines recommending the use of hydroxyurea in all patients above 2 years of age.

We analyzed the modifying effect of HbF-related genetic polymorphisms in 417 patients with homozygous SCD >2 years who received hydroxyurea. HbF levels were correlated with higher total hemoglobin levels, lower rates of hemolysis, a lower frequency of painful crises and of red blood cell transfusions. The minor alleles of the polymorphisms in the γ-globin promoter (rs7482144), BCL11A (rs1427407) and HMIP (rs66650371) were strongly associated with increased HbF levels. However, these associations did not translate into lower frequencies of vasoocclusive events that did not differ between patients either carrying or not carrying the HMIP and BCL11A polymorphisms. Patients on hydroxyurea carrying the γ-globin promoter polymorphism demonstrated substantially higher hemoglobin levels (p<10⁻⁴) but also a higher frequency of painful crises and hospitalizations (p<0.01) when compared to patients without this polymorphism.

Taken together, these data indicate that the γ-globin, HMIP and BCL11A polymorphisms correlate with increased HbF in SCD patients on hydroxyurea. While HbF is negatively
correlated with the frequency of painful crises and hospitalizations, this was not observed for the presence of known HbF boosting alleles.

**Introduction**

Sickle Cell Disease (SCD) is a multiorgan disorder that is characterized by a broad spectrum of clinical presentations. While some patients reach adulthood with few symptoms, others die early from complications such as acute anemia, infection or acute chest syndrome. Besides the β-globin and α-globin genotypes, the most important modifier of SCD is the persisting expression of fetal hemoglobin (HbF), a heritable quantitative trait determined mainly by the three loci **BCL11A, HMIP** and **HBG**. While α-thalassemia, if coinherited with the HbS mutation, slows down HbS polymerization by reducing the cellular hemoglobin concentration, persisting HbF can interfere with the polymerization of HbS. Genetic modifiers of HbF synthesis have generally shown a beneficial effect on the phenotype of SCD. However, some studies have resulted in conflicting results and most had exclusively included patients who did not receive the disease-modifying drug hydroxyurea. Several studies analyzing the effects of α-thalassemia and HbF-modifiers in patients treated with hydroxyurea suggested that the effect of hydroxyurea on laboratory and clinical outcomes largely supersedes the effect of the genetic modifiers.

Both the effects of polymorphisms identified by genome-wide association studies to modify the phenotype of SCD and the pharmacologic effects of hydroxyurea were originally considered to be mediated via the expression and distribution of HbF. Genetic modifiers of HbF synthesis generally interfere with the expression or the binding activity of **BCL11A**. While this transcription factor is required for the perinatal “hemoglobin switch”, its actions are not limited to the β-globin locus, leaving room for effects on red blood cells and on the phenotype of SCD that are independent from HbF expression. Similarly, hydroxyurea does not exclusively target HbF expression but in addition exerts effects such as myelosuppression and NO release that may be equally important in ameliorating SCD.

Considering the pleiotropic effects of both, genetic modifiers and pharmacotherapy, the association of genetic modifiers with a certain phenotype may vary with the treatment that is applied. Thus, the actual importance of genetic modifiers for the clinical course of SCD needs to be assessed in the context of pharmacological treatment in addition to previous studies in treatment-naïve patients.

In Germany, treatment guidelines encourage the use of hydroxyurea in all symptomatic patients with SCD starting at the age of 2 years. Therefore, approximately 90% of patients with homozygous SCD registered in the German SCD registry are prescribed hydroxyurea. We made use of laboratory and clinical data collected in this registry to identify the effect of genetic modifiers on the phenotype of homozygous SCD. To this end, we selected polymorphisms known to modify either the HbF expression or the phenotype of SCD, to be independent from each other and to be functionally relevant, for instance by altering transcription factor binding. We focused on the polymorphisms rs1427407 and rs7606173 in **BCL11A**, on the 3 bp deletion delCTA rs66650371 in **HMIP** and on the **XmnI** polymorphism in the γ-globin promoter, rs7482144. The allele **BCL11A** rs1427407 T was associated with increased HbF in genome-wide association studies and was shown to reduce binding of **GATA1** and **TAL1** to a DNase-hypersensitive site that regulates **BCL11A** expression. After conditioning for the association with rs1427407, rs7606173 G is the **BCL11A** allele that remains most significantly associated with high HbF expression. It is located in a DNase hypersensitive site 7 kb closer to the **BCL11A** transcription start site than...
rs142740720. The deletion of three base pairs, CTA, in *HMIP* rs66650371 is considered to cause the strong association of the *HMIP* locus on chr6 with HbF levels by augmenting an enhancer-like activity located between the *HBS1L* and the *MYB* genes21. The polymorphism in the γ-globin promoter that creates an *XmnI* restriction site, *HGB2* rs7482144 A, has long been a candidate for being the HbF boosting sequence within the high-HbF β-globin haplotypes (‘Senegal’ and ‘Arab-Indian’)24, 25. Together, polymorphisms in *BCL11A, HMIP*, and the γ-globin promoter were estimated to explain approximately 22% of the variability in HbF expression26. In addition, we analyzed the coinheritance of the α-thalassemia trait that has been shown in multiple studies to be associated with a reduced risk of cerebrovascular complications, but an increased risk of painful crises5. We restricted our analyses to patients of at least two years of age with homozygous SCD who are treated with hydroxyurea, independent from the dose used.

