

Newborn Identification: Analysis of DNA Polymorphism in Samples taken from Newborn and Mother at the Moment of Delivery and When They Leave the Maternity Ward

Raimondi, E., Toscanini U, Vidales, J, Haas, E.

PRICAI (Primer Centro Argentino de Immunogenetics), Av. Belgrano 1746 2° piso (1093)

Bs.As.-Argentina. Laboratorie de Immunogenetica del ICYCC de la Fundacion Favaloro



INTRODUCTION

Newborn identification is still an unsolved problem since methods used nowadays (footprinting, bracelets, etc.) have shown to be inefficient and unsecure. If a demand for baby change occurs, the clinic has no defense since it registers the child that was born but not the one who leaves the maternity ward. We propose a simple method for keeping one blood sample of the baby and one blood sample of the mother, both of them taken in the moment of delivery before cutting the umbilical cord, and a mucosal cheek swab taken from the baby when he leaves the maternity ward. If there is a legal action, DNA patterns from blood samples and swabs are compared in order to determine if a change has occurred.

MATERIALS AND METHODS

A) Collection Kit: It consists of: 1) a filter paper adhered to a sticker (inviolable) with two perforations on it that let enough space to deposit ~300ul of blood from mother and child in each sector, respectively. In the same card, data from mother, day and time of birth, number of clinical history and the responsible physician signature are recorded; 2) a swab in whose distal extreme data concerning day of birth and day of departure from maternity ward are registered and mother signs. The whole kit is stored at -20°C in an inviolable bag and registered in a database for 1 year. B) A mucosal cheek swab and blood sample (200-300ul) were taken to each of 100 individuals. Blood samples were allowed to dry on the filter and both, the swabs and the filters were stored at -20°C for 8 months. After that period, DNA was extracted from stored samples by organic procedure. DNA polymorphism were analyzed at 3 RFLP loci and 6 STR loci and the patterns obtained were compared.

RESULTS

DNA suitable for PCR amplification and restriction enzyme digestion was extracted from 100% of samples, yielding an average of 1 µg per sample. DNA profiles were clear and patterns obtained from swabs matched the pattern obtained from the corresponding blood sample at each locus.

CONCLUSIONS

We think that this is a good method for newborn identification since it is non-invasive, low-cost (since in most cases the material is kept without processing it) and assures the identity of the child that leaves the maternity ward, protecting in this way to the parents and to the intervening professionals. If the possibility of a baby change exists, a screening is performed of all children born on the same day in that institution to identify the true parents by simply analyzing the stored material.