Accepted Manuscript

A bioinformatics transcriptome meta-analysis highlights the importance of trophoblast differentiation in the pathology of hydatidiform moles

Christophe Desterke, Rima Slim, Jean-Jacques candelier

PII: S0143-4004(18)30140-1

DOI: 10.1016/j.placenta.2018.04.002

Reference: YPLAC 3806

To appear in: *Placenta*

Received Date: 23 January 2018

Revised Date: 26 March 2018

Accepted Date: 6 April 2018

Please cite this article as: Desterke C, Slim R, candelier J-J, A bioinformatics transcriptome meta-analysis highlights the importance of trophoblast differentiation in the pathology of hydatidiform moles, *Placenta* (2018), doi: 10.1016/j.placenta.2018.04.002.

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.

ACCEPTED MANUSCRIPT

A bioinformatics transcriptome meta-analysis highlights the importance of trophoblast differentiation in the pathology of hydatidiform moles

Abstract

Introduction: Hydatidiform mole (HM) is an aberrant human pregnancy with abnormal trophoblastic development, migration / invasion of the extravillous trophoblast in the decidua. These abnormalities are established in a hypoxic environment during the first trimester of gestation.

Methods: Using text mining, we identified 72 unique genes that are linked to HM (HM-linked genes) that we studied by bioinformatic analysis in publicly available transcriptomes of primary chorionic villous cells (cytotrophoblast, syncytiotrophoblast, extravillous trophoblast, and arterial and venous endothelial) isolated from normal placentas or established trophoblastic cell lines cultured under different oxygen concentrations.

Results: We show that the majority of HM-linked genes (75%) are involved in normal trophoblastic differentiation, arranged in clusters, and some of them are implicated in chorionic villous invasion or regulated by oxygen concentrations.

Discussion: Our analysis integrates the various aspects of the pathophysiology of HM and highlights the importance of trophoblastic differentiation in this pathology.

ACCEPTED MANUSCRIPT

Download English Version:

https://daneshyari.com/en/article/8626399

Download Persian Version:

https://daneshyari.com/article/8626399

Daneshyari.com