**Methods**

*Patient recruitment & data collection*

Patients were recruited through the nationwide German SCD registry (NCT03327428) that collects prospective and retrospective data on patients with SCD in Germany. The study was performed according to the Declaration of Helsinki and approved by the institutional review board of the Medical Faculty of Heidelberg University (S-416/2014). Written informed consent was obtained from patients or legal guardians, respectively.

The data include demographic information, diagnosis and genotype, treatment, laboratory parameters and clinical events. At the time of the data cutoff, May 13th 2020, 425 patients with homozygous SCD from 28 different institutions were enrolled in the registry. Data were analysed by P.A., J.K., N.A. and A.K.-S.. All co-authors had access to all registry data.

Treatment guidelines implemented in 2014 recommend parental education, the use of penicillin prophylaxis at least until the age of five years, and annual screening with transcranial Doppler ultrasound starting from 2 until 18 years of age. The use of hydroxyurea is encouraged in all patients with SCD who ever experienced a painful vasoocclusive crisis, including mild ones. The recommended hydroxyurea starting dose is 15 mg/kg*d for adults and 20 mg/kg*d for children. In case of insufficient efficacy, a dose escalation up to the maximum tolerated dose or to 35 mg/kg*d is recommended.

For the analysis of the frequency and distribution of genetic modifiers, patients with homozygous SCD of all ages and irrespective of treatment were included. Patients with compound heterozygous SCD (HbSC, HbS/β-thalassemia, others) were excluded. For the analysis of laboratory parameters and complications of SCD, only patients of at least two years of age and with ongoing treatment with hydroxyurea were considered. Patient data collected after stem cell transplantation were excluded. Data on complications and treatment of SCD were documented annually, together with routine laboratory parameters (Hb, MCV, reticulocytes, LDH, bilirubin and HbF, Table 1). The latter were only considered if the patient had not received red blood cell transfusions within 100 days before laboratory assessment. All laboratory parameters were taken while the patient was on hydroxyurea and followed for clinical complications. If more than one laboratory data point fulfilled these criteria, we used the average of all available data.

Patients registered by May 13th 2020 were included in the analysis. For the correlation of HbF with laboratory parameters and clinical course, all patients with available data were analysed (n=193 to n=202, Figures 1 and 2). All patients for whom the complete set of genetic traits of interest (α-thalassemia, *HBG2*-polymorphism rs7482144, *BCL11A* polymorphisms rs1427407 and rs7606173, *HMIP* polymorphism rs66650371) was available in combination with the respective parameter (n=121 for HbF to n=164 for MCV, Table 2) were included in the analyses that correlated genetics with laboratory parameters and clinical course.
In order to investigate geographic and ethnic differences in the phenotypic expression of SCD, we categorized patients according to the origins of their parents from one of the three regions Mediterranean Sea, Sub-Saharan Africa and “rest of the world”. The latter included mainly patients from Iraq (n=13), all other countries contributed at most two patients. Pain crises were defined as pain requiring pharmacologic treatment and hospitalization with no other obvious cause besides SCD. This definition does not include visits in the emergency department that did not result in hospital admission. Clinical events were considered from the first dose of hydroxyurea until last follow up (median/mean observation period per patient 1.8/1.1 years, range 0.5 to 5.3 years), independent from changes in the hydroxyurea dose. In 313 patients with at least one year of follow up on hydroxyurea, the severity of SCD was graded as “severe” (n=83) if 1.5 or more pain crises requiring hospitalization per year or 0.5 or more acute chest syndromes (ACS) per year were documented. In addition, any stroke, sepsis, chronic pain or the need of chronic red blood cell transfusions occurring on hydroxyurea defined a severe course.

