Physiological Genomics 2017 vol.49 N3, pages 193-200

HLA gene expression is altered in whole blood and placenta from women who later developed preeclampsia

Small H., Akehurst C., Sharafetdinova L., McBride M., McClure J., Robinson S., Carty D., Freeman D., Delles C.

Kazan Federal University, 420008, Kremlevskaya 18, Kazan, Russia

Abstract

© The American Physiological Society. Preeclampsia is a multisystem disease that significantly contributes to maternal and fetal morbidity and mortality. In this study, we used a non-biased microarray approach to identify dysregulated genes in maternal whole blood samples which may be associated with the development of preeclampsia. Whole blood samples were obtained at 28 wk of gestation from 5 women who later developed preeclampsia (cases) and 10 matched women with normotensive pregnancies (controls). Placenta samples were obtained from an independent cohort of 19 women with preeclampsia matched with 19 women with normotensive pregnancies. We studied gene expression profiles using Illumina microarray in blood and validated changes in gene expression in whole blood and placenta tissue by qPCR. We found a transcriptional profile differentiating cases from controls; 336 genes were significantly dysregulated in blood from women who developed preeclampsia. Functional annotation of microarray results indicated that most of the genes found to be dysregulated were involved in inflammatory pathways. While general trends were preserved, only HLA-A was validated in whole blood samples from cases using qPCR (2.30-± 0.9-fold change) whereas in placental tissue HLA-DRB1 expression was found to be significantly increased in samples from women with preeclampsia (5.88-± 2.24-fold change). We have identified that HLA-A is upregulated in the circulation of women who went on to develop preeclampsia. In placenta of women with preeclampsia we identified that HLA-DRB1 is upregulated. Our data provide further evidence for involvement of the HLA gene family in the pathogenesis of preeclampsia.

http://dx.doi.org/10.1152/physiolgenomics.00106.2016

Keywords

Gene expression, Microarray, Placenta, Preeclampsia

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