Background and Aims The traditional mercury thermometer has been replaced by the more “user friendly” digital thermometer. As accuracy is comparable with both instruments and mercury remains an environmental hazard they are no longer recommended. New non invasive method of measuring temperature may reduce infection rate as well as intangible pain and suffering of neonate.

Methods The body temperature of patients admitted in Neonatal Intensive Care Unit was measured using axillary digital thermometer as well as a handheld infrared non touch thermometer. Patients placed under radiant warmers were included. Temperature recordings were taken as required routinely for clinical care. Axillary temperature was recorded within 30 seconds and the forehead temperature within 5 seconds.

Results The body temperature measured by Axillary digital thermometer and forehead method do not agree well (95% limits of agreement: –4.2, 2.2). A trend was observed suggesting that agreement depends on the magnitude of the temperature. The agreement slightly improved when patients in warmer were excluded (95% limits of agreement: –4.1, 2.1) with similar trend. The best possible agreement was observed between warmer and axillary temperature but was not clinically acceptable (95% limits of agreement: –0.99, 2.36).

Conclusion Forehead temperature due to non touch may appear less disturbing to the neonate and also time saving for the nurse but they are misleading. The infrared technology needs further improvement before it can be used in our setting. Although advent of technology is tempting, a scientific validation of new technology under different settings is caveat before adapting it.

1412 TRANS Cutaneous B Irl R ubinometers used within a Structured Pathway predicts high Serum Bilirubin levels in Healthy Term Jaundiced Neonates monitored at home

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Background 1NICE) guidelines recommend that bilirubin is monitored in all jaundiced babies. We implemented a home based integrated care pathway to monitor healthy term jaundiced neonates with transcutaneous bilirubinometers (TcB). Babies were readmitted to hospital for phototherapy at total serum bilirubin (TsB) ≥340 µmol/l. TsB ≤250 µmol/l correlates highly with TcB and correlated. High TcB ≤250 µmol/l predicts ability to exceed 340 µmol/l.

Aim To determine the TcB values in term babies monitored at home that could predict TsB values ≥340 µmol/l.

Methods Healthy jaundiced neonates were monitored at home using BiliChek® (Ver 6.12) bilirubinometer. Babies with TcB > 250 µmol/l had TsB measured using the Beckman Coulter timed endpoint diazo method within 4 hours to confirm result. We carried out statistical analysis of the paired samples to determine the TcB value with the best predictive value for TsB ≥ 340 µmol/l.

Results Eighty-three paired samples were analysed from 63 babies. 6 (7%) had TcB values of ≥ 340 µmol/l. The Receiver Operating Characteristics (ROC) curve analysis suggested an area under the curve (AUC) of 0.9037. TcB values ≥ 315 µmol/l predicted TsB ≥ 340 µmol/l with sensitivity of 0.83 (0.36, 1.00); specificity of 0.82 (0.71, 0.90); positive predictive value of 0.26 (0.09, 0.51) and overall accuracy of 0.82 (0.72, 0.90). TcB values ≥ 303 µmol/l predictive ability had a sensitivity of 1.00 (0.54, 1.00); specificity of 0.71 (0.60, 0.81), positive predictive value of 0.21 (0.08, 0.41) and overall accuracy 0.73 (0.63, 0.83).

Conclusion BiliChek® TcB ≥ 303 µmol/l had higher sensitivity but lower specificity than TcB ≥ 315 µmol/l for predicting TsB values ≥ 340 µmol/l in healthy term jaundiced neonates monitored at home.

1414 INSIGHTS INTO NEONATAL ORAL FEEDING PATHOLOGY THROUGH RNA SEQUENCING OF SALIVARY SAMPLES

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Background and Aims To improve our understanding of newborn feeding pathophysiology at the molecular level, our laboratory studies transcripts in neonatal saliva. Previously, we used whole transcriptome microarrays. Here, we tested the hypothesis that sequencing of RNA would provide additional and more specific information.

Methods RNA was extracted and prepared for sequencing from salivary samples (10 µL) collected from newborns matched for gestational age, postnatal age, and feeding status. Paired-end 100 x 100 base pair sequencing was performed on the Illumina HiSeq 2000. Sequence data were aligned against human reference genome GRCh37/hg19. Cuffdiff analysis identified differentially expressed genes, promoters, and splicing variants between subjects. Ingenuity Pathway Analysis was performed on statistically significantly differentially expressed genes.