**Genetic analysis**

The HBG2-polymorphism rs7482144 was identified by PCR amplification (forward primer: ATA GCA CTT CTT ATT TGG AAA CCA A, reverse primer: TGT CTA AGT TGC CTC GAG ACT AAA G), XmnI digestion and restriction fragment length analysis. The BCL11A polymorphisms (rs1427407 and rs7606173) were analyzed using sequence specific TaqMan Genotyping. The 3 bp deletion in HMIP (rs66650371) was diagnosed by sequence specific PCR and agarose gel electrophoresis. α-thalassemia deletions (-α3.7, -α4.2, -α20.5, --SEA and --MED) were detected by PCR and subsequent agarose gel electrophoresis.

**Statistical analysis**

To evaluate the effect of HbF levels on laboratory parameters we used linear model analysis. To obtain approximately normally distributed variables, LDH, bilirubin and reticulocytes were log-transformed. The association of HbF and clinical course was analyzed using a Poisson regression. The impact of the combination of SNPs on HbF and on the laboratory parameters was analyzed by linear multivariable regression analysis. The presence of a SNP-variant was coded with 0 (no polymorphism - wildtype), 1 (heterozygous) and 2 (homozygous) for each studied polymorphism. A Poisson regression was used to estimate the contribution of each SNP on the clinical course. All statistical analyses were conducted using R version 4.0.2 (The R Foundation for Statistical Computing 2020).

**Data sharing statement**

The protocol of the SCD registry is available in German language at www.sichelzellkrankheit.info. For original data, please contact joachim.kunz@med.uni-heidelberg.de. As the informed consent does not allow disclosing individual patient data, only aggregated data can be provided upon request.

**Results**

**Patient characteristics**

We restricted our analysis to patients of at least two years of age and on hydroxyurea, corresponding to 77.6% (n=330) of all patients with homozygous SCD in the registry. Of all patients with homozygous SCD (n=425), 19 were excluded because of young age (<2 years), 36 were excluded because they were not on hydroxyurea, 16 were excluded from the analysis of laboratory parameters because they had received red blood cell transfusions within 100 d before blood sampling, three were excluded because no data prior to allogeneic stem cell transplantation were documented and 13 did not have complete data on clinical complications.
The age cut off was set at two years because hydroxyurea is licensed for use in Europe starting at this age and because HbF levels were not correlated with age and sex in this patient group (Figure S1 and S2). The mean daily hydroxyurea dose was 23.2 mg/kg (SD 5.9, range 7.7-39.0).

Mean HbF levels among these patients were higher than those reported in hydroxyurea-naïve patients of West African origin²⁸, ²⁹ and comparable to hydroxyurea-naïve patients from India³⁰. Most patients had initiated hydroxyurea treatment before they were enrolled in the registry, but in 25 patients paired HbF measurements from before and after initiation of hydroxyurea treatment were available. During hydroxyurea treatment, HbF was on average 1.8-fold higher than before (mean HbF 23.7% vs. 13.2%, p<10⁻⁴ (T-test); Figure S3)

While α-thalassemia deletions and polymorphisms in BCL11A were present in at least a third of all patients, the HBG2-polymorphism rs7482144 and the polymorphism rs66650371 in HMIP affected only a minority of 10 to 15% of patients (Table 1). These less frequent traits were exceedingly rare among patients originating from sub-Saharan Africa but enriched in patients originating from the Mediterranean region (28% allele frequency for HMIP rs66650371) and from the rest of the world (47% allele frequency for the HBG2-polymorphism rs7482144, Table S1). Of note, the minor allele frequencies of these polymorphisms were paralleled by higher levels of HbF and total Hb in patients not originating from sub-Saharan Africa (Table S2). As expected for polymorphisms that are differentially enriched in specific ethnicities and, as is the case for the HBG2-polymorphism rs7482144, are linked to the HbS-mutation, the frequency of homozygous carriers of the minor allele significantly (p<10⁻⁴) exceeded that predicted by the Hardy-Weinberg equilibrium. In contrast, α-thalassemia deletions were detected significantly more frequently among patients originating from sub-Saharan Africa in comparison to all other patients (allele frequency 25.2% vs. 7.1%, p<10⁻⁴). Compatible with a linkage disequilibrium, both polymorphisms in BCL11A were significantly associated with each other (p<10⁻⁴). As expected for independently inherited traits, we did not identify any significant associations between polymorphisms in BCL11A and in HMIP or HBG2. However, the polymorphisms that occurred preferentially in the non-sub-Saharan patients, HMIP and HGB2, were significantly associated with each other (p = 0.008, Chi Square).

