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A laboratory strategy for genotyping haemoglobin H disease in the Chinese

Amy Yuk-Yin Chan, Chi-Chiu So, Edmond Shiu-Kwan Ma and Li-Chong Chan

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A laboratory strategy for genotyping haemoglobin H disease in the Chinese

Amy Yuk-Yin Chan, Chi-Chiu So, Edmond Shiu-Kwan Ma, Li-Chong Chan

Background: The thalassaemias are the commonest blood disorders worldwide, with South East Asia and southern China as areas of high prevalence. Accurate diagnosis of these disorders helps in clinical management with improved outcome.

Methods: The α-globin genotypes of 100 Chinese patients in Hong Kong with haemoglobin H (Hb H) disease were characterised. Single-tube multiplex gap-PCR was used to detect −−SEA, −α3.7 and −α4.2, while Hb CS, Hb QS and codon 30 (ΔGAG) were identified by single-tube multiplex amplification refractory mutation system (ARMS). Automated direct nucleotide sequencing of the amplified α2- and α1-globin genes was performed to characterise other non-deletional α-thalassaemia determinants.

Results: In the 100 cases studied, 99 cases had −−SEA in combination with deletional αα-thalassaemia or non-deletional αα-globin mutation involving the α2-globin gene. In 70 cases of the deletional form, 43 cases showed the genotype of (−−SEA/−α3.7) and 27 cases of (−−SEA/−α4.2). Three of the 27 cases of (−−SEA/−α4.2) were found to have Hb Q-Thailand linked in-cis with −α4.2. The remaining 30 cases were of non-deletional form with the following genotypes: 11 cases of (−−SEA/αHbCSαHbCS), 9 cases of (−−SEA/αHbQSαHbQS), 3 cases of (−−SEA/αD171EαD171E), 3 cases of (−−SEA/αββ30Dαββ30D), 2 cases of (−−SEA/αββ30Dαββ30D), 1 case of (−−SEA/αβ6Westmeadαβ6Westmead) and 1 case of (−−non-SEA/−αHbQαHbQ).

Conclusions: Based on two rapid diagnostic tests, multiplex gap-PCR and multiplex ARMS, more than 90% of the cases were genetically characterised. This laboratory strategy should be widely applicable for genetic diagnosis of α-thalassaemia.

MATERIALS AND METHODS

Patient samples
Between 1998 and 2003, 100 cases of Hb H disease (97 Chinese, 2 Thais, 1 Filipino) were diagnosed by routine haemoglobin study. Seven cases were related, coming from three families with Hb H disease. The age range was 1–84 years, with more than two-thirds of the patients older than 20 years and one-third older than 40 years.

DNA analysis
Genomic DNA was extracted from peripheral blood of patients. Multiplex gap-PCR was adopted and modified to detect −−SEA, −α3.7 and −α4.2. Genomic DNA samples were amplified in a GeneAmp9700 thermocycler using the following cycling parameters: initial denaturation at 95°C for 15 min, followed by 30 cycles of 98°C denaturing for 45 s, 60°C annealing for 1 min 30 s, and 72°C extension 2 min 15 s. A final 5 s extension completed the reaction. Each PCR was set up in a total volume of 50 μl containing: 300–600 ng genomic DNA, 200 μM each of dNTP, 1.5 mM MgCl2, 1× Q-solution (Qiagen, Hilden, Germany), 2.5 U HotStarTaq DNA polymerase in supplied reaction buffer (Qiagen) and 9 different primers at various concentrations (table 1). A 10 μl aliquot of each amplified product was analysed by electrophoresis on a 1% agarose gel after staining with ethidium bromide.

For the detection of the three common non-deletional α2-thalassaemia determinants, Hb CS, Hb QS and codon 30 (ΔGAG), the multiplex amplification refractory mutation system (ARMS) was performed to characterise other non-deletional α-thalassaemia determinants.

Abbreviations: ARMS, amplification refractory mutation system; Hb, haemoglobin
system (ARMS) approach was modified and used. Genomic DNA samples were amplified in a GeneAmp9700 thermocycler using the following cycling parameters: initial denaturation at 94°C for 12 min, followed by 32 cycles of 94°C denaturing for 40 s, 62°C annealing for 20 s, and 72°C extension 3 min. A final 7 minutes extension completed the reaction. Each PCR was set up in a total volume of 20 μl containing: 200 μM of each dNTP, 2.0 mM MgCl₂, 10% dimethylsulphoxide, 16.5 mM ammonium sulphate, 0.01% (v/v) gelatin, 10 mM Tris-HCL, pH 8.3, 50 mM KCl, 5 U AmpliTaq Gold DNA polymerase and 6 different primers at various concentrations (table 1). A 10 μl aliquot of each amplified product was analysed by electrophoresis on a 8% non-denaturing polyacrylamide gel. Three fragments were caused by co-inheritance of −SEA with either deletional or non-deletional α-thalassemia determinants. Deletional Hb H disease, that is −SEA in association with α²-deletion (−α²7 and −α²2), accounted for 70% of the cases. Figure 2 shows the electrophoretic results of multiplex gap-PCR product in deletional Hb H disease on 1% agarose gel. Three cases of (−SEA)/−α² by direct nucleotide sequencing of the amplified α⁰-globin gene.

