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Data in Brief

# Glomerulonephritis-induced changes in kidney gene expression in rats

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ABSTRACT

We investigated a glomerulonephritis (GN) model in rats induced by nephrotoxic serum (NTS) which contains antibodies against the glomerular basement membrane (GBM). The anti-GBM GN model in rats is widely used since its biochemical and histopathological characteristics are similar to crescentic nephritis and Goodpasture's disease in humans (Pusey, 2003 [2]). Male Wistar Kyoto (WKY) and Sprague–Dawley (SD) rats were dosed once with 1, 2.5 and 5 ml/kg nephrotoxic serum (NTS) or 1.5 and 5 ml/kg NTS, respectively. GN and tubular damage were observed histopathologically in all treated rats after 14 days. To obtain insight into molecular processes during GN pathogenesis, mRNA expression was investigated in WKY and SD kidneys using Affymetrix's GeneChip Rat genome 230_2.0 arrays (GSE64265). The immunopathological processes during GN are still not fully understood and likely involve both innate and adaptive immunity. In the present study, several hundred mRNAs were found deregulated, which functionally were mostly associated with inflammation and regeneration. The β-chain of the major histocompatibility complex class II RT1.B (Rt1-Bb) and complement component 6 (C6) were identified as two mRNAs differentially expressed between WKY and SD rat strains which could be related to known different susceptibilities to NTS of different rat strains; both were increased in WKY and decreased in SD rats (Pavkovic et al., 2015 [1]). Increased Rt1-Bb expression in WKY rats could indicate a stronger and more persistent cellular reaction of the adaptive immune system in this strain, in line with findings indicating adaptive immune reactions during GN. The complement cascade is also known to be essential for GN development, especially terminal cascade products like C6.



| Specifications | |
|---|---|
| Organism/cell line/tissue | Wistar Kyoto (WKY/NCrl) and Sprague–Dawley® (Crl:SD) rats |
| Sex | Male |
| Sequencer or array type | GeneChip Rat genome 230_2.0 arrays (Affymetrix, Santa Clara, California) |
| Data format | Raw |
| Experimental factors | Untreated vs. nephrotoxic serum treated |
| Experimental features | Male Wistar Kyoto (WKY) and Sprague–Dawley (SD) rats were dosed once with 1, 2.5 and 5 ml/kg nephrotoxic serum (NTS) or 1.5 and 5 ml/kg NTS, respectively. After 14 days rats were euthanized and kidneys were removed for RNA extraction and hybridization on Affymetrix microarrays. |
| Consent | Not required (animal sample) |
| Sample source location | N/A |

## 1. Direct link to deposited data

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE64265.

## 2. Experimental design, materials and methods Pavkovic et al., 2015 [1]

All animal experiments were performed according to the German guidelines for care and use of laboratory animals. Male WKY and SD rats, 8 weeks old, were purchased from Charles River laboratories (Sulzbach, Germany). Animals were individually housed in type III Makrolon cages, with a 12-h light–dark cycle. Standard rodent chow pellets and water were provided ad libitum. Rats were randomly grouped (WKY: control group n = 3, treatment groups n = 5; SD: all groups n = 6) and dosed once i.v. with 0, 1.0 (WKY), 1.5 (SD), 2.5 (WKY), or 5.0 ml/kg NTS (Sheep Anti-Rat GBM Serum [PTX-001S]; Probetex, San Antonio, Texas). Control groups received appropriate volumes of normal saline solution. Doses were selected based on Probetex recommendations and dose finding studies performed in house. On day 14 rats were euthanized and the kidneys

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were removed for histopathological examination and RNA isolation. Kidney tissue for RNA isolation was shock frozen with liquid nitrogen and stored at −80 °C.

Total kidney RNA (mRNA) was isolated with the RNeasy Mini Kit (Qiagen) from 70 mg kidney tissue according to the manufacturer's instructions. The quality of isolated RNAs was assessed using Bioanalyzer Nano RNA Kits (Agilent, Santa Clara, California), and the quantity was determined with a spectrophotometer.

For microarray expression profiling, biotin-labeled copyRNA samples prepared from 500 ng high quality total kidney RNA were hybridized on GeneChip Rat genome 230_2.0 arrays (Affymetrix, Santa Clara, California) according to the manufacturer's instructions. After scanning of the fluorescent GeneChip images with the Affymetrix GeneChip Scanner 3000, raw data image files (dat) were converted into cel-files. Finally, one intensity value per probe set was derived with Affymetrix Microarray Suite (MAS) 5.0. The GeneChip Rat genome 230_2.0 array comprises over 31,000 probe sets representing approximately 28,700 well-annotated rat genes. Using Genedata's Analyst, genes encoding mRNAs, whose levels were significantly changed, were selected separately for each rat strain using ANOVA based on the factor treatment (BHQ < 0.005 considered as significant), Student's t test ($p < .001$ considered as significant), and a 2-fold deregulation cutoff between treated and control groups. Ingenuity pathway analysis (IPA, Ingenuity Systems, www.ingenuity.com) was employed for pathway analysis.

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