High HbF levels are associated with a milder phenotype of SCD

All hematological parameters tested were strongly associated with HbF levels (Figure 1). While patients with an HbF of 5% had a mean total hemoglobin of 7.9 g/dL (MCV 85 fL), patients with an HbF of 25% had a mean total hemoglobin of 9.4 g/dL (MCV 94 fL). Indicators of hemolysis showed an inverse relation (patients with HbF 5% vs 25%: LDH 560 vs. 441 U/L, bilirubin 2.34 vs 1.51 mg/dL, reticulocytes 87‰ vs 53 ‰, Figure 1).

Simultaneously, the frequency of pain crises and of red blood cell transfusions decreased with increasing HbF (Figure 2). The frequency of hospitalizations paralleled that of pain crises, reflecting our definition of “pain crisis” as requiring hospitalization and the fact that most admissions in patients with SCD are due to acute pain. In contrast, ACS was not correlated with HbF levels, indicating a differential effect of HbF on these complications.

In order to analyze if adherence to hydroxyurea- reflected by increased MCV, but also HbF and total hemoglobin- is associated with the phenotype, we compared laboratory and clinical parameters in patients with severe SCD to those with non-severe SCD (Table S 3). While severely affected patients were slightly older than non-severely affected patients and carried more HbF-modifying alleles, they did not differ in any other laboratory parameter, most importantly MCV, indicating that potential differences in adherence to hydroxyurea were too small to be detected.
Effects of genetic modifiers can be either mediated by HbF or independent from HbF

In order to assess if the effects of genetic modifiers on SCD are mediated by boosting HbF expression, we next compared the correlation of genetic traits with HbF levels, with laboratory parameters and with complications of SCD (Table 2, Figures S4- S11, Tables S4- S7).

As expected, the co-inheritance of α-thalassemia results in lower MCV and reduced rates of hemolysis without significantly affecting HbF or total hemoglobin. However, the α-thalassemia trait is not linked to the frequency of complications in these patients. The rarer alleles of the polymorphic loci BCL11A rs1427407, HMIP rs66650371 and HBG2-polymorphism rs7482144 were significantly associated with increased HbF levels. In addition, the BCL11A rs1427407 and HBG2 rs7482144 polymorphisms were associated with increased total hemoglobin concentrations. Consistent with this observation, patients carrying the HBG2-polymorphism rs7482144 received red blood cell transfusions less frequently than others. However, neither the increases in HbF nor in total hemoglobin are reflected in a reduced frequency of complications of SCD. In contrast, pain crises and hospitalization were strikingly and highly significantly (p<0.01) more frequent in patients carrying the HBG2-polymorphism rs7482144 than in others (Table 2, Figure 3C-D). The coinherense of two or more HbF-boosting alleles appears to be associated with an additive effect on HbF levels (Figure S12). While small patient numbers precluded definitive statistical analyses that combine patients’ origins and genotypes, the association of rs7482144 with increased HbF and frequent complications appears to be independent from the region of origin (Figure S13).

The association of genetic traits with HbF does not correlate with the association of genetic traits on the rate of hemolysis or the frequency of complications of SCD (Table 2). While decreased LDH levels in patients with BCL11A rs1427407 and HMIP rs66650371 are concordant with increased HbF, BCL11A rs7606173 is not correlated with HbF levels but with increased LDH. At the same time, the HBG2-polymorphism rs7482144, which is clearly associated with high HbF, is not significantly associated with changes in any of the parameters that are informative of hemolysis. Without having any detectable effect on HbF levels, BCL11A rs7606173 shows a trend towards higher LDH and more frequent hospitalizations and ACS. Although there was no association between increased HbF and a reduced frequency of ACS, patients carrying BCL11A rs1427407 T showed a significant reduction in the frequency of ACS (Table 2), suggesting an HbF-independent modulation of the SCD phenotype.

We conclude that the induction of HbF expression is only one of several effects that modify the clinical phenotype of SCD in patients treated with hydroxyurea. As BCL11A, a key player that is influenced by polymorphisms in HMIP and BCL11A itself, is a pleiotropic transcription factor, its effects will not be limited to the regulation of HbF expression. In contrast, the HBG2-polymorphism rs7482144 is localized in the γ-globin promoter and shows a strong association with HbF but is not correlated with a milder course of SCD in this group of patients on hydroxyurea.

