

## **Genetic modifiers of sickle cell anaemia in patients from Nigeria: A pilot study**

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The variable clinical phenotype in sickle cell anaemia (SCA) is well documented, with severity in presentation partly associated with the persistence of fetal haemoglobin (HbF) and co-inheritance of  $\alpha$ -thalassemia ( $\alpha$ -3.7 globin gene deletion). Understanding genetic factors that contribute to clinical variability and severity in SCA is one step towards tackling health issues in SCA, as well as advancing knowledge about the disease, and research geared towards novel therapeutic targets. Genetic modifiers of HbF have been identified in several global populations, with a few studies reported from Nigeria.

We conducted a pilot study in the Federal Capital Territory of Nigeria to: (1) survey the prevalence of known genetic modifiers of HbF and the co-inheritance of  $\alpha$ -thalassemia in a different region of Nigeria; (2) boost capacity for sickle cell disease (SCD) research in Nigeria through collaborative studies; and (3) troubleshoot procedures for the investigation.

Our findings indicate: (a) differences in the frequencies of HbF-boosting alleles between the Abuja and Lagos patient groups; (b) associations between HbF levels and, *HMIP-2A* (rs66650371) and *Xmn1-HBG2* (rs7482144); (c) HbF-boosting alleles observed in *cis* within *BCL11A* in the Abuja study; (d) negative correlation between 3.7kb alpha globin gene deletion and, MCV and MCH; and (e) no major administrative or operational obstacles in this collaborative study. This study presents the basis for a larger and regional SCD study to aid the management of patients with SCD, and the development and implementation of relevant healthcare policies incorporating the genomics of SCD in Nigeria.

**Key words:** Sickle cell anaemia, genetic modifiers, co-inheritance of alpha-thalassemia, Nigeria

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