Series GSE145974

Query DataSets for GSE145974

Status	Public on Apr 03, 2020
Title	Global transcriptome analysis identifies a signature for early disseminated Lyme disease and its resolution
Organism	Homo sapiens
Experiment type	Expression profiling by array
Summary	Lyme disease (LD), caused by Borrelia burgdorferi, is the most common tick-borne infectious disease in the United States. We examined gene expression patterns in the blood of individuals with early disseminated LD at the time of diagnosis (Acute LD) and also at approximately 1 month and 6 months following antibiotic treatment. A distinct acute LD profile was observed that was sustained during early convalescence (1 month) but returned to control levels six months after treatment. Using a computer learning algorithm, we identified sets of 20 classifier genes that discriminate LD from other bacterial and viral infections. In addition, these novel LD biomarkers are highly acurate in distinvuishing patients with acute LD from healthy subjects and in discriminating between individuals with active and resolved infecitons. This computational approach offers the potential for more accurate diagnosis of early dissminated Lyme disease. It may also allow improved monitoring of treatment efficacy and disease resolution.
Overall design	A bioinformatics approach was employed to identify transcriptome alterations in the peripheral blood mononuclear cells of well-characterized human subjects who were diagnosed with early disseminated Lyme disease (LD) based on stringent microbiological and clinical criteria. Transcriptomes were assessed at the time of presentation, and at approximately 1 month (early convalescence) and 6 months (late convalescence) following initiation of an appropriate antibiotic regimen. Comparative transcriptomics identified 335 transcripts, representing 233 unique genes, with significant alterations of at least 2-fold expression in acute or convalescent blood samples from LD subjects relative to healthy donors. Acute phase blood samples from LD subjects had the largest number of differentially expressed transcripts (187 induced, 54 repressed). This transcriptional profile, which was dominated by interferon-regulated genes, was sustained during early convalescence. Six months after antibiotic treatment the transcriptome of LD subjects was indistinguishable from that of healthy controls based on two separate methods of analysis. Return of the LD expression profile to levels found in control subjects was concordant with disease outcome; 82% of subjects with LD experienced at least one symptom at the baseline visit, as compared to 43% at the early convalescence time point and only a single patient (9%) at the six-month convalescence time point. Using the random forest machine learning algorithm, we developed an efficient computational framework to identify sets of 20 classifier genes that discriminated LD from other bacterial and viral infections. These novel LD

biomarkers not only differentiated subjects with acute disseminated LD from healthy controls with 96% accuracy, but also distinguished between subjects with acute and resolved (late convalescent) disease with 97% accuracy.

Contributor(s)	Petzke MM, Schwartz I
Citation(s)	Petzke MM, Volyanskyy K, Mao Y, Arevalo B et al. Global Transcriptome Analysis Identifies a Diagnostic Signature for Early Disseminated Lyme Disease and Its Resolution. *mBio* 2020 Mar 17;11(2). PMID: 32184234
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Contact name	Mary Petzke
E-mail(s)	mary_petzke@nymc.edu
Organization name	New York Medical College
Department	Microbiology and Immunology
Lab	BSB 306
Street address	15 Dana Road
City	Valhalla
State/province	NY
ZIP/Postal code	10595
Country	USA

Platforms (1)	GPL13667 [HG-U219] Affymetrix Human Genome U219 Array
Samples (86)	GSM4340492 PBMC total RNA-Healthy control 1
More...	GSM4340493 PBMC total RNA-Healthy control 2
	GSM4340494 PBMC total RNA-Healthy control 3

Relations

BioProject	PRJNA608899

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SOFT formatted family file(s)	SOFT
MINiML formatted family file(s)	MINiML
Series Matrix File(s)	TXT

Supplementary file	Size	Download	File type/resource
GSE145974_RAW.tar	171.4 Mb	(http)(custom)	TAR (of CEL)
Raw data provided as supplementary file			
Processed data included within Sample table			