The HBG2-polymorphism rs7482144 defines a group of patients with high risk for painful crises

As has been observed in several studies of patients not on hydroxyurea, patients on hydroxyurea and with the HBG2-polymorphism rs7482144 (heterozygous or homozygous) are characterized by significantly higher mean HbF (23.6 ± 8.6 % vs 17.5 ± 10 %, p=0.0061, Figure 3A) and mean total hemoglobin (10.1 ± 1.3 g/dL vs 8.8 ± 1.4 g/dL, p<10⁻⁴, Figure 3B) when compared to all other patients. At the same time, MCV, reticulocyte counts, bilirubin and LDH levels did not differ between patients who do or do not carry at least one HBG2-polymorphism rs7482144, indicating that the rate of hemolysis is not reduced by the HBG2-
polymorphism rs7482144. While among patients who did not carry the HBG2-polymorphism rs7482144 higher levels of fetal hemoglobin and total hemoglobin were significantly associated with fewer hospitalizations (Tables S8 and S9), such a correlation was not detected among carriers of the HBG2-polymorphism rs7482144 (Table S10 and S11). In contrast, among patients carrying the HBG2-polymorphism rs7482144, there was a slight trend towards a higher total hemoglobin in those who suffered from severe disease (10.8 ± 1.6 g/dL vs 10.0 ± 1.1 g/dL, p=0.21). The comparison of hydroxyurea doses prescribed to patients with or without the HBG2-polymorphism rs7482144 A confirmed that hydroxyurea doses were similar in both groups, indicating that the higher rate of complications in patients carrying rs7482144 A was not related to low hydroxyurea doses (Table S7). In contrast, patients who carried either BCL11A rs1427407 T or HMIP rs66650371 delCTA were prescribed lower doses of hydroxyurea (Tables S4 and S6), compatible with the notion that the hydroxyurea dose may be titrated according to HbF response.

Discussion

The negative correlation between HbF levels and the frequency of pain crises and of red blood cell transfusions confirms that the HbF level is a favorable prognostic marker in patients with SCD who are on treatment with hydroxyurea. At the same time, the polymorphisms rs1427407 in BCL11A, rs66650371 in HMIP and rs7482144 in the γ-globin promoter are strongly correlated with HbF levels in patients on hydroxyurea, indicating that γ-globin induction by hydroxyurea does not override the effects of genetic modifiers on HbF levels in this patient cohort. This observation contrasts with results from trial cohorts that did not identify a significant effect of the genetic modifiers analyzed here on HbF levels in patients who had been treated with hydroxyurea. A possible explanation for this discrepancy may be the younger age of patients in these studies in comparison to our registry patients.

Despite the strong effect of HbF on the frequency of complications of SCD, the correlation of genetic modifiers with HbF does not translate into a reduced frequency of pain crises and hospitalizations in those patients who carry HbF-boosting alleles. In contrast, the presence of rs7482144 in the γ-globin promoter is associated with higher total hemoglobin but, unexpectedly, also with increased frequencies of pain crises and hospitalizations. This is in contrast to several earlier series of patients with SCD not treated with hydroxyurea that carry rs7482144 in the γ-globin promoter. These patients were characterized by increased HbF levels and, in contrast to our findings, also less frequent vasoocclusive events. Studies on the association of rs7482144 with complications of SCD in patients treated with hydroxyurea are scarce. Consistent with our observations, the results of the BABY HUG trial show a trend towards a higher frequency of vasoocclusive events in patients who carry rs7482144 if treated with hydroxyurea. We can only speculate on the reason of the discordant effect of rs7482144 on HbF and on the frequency of pain crises. Possibly the protective effect of HbF induction is counterbalanced by the increase in total hemoglobin that results in high blood viscosity and precipitates vasoocclusion. Such an effect would result in an optimal dose level for hydroxycarbamide below the frequently used maximum tolerated dose. Patients presenting with frequent pain episodes despite high HbF and high total hemoglobin may benefit from a transient reduction of blood viscosity by cautious phlebotomy. Another possible explanation why high HbF levels and also the HbF boosting polymorphism BCL11A rs1427407 are associated with a lower frequency of vasoocclusive complications but rs7482144 in contrast is associated with a higher frequency of vasoocclusive complications may result from the distribution of HbF. If HbF were distributed in a heterocellular manner in patients carrying the minor allele of rs7482144, the protection against vasoocclusive crises would be inferior to patients with elevated HbF that is distributed pancellularly. As we do
not have any data on the cellular distribution of HbF in our patients, we were not able to test this hypothesis.

