**RESEARCH ARTICLE**

# Distribution of Rh Subgroups and Kell Antigens in Patients with Thalassemia

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**ABSTRACT**

First-line therapy for thalassemia patients is blood transfusion. Patients who get repeated transfusions of red blood cells (RBCs) risk developing an immune response to the RBCs, resulting in a hemolytic transfusion reaction and even death. Patients who get phenotype blood transfusions are less likely to experience these side effects. Between 2014 and 2015, researchers at Baghdad's Ibn Al-Baladi Thalassemia Hospital performed a prospective survey and collected samples. Enrollment in this trial included (903) patients (males were 477 and females were 426). Patients' venous blood samples were taken and processed using a novel procedure known as the (gel method). A lot of data was collected, including gender, ABO blood groups, Rh typing, and blood phenotypes. In thalassemia, the most frequent blood group was (O), and the most common blood antigen (phenotype) was (A) (e). Typed blood units can be provided with a lower risk of alloimmunization and other complications by typing patient RBCs before transfusing, according to this study. Blood transfusion patients must have access to a database of blood donors who have been phenotyped.

**Keywords:** Blood group, Blood transfusion, Drugs, Gel method, Phenotyped, Thalassemia.

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## INTRODUCTION

Hereditary blood illnesses known as thalassemia syndromes are associated with the reduced or missing synthesis of the beta-globin chain, which results in lower Hb levels in red blood cells, decreased RBC production, and anemia. Three primary types of -thalassemia exist: Cooley's Anemia, or "Mediterranean Anemia," Thalassemia Intermedia and Thalassemia Minor, or "heterozygous -thalassemia," are all forms of the same disease, which is also known as Thalassemia Major, Thalassemia Intermedia, or "Mediterranean Anemia".[1-4] The Hb molecule has piqued researchers' interest because of the numerous clinical disorders that it affects, including those caused by structural variations (hemoglobinopathies), synthesis abnormalities (thalassemias), and a wide range of developmental problems (HPFH).[2,4] Many complicated disease phenotypes cannot be explained in such detail, and predicting patient risk as a function of their unique genetic background already provides help in clinical settings for -thalassemia, unlike other complex illnesses.[4-7]

DNA sequencing can be used in patients with homozygous -thalassemia to identify genetic moderators and better understand phenotypic modulation abilities. Genetic modifiers will soon re-evaluate our current phenotypic definition, which will allow us to re-define the disease on a genetic foundation.[4,8,9] It is common for thalassemia carriers to exhibit hypochromic microcytosis, with MCV 80 FL and MCH 27 pg. Thalassemia mutations, genetic interplay between thalassemic genes, and blood cell counts can all affect these results.[5,9] These indicators have been tested to see if they are useful in detecting thalassemia.[6,10] The phenotypic -thalassemia is caused by recessive mutations in the HBA1 and HBA2 genes.[7,8,10] There are four alleles since there are two gene loci. -globin has two genetic loci, hence four alleles are present in diploid cells.

Two alleles originate from the mother and two from the father. The bigger the number of -globin; alleles impacted, the more severe the symptoms of the disease will be.[9] Alpha-thalassemias cause a reduction in alpha-globin production, which results in an overproduction of chains in adults and an overproduction of chains in infants, respectively. If the beta chain counts exceed four, hemoglobin H or HbH of four forms an unstable tetramer with aberrant oxygen dissociation curves, known as hemoglobin H (HbH of four).[10]

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## MATERIALS AND METHODS

The Ibn Al-Baladi Hospital for Thalassemia in Baghdad was surveyed and samples were gathered from 2014 to 2015. Patients' demographics (age, gender, and species) were collected. Patients are the only ones included in the studies. The positive and negative species that they carry were discovered via the analysis. Patients with Thalassemia can get blood transfusions. Using the gel method, a disc having drilling, each hole has a distinct type of gene that affects the patient when blood is introduced to it, patients' venous blood samples were analyzed. These holes are filled with blood serum, which is then spun in a centrifuge to separate the serum-mixed material and determine if the patient has any of this particular type of serum. It delivers a positive result if it matches and a negative result if it doesn't match. Using this procedure, the patient's sensitivity to the blood collected is reduced, and their condition is improved.

### Statistical Analysis

Data was collected and analyzed statistically using the SPSS (Statistical Package for Social Science) application.

There have been two sorts of statistics conducted:

- Descriptive statistics: where quantitative data were shown as mean and standard deviation, The quantitative and qualitative data were reported as frequency and percentage.
- Analytical statistics: the test was used to compare the mean and standard deviation (SD) of two sets of quantitative normally distributed data.

In this Table 1, more males were infected than females, as it was noted that the number of infected males reached (477), and the number of infected females amounted to (426).