Among the remaining 30% of cases with Hb H disease, six different types of non-deletional determinants were found, all in the α²-globin gene. They were Hb CS, Hb QS, codon 30 (ΔGAG),12 codon 31 (AGG→AAG),13 poly-A signal (AATAAA→AATGAA)14 and Hb Westmead (codon 122 CAC→CAG).14 15 Our multiplex ARMS detected Hb CS, Hb QS and codon 30 (ΔGAG) and resolved 80% (ie 24/30) of the non-deletional cases. Figure 3 shows the electrophoretic results of three common non-deletional Hb H disease as detected by our multiplex ARMS in an aqueous 8% polyacrylamide gel.

The remaining three non-deletional determinants were characterised by direct nucleotide sequencing of the amplified α²-globin gene. They were codon 31 (AGG→AAG),13 poly-A signal (AATAAA→AATGAA)14 and Hb Westmead (codon 122 CAC→CAG).14 15 Figure 4 illustrates the automated sequencing result of codon 31 (AGG→AAG).

**DISCUSSION**

The clinical severity of Hb H disease is known to be variable. There is evidence to show a more severe phenotype with non-deletional forms (−/−α⁰) compared with deletional forms (−/−α⁰), which leads to the view that Hb H disease is not as benign a disorder as previously thought.18 Patients with non-deletional forms of Hb H may have significant anaemia, iron overload and multi-organ morbidity. An early and accurate diagnosis of Hb H disease is therefore warranted. Many methods for genetic diagnosis of α-thalassaemia are currently in use, including Southern blot analysis, direct nucleotide sequencing and reverse dot-blotting.19 However, these approaches are labour-intensive and time-consuming. With our diagnostic strategy (fig 1), more than 90% of Hb H disease in our population can be characterised.
by performing only two multiplex PCRs, and direct sequencing is needed in <10% of cases. With adaptation to detect prevalent \( \alpha \)-globin mutations in their localities, our approach should also be applicable in other South East Asian countries. This strategy can be further modified by including primers for the detection of the \( -^2 \text{MED} \) and \( -^4 \) double-gene deletions and becomes applicable in the Mediterranean area. However, this strategy may be less applicable in places like Cambodia or Papua New Guinea where access to fluorescent dye chemistry sequencing is much more limited.

Prenatal diagnosis for Hb H disease is not routinely performed as it is not generally regarded as a severe condition. Whether genetic risk prediction is indicated for a non-fatal disorder that is associated with significant morbidity, such as Hb H disease, will have to be considered in light of recent evidence of more severe forms of the disease, such as Hb H hydrops. However, current antenatal thalassaemia screening does not usually identify couples at risk of Hb H disease because \( -^2 \) or \( -^4 \) heterozygous carrier state cannot be reliably detected by phenotypic tests. Hence genetic counselling will not be offered even if Hb H disease is included as a target for screening.

The availability of a simple and effective \( \alpha \)-thalassaemia genotyping strategy as proposed in the present study will greatly facilitate carrier detection and its potential use in antenatal screening, molecular characterisation of Hb H disease, genotype–phenotype correlation as well as longitudinal studies on the natural history of clearly defined deletional and non-deletional Hb H disease.

Figure 1 Strategy for genotypic diagnosis of Hb H disease by multiplex gap-PCR, multiplex ARMS-PCR and automated direct nucleotide sequencing of the amplified \( \alpha_2 \) and \( \alpha_1 \) globin genes.

Figure 2 Electrophoretic results of multiplex gap PCR products on 1% agarose gel in deletional Hb H disease.
Figure 4 Result of direct automated sequencing of the $\alpha$2-globin gene, showing AGG$\rightarrow$AAG mutation at codon 31. The normal allele is absent since the patient harbours SEA deletion on the other chromosome 16.

Take-home messages

- A total of 100 haemoglobin H (Hb H) disease patients in Hong Kong have been characterised at the DNA level.
- Single-tube multiplex gap-PCR was used to detect $\alpha$-SEA, $\alpha^{+}3.7$ and $\alpha^{0.2}$, while Hb CS, Hb QS and codon 30 (\DeltaGAG) were identified by single-tube multiplex amplification refractory mutation system (ARMS).
- Automated direct nucleotide sequencing of the amplified $\alpha$2- and $\alpha$1-globin genes was performed to characterise other non-deletional $\alpha$-thalassaemia determinants.
- Based on two rapid diagnostic tests, namely multiplex gap-PCR and multiplex ARMS, $\geq$90% of the cases were genetically characterised.
- This laboratory strategy should be widely applicable for genetic diagnosis of $\alpha$-thalassaemia.

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