The major limitation of our study is the selection of few genetic markers that, with the exception of α-thalassemia trait\textsuperscript{2}, focus on the expression of HbF\textsuperscript{20-22} but do not consider other mechanisms that may modify the phenotype of SCD\textsuperscript{40}. As HbF boosting polymorphisms are enriched in patients who do not originate from sub-Saharan Africa, we cannot fully discriminate between the effects of single polymorphisms, of the genetic background or even of social and behavioral factors. For future studies, a genome-wide characterization of patients may help in the identification of genetic traits causally related to the phenotype of SCD even in ethnically heterogeneous patient groups. In addition, we observed a relatively short period of a maximum of four years in young patients, who were enrolled in a registry, not a controlled clinical trial. Because the registry design does not intend source data verification, we do not expect the laboratory parameters and the data on clinical complications to be as complete as in a clinical trial. Similarly, we do not have direct data monitoring patient adherence to hydroxyurea treatment. However, HbF levels and mean corpuscular volumes in these patients are consistently higher than in hydroxyurea-naive patients\textsuperscript{39,41}, compatible with a good adherence to treatment in the majority of patients.

The γ-globin promoter polymorphism rs7482144 was strongly associated with both pain crises and a reduced need for transfusions, indicating that the same genetic trait may have divergent effects on different phenotypic aspects of SCD. This is one reason why general conclusions on the course of SCD in an individual patient cannot be drawn from the presence of certain genetic markers. Second, while the genetic signature specifies relative risks in the subgroups, the overlap between subgroups is too large to allow for the prediction of individual risks for complications of SCD. Third, in the present study we only considered acute complications of SCD in a young patient group but cannot yet evaluate the impact of the polymorphisms on long term sequelae such as chronic kidney failure or pulmonary hypertension. Therefore, the decision as to whether hydroxyurea or even curative treatment options such as allogeneic SCT or gene therapy should be offered cannot be confidently based on the genetic profile analyzed here.

We conclude that polymorphisms in BCL11A, HMIP and HGB2 increase HbF levels in patients with SCD on hydroxyurea. However, the impact of these polymorphisms on the complications of SCD treated with hydroxyurea was not observed to be correlated with their effect on HbF.

**Appendix: Members of the German Sickle Cell Disease Study Group (in alphabetical order)**

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References

Tables

Table 1 Patient characteristics. *n* refers to the number of evaluable patients for each parameter. The data sets of some patients were incomplete, either because of incomplete documentation or because laboratory parameters could not be analyzed as the patient had received a red blood cell transfusion within 100 days before blood sampling.

<table>
<thead>
<tr>
<th>Variables</th>
<th><em>n</em></th>
<th>Mean ± SD</th>
<th>Range</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sex</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Female</td>
<td>208</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Male</td>
<td>209</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Age at last observation under treatment (years)</td>
<td>330</td>
<td>12.6 ± 8.5</td>
<td>2.3 – 54.1</td>
</tr>
<tr>
<td>Hematological parameters in patients on hydroxyurea</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>HbF (%)</td>
<td>208</td>
<td>17.9 ± 9.5</td>
<td>0 – 46.7</td>
</tr>
<tr>
<td>Hb (g/dL)</td>
<td>300</td>
<td>9.0 ± 1.5</td>
<td>5 – 14.3</td>
</tr>
<tr>
<td>MCV (fL)</td>
<td>300</td>
<td>92.6 ± 13.6</td>
<td>60.6 – 134.7</td>
</tr>
<tr>
<td>Reticulocytes (%)</td>
<td>279</td>
<td>75.3 ± 44.1</td>
<td>12.7 – 360</td>
</tr>
<tr>
<td>Bilirubin (mg/dL)</td>
<td>281</td>
<td>2.1 ± 1.5</td>
<td>0.2 – 12.5</td>
</tr>
<tr>
<td>LDH (U/L)</td>
<td>280</td>
<td>509.2 ± 189.4</td>
<td>167 – 1545</td>
</tr>
<tr>
<td>Region of origin</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Sub-Saharan Africa</td>
<td>285</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Mediterranean Sea</td>
<td>62</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Rest of the World*</td>
<td>25</td>
<td></td>
<td></td>
</tr>
<tr>
<td>α-globin-deletions**</td>
<td>0 / 1 / 2</td>
<td>243 / 107 / 23</td>
<td></td>
</tr>
<tr>
<td>BCL11A rs1427407</td>
<td>GG / GT / TT</td>
<td>135 / 88 / 15</td>
<td></td>
</tr>
<tr>
<td>BCL11A rs7606173</td>
<td>CC / CG / GG</td>
<td>47 / 117 / 74</td>
<td></td>
</tr>
<tr>
<td>HBG2-polymorphism rs7482144</td>
<td>WT / het. / hom.</td>
<td>207 / 14 / 24</td>
<td></td>
</tr>
<tr>
<td>HMIp rs66650371 3bp del</td>
<td>WT / het. / hom.</td>
<td>211/ 23 / 6</td>
<td></td>
</tr>
<tr>
<td>Clinical events while on hydroxyurea***</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Pain crises/year</td>
<td>299</td>
<td>0.7 ± 1.2</td>
<td>0 – 10</td>
</tr>
<tr>
<td>ACS /year</td>
<td>300</td>
<td>0.1 ± 0.4</td>
<td>0 – 3</td>
</tr>
<tr>
<td>RBC transfusion /year</td>
<td>298</td>
<td>0.4 ± 1.1</td>
<td>0 – 10</td>
</tr>
<tr>
<td>Hospitalization /year</td>
<td>298</td>
<td>0.9 ± 1.4</td>
<td>0 – 11</td>
</tr>
<tr>
<td>Severity of SCD while on hydroxyurea</td>
<td></td>
<td>Not severe / severe</td>
<td>230 / 83</td>
</tr>
</tbody>
</table>

