Platform-based concordance test to evaluate EcoToxChips – technical calibration

BACKGROUND INFORMATION

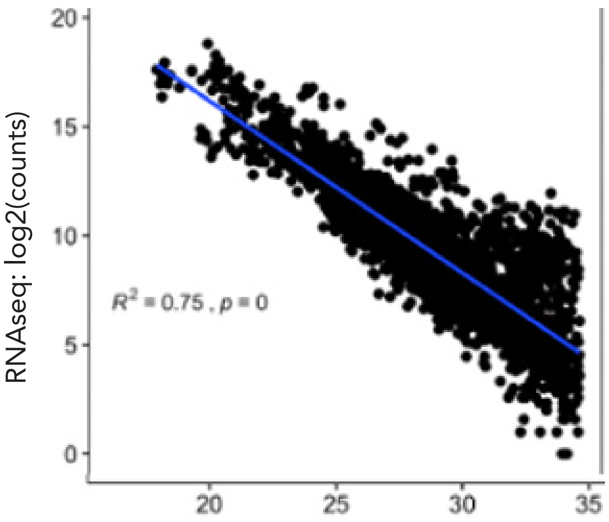
EcoToxChips are a qPCR-based tool. There are several molecular biological approaches to determine changes in gene expression, and therefore it is important to determine how one technology (e.g., qPCR) compares to another widely used approach, whole transcriptome RNA-sequencing.

OBJECTIVE

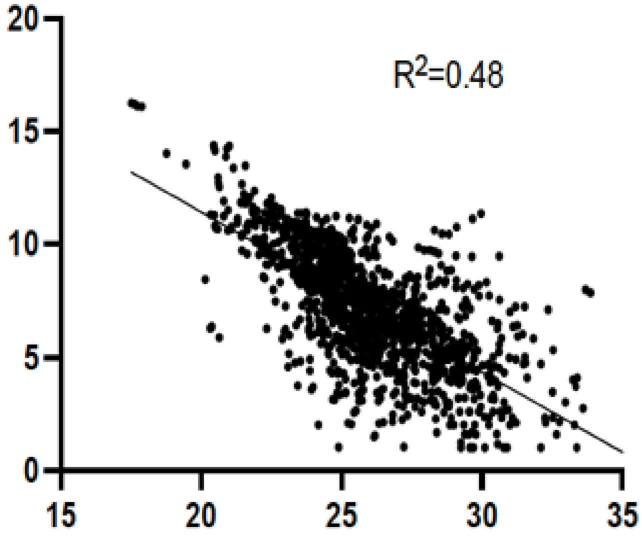
Compare gene expression of the 384 genes on the species-specific EcoToxChips (Ct values) with project-derived RNAseq data (raw counts) for the same samples.

RESULTS

Japanese quail (JQ) Version 1 EcoToxChip
Source tissue: Liver from embryonic day 9
n = 10 Chlorpyrifos-exposed samples
$R^2 = 0.75$



Xenopus laevis (XL) Version 1 EcoToxChip
Source tissue: Pooled whole body larvae (5 dpf)
n = 4 Lead (Pb)-exposed samples
$R^2 = 0.48$



EcoToxChip: Ct values

TAKEAWAYS

EcoToxChips yielded data that were highly correlated with those from RNAseq providing additional confidence in the qPCR array approach for gene expression analysis. The inter-platform correlation of gene expression data is comparable with the $R^2=0.48$ reported in the MAQC Phase 1 study.

Notes
MAQC Phase 1 results at www.ncbi.nlm.nih.gov/pmc/articles/PMC3272078/

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