**Table 1:** Details of patients' genders

| | | *Frequency* | *Percent* | *Valid percent* | *Cumulative percent* |
|---|---|---|---|---|---|
| | male | 477 | 52.8 | 52.8 | 52.8 |
| Valid | Female | 426 | 47.2 | 47.2 | 100.0 |
| | Total | 903 | 100.0 | 100.0 | |

**Table 2:** This table shows the statistics for the percentage of each blood type

| *Blood_group* | | *Frequency* | *Percent* | *Valid percent* | *Cumulative percent* |
|---|---|---|---|---|---|
| | A | 246 | 27.2 | 27.2 | 27.2 |
| | O | 364 | 40.3 | 40.3 | 67.6 |
| Valid | AB | 53 | 5.9 | 5.9 | 73.4 |
| | B | 240 | 26.6 | 26.6 | 100.0 |
| | Total | 903 | 100.0 | 100.0 | |

**Table 3:** This table shows the percentage of Rh factor in patients

| | | *Frequency* | *Percent* | *Valid percent* | *Cumulative percent* |
|---|---|---|---|---|---|
| | P | 821 | 90.9 | 90.9 | 90.9 |
| Valid | N | 82 | 9.1 | 9.1 | 100.0 |
| | Total | 903 | 100.0 | 100.0 | |

**Table 4:** Details of the subgroups that appear in patients

| *C* | | *Frequency* | *Percent* | *Valid percent* | *Cumulative percent* |
|---|---|---|---|---|---|
| | P | 803 | 88.9 | 88.9 | 88.9 |
| Valid | N | 100 | 11.1 | 11.1 | 100.0 |
| | Total | 903 | 100.0 | 100.0 | |
| C | | Frequency | Percent | Valid percent | Cumulative percent |
| | p | 719 | 79.6 | 79.6 | 79.6 |
| Valid | N | 184 | 20.4 | 20.4 | 100.0 |
| | Total | 903 | 100.0 | 100.0 | |
| E | | Frequency | Percent | Valid percent | Cumulative percent |
| | P | 404 | 44.7 | 44.7 | 44.7 |
| Valid | N | 499 | 55.3 | 55.3 | 100.0 |
| | Total | 903 | 100.0 | 100.0 | |
| E | | Frequency | Percent | Valid percent | Cumulative percent |
| | P | 894 | 99.0 | 99.0 | 99.0 |
| Valid | N | 9 | 1.0 | 1.0 | 100.0 |
| | Total | 903 | 100.0 | 100.0 | |
| K | | Frequency | Percent | Valid percent | Cumulative percent |
| | P | 55 | 6.1 | 6.1 | 6.1 |
| Valid | N | 848 | 93.9 | 93.9 | 100.0 |
| | Total | 903 | 100.0 | 100.0 | |

**Table 5:** Shows Sex* Blood_group crosstabulation

| *Count A* | | *Blood_group* | | | | *Total* |
|---|---|---|---|---|---|---|
| | | *O* | *AB* | *B* | | |
| Sex | male | 123 | 200 | 29 | 125 | 477 |
| | Female | 123 | 164 | 24 | 115 | 426 |
| Total | | 246 | 364 | 53 | 240 | 903 |

## RESULTS

In Tables 2 to 4, it was counted and explored that the patients carrying the Rh factor of a positive type are more than the patients carrying the Rh factor of a negative type, as the negative type are few and getting them to donate blood is difficult.[11]

Tables 5 to 7 showed that the blood subgroup (e) was the type that most affects the patients while the blood subgroup K was the least affected the patients.

## DISCUSSION

Samples were collected, processed, and data were compiled from Thalassemia patients at Baghdad's Ibn Al-Balad Hospital who require periodic blood transfusions. A recent investigation (gel technique) verified that the donor blood matched. It was

**Table 6:** Shows sex vs RH

| *Group Statistics* | *Sex* | *N* | *Mean* | *Std. deviation* | *Std. error mean* |
|---|---|---|---|---|---|
| Rh | male | 477 | 1.07 | .261 | .012 |
| | Female | 426 | 1.11 | .314 | .015 |

**Table 7:** Shows subgroups vs blood groups

| *C * Blood_group crosstabulation* | | *Blood_group* | | | | *Total* |
|---|---|---|---|---|---|---|
| | | *A* | *O* | *AB* | *B* | |
| C | P | 213 | 328 | 46 | 216 | 803 |
| | N | 33 | 36 | 7 | 24 | 100 |
| Total | | 246 | 364 | 53 | 240 | 903 |

discovered that persons with blood type O are the majority, while those with blood type AB are the minority.

Additionally, our research identified significant blood subgroups that are associated with thalassemia patients in particular. These subtypes are a collection of antigens referred to as (subgroup, phenotypic, or Rh system) (C, c, E, e, Kill). This affects the patient's blood since it might produce allergic responses or sensitivity and can result in alloimmunization in individuals who get frequent blood transfusions.

## CONCLUSION

Through this study and quantitative information with average values, 903 patients with this disease were monitored and when they need a blood transfusion from a donor, it must be ensured that the groups match and that the dominant type on patients is O-positive, amounting to 40.3%, as well as the sub-group of the patient and the donor, which increases his health condition is poor if these species do not match

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