ACS- acute chest syndrome, RBC- red blood cells, WT- wild type, het.- heterozygous, hom.- homozygous
* Iraq n=13, all others *n*≤2
** No patients with homozygous SCD and deletion of three α-globin genes were registered
*** Clinical events were only evaluated in patients with at least 6 months of follow up while on hydroxyurea, age >2 years.
Table 2 Multivariable analysis of the effect of genetic traits on laboratory parameters and complications of SCD. Coefficients (95% Confidence Intervals) of a linear regression model are reported for endpoints HbF, Hb, MCV, LDH, Bilirubin, Reticulocytes- positive values indicate a positive correlation, negative values indicate a negative correlation. Exponentiated coefficients (95% Confidence Intervals) of Poisson regression are reported for endpoints hospitalization, pain crises, ACS, transfusions- values greater than 1 indicate a positive correlation, values smaller than 1 indicate a negative correlation. Blue- positive correlation; red- negative correlation; dark blue/dark red\(^1\) p<0.01; blue/red\(^2\) p<0.05; light blue/ light red\(^3\) p<0.1; all other p>0.1; n- number of patients available for analysis

<table>
<thead>
<tr>
<th>Genetic Trait</th>
<th>HbF (%) (n = 121)</th>
<th>Mean Hb (g/dL) (n = 163)</th>
<th>Mean MCV (fL) (n = 164)</th>
<th>ln LDH (U/L) (n = 150)</th>
<th>ln Bilirubin (mg/dL) (n = 151)</th>
<th>ln Reticulocytes (%) (n = 150)</th>
<th>Hospitalization (per year) (n = 161)</th>
<th>Pain crises (per year) (n = 162)</th>
<th>ACS (per year) (n = 163)</th>
<th>Transfusions (per year) (n = 163)</th>
</tr>
</thead>
<tbody>
<tr>
<td>α-thalassemia</td>
<td>-1.490</td>
<td>0.023</td>
<td>-9.42(^4) (-12.273 – -6.567)</td>
<td>-0.075(^3) (-0.155 – -0.005)</td>
<td>-0.124 (-0.277 – -0.030)</td>
<td>-0.232(^2) (-0.362 – -0.103)</td>
<td>0.933 (0.764 – 1.132)</td>
<td>0.959 (0.772 – 1.118)</td>
<td>0.589 (0.275 – 1.119)</td>
<td>0.832 (0.579 – 1.171)</td>
</tr>
<tr>
<td>BCL11A</td>
<td>3.894(^2) (0.939 – 6.849)</td>
<td>0.597(^1) (0.222 – 0.972)</td>
<td>3.278(^1) (0.043 – 6.512)</td>
<td>-0.087(^3) (-0.175 – -0.001)</td>
<td>0.061 (-0.106 – 0.228)</td>
<td>-0.239(^1) (-0.362 – -0.001)</td>
<td>0.852 (0.686 – 1.055)</td>
<td>0.909 (0.719 – 1.144)</td>
<td>0.589 (0.275 – 1.119)</td>
<td>0.473(^2) (0.217 – 0.952)</td>
</tr>
<tr>
<td>BCL11A</td>
<td>-0.403</td>
<td>0.075</td>
<td>-1.991 (-4.838 – 0.855)</td>
<td>0.067(^1) (-0.011 – 0.145)</td>
<td>0.038 (-0.112 – 0.228)</td>
<td>-0.239(^1) (-0.362 – -0.001)</td>
<td>1.194(^3) (0.993 – 1.438)</td>
<td>1.156 (0.945 – 1.415)</td>
<td>1.646(^2) (0.939 – 2.942)</td>
<td>0.907 (0.657 – 1.248)</td>
</tr>
<tr>
<td>HMIP</td>
<td>6.098(^2) (0.838 – 11.359)</td>
<td>0.437</td>
<td>0.964 (-3.690 – 5.619)</td>
<td>-0.160(^3) (-0.284 – -0.036)</td>
<td>-0.391(^4) (-0.629 – -0.153)</td>
<td>-0.306(^1) (-0.512 – -0.101)</td>
<td>0.735(^3) (0.497 – 1.033)</td>
<td>0.780 (0.519 – 1.111)</td>
<td>0.585 (0.101 – 1.713)</td>
<td>0.112(^2) (0.006 – 0.479)</td>
</tr>
<tr>
<td>HBG2</td>
<td>2.961(^2) (0.278 – 5.644)</td>
<td>0.807(^1) (0.435 – 1.180)</td>
<td>0.731 (-2.481 – 3.943)</td>
<td>-0.056 (-0.142 – -0.029)</td>
<td>0.020 (-0.144 – 0.214)</td>
<td>0.071 (-0.072 – 0.214)</td>
<td>1.577(^1) (1.329 – 1.853)</td>
<td>1.680(^1) (1.403 – 1.991)</td>
<td>1.190 (0.574 – 2.075)</td>
<td>0.252(^2) (0.050 – 0.608)</td>
</tr>
</tbody>
</table>
**Figure Legends**

**Figure 1. Linear Regression of HbF on laboratory parameters.** (A) Linear Regression of HbF on Hb (n=202). (B) Linear Regression of HbF on MCV (n=202). (C) Linear Regression of HbF on ln LDH (n=194). (D) Linear Regression of HbF on ln Bilirubin (n=195). (E) Linear Regression of HbF on ln Reticulocytes (n=195). Hb – total hemoglobin; HbF – fetal hemoglobin; LDH – lactate dehydrogenase; MCV – mean corpuscular volume.

**Figure 2. Correlation between HbF level and complications of SCD** (Poisson regression). Number of patients available for analysis: n=193 for hospitalization, n=194 for pain crisis and red blood cell transfusion. Thick line- predicted, thin line- 95% confidence interval.

**Figure 3. Mean values of laboratory parameters and complications from the γ-globin promoter polymorphism rs7482144-negative patients compared to the γ-globin promoter polymorphism rs7482144-positive patients.** (A) Negative patients (n=105): mean HbF 17.5 ± SD 10 % vs positive patients (n=24); mean HbF 23.6 ± SD 8.6 %; T-Test p=0.0061. (B) Negative patients (n=143): mean Hb 8.9 ± SD 1.5 g/dL vs positive patients (n=29); mean Hb 10.1 ± SD 1.3 g/dL; T-Test p<10⁻⁴. (C) Negative patients (n=142): mean frequency of hospitalizations per year 0.8 ± SD 1.3 vs positive patients (n=27): mean frequency of hospitalizations per year 1.9 ± SD 2.6; T-Test p=0.0011. (D) Negative patients (n=143): mean frequency of pain crises per year 0.6 ± SD 1.1 vs positive patients (n=27): mean frequency of hospitalizations per year 1.7 ± SD 2.5; T-Test p=0.0003. Hb – total hemoglobin; HbF – fetal hemoglobin; SD – standard deviation.
A

hospitalisation frequency(HbF) = \( \exp(0.912 - 0.03 \times \text{HbF}) \)

B

pain crises frequency(HbF) = \( \exp(0.753 - 0.031 \times \text{HbF}) \)

C

RBC transfusions frequency(HbF) = \( \exp(0.262 - 0.063 \times \text{HbF}) \)