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(54) **PREDICTIVE RENAL SAFETY BIOMARKERS AND BIOMARKER SIGNATURES TO MONITOR KIDNEY FUNCTION**

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(57) **ABSTRACT**

Biomarker signatures were identified which can be used to diagnose or predict kidney or liver toxicity and more specifically renal tubular toxicity as a consequence of disease or drug treatment.
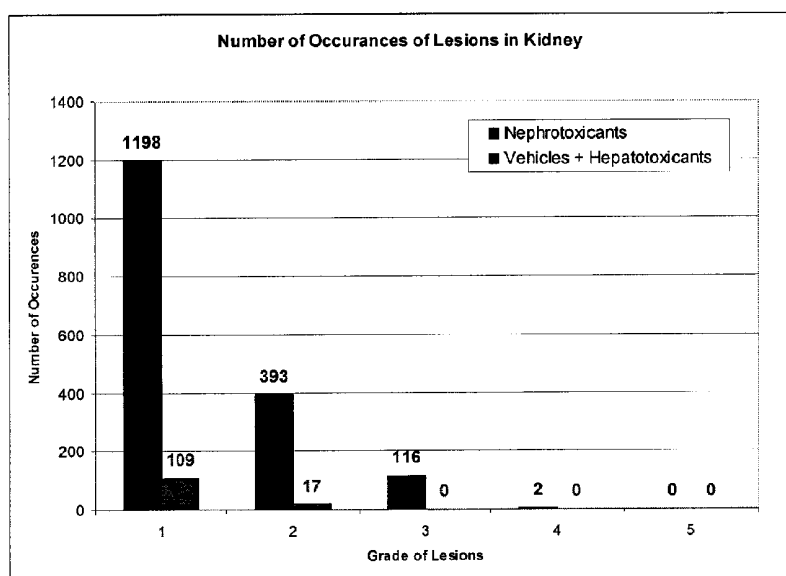
Nephrotoxicants

Compound	Tubul.	Glom.	Coll. D.	Mode of Toxicity
Gentamycin	x			Lysosomal phospholipidosis
Puromycin	x (2nd)	x		Damage to podocytes
Vancomycin	x	x		Oxidative stress (free radicals)
Doxorubicin	x (2nd)	x		Oxidative stress to glom. filtr. membrane
Furosemide	x			Mineralization
Lithium carbonate	x	(x)	(x)	Influences formation of intracellular cyclic adenosine monophosphate
Cisplatin	x	(x)	(x)	Direct DNA alkylation of DNA, Ox. stress
FK506	x	(x)		Complex (vasoconstrict., calcification...)

Hepatotoxicants

α-Naphthyisothiocyanate (ANIT)	Cholangitis
Methapyrilene	Hepatocarcinogen (upon chronic treatment)

FIG. 1

COMPOUNDS ADMINISTERED IN THE *IN VIVO* STUDIES

FIG. 2

NUMBER OF KIDNEY LESIONS REPORTED IN ALL 10 STUDIES

Primary Histopathology Process	Secondary Lesion	Structural Element / Segment	Nephrotoxicants						Controls						All					
			0	1	2	3	4	5	0	1	2	3	4	5	0	1	2	3	4	5
Tubular Cell Degeneration/Necrosis/Apoptosis	Necrosis	No precise localization possible	412	19	14	2	0	0	291	1	0	0	0	0	703	20	14	2	0	0
		Prox. convoluted tubule (PCT, s1-s2)	396	41	10	0	0	0	292	0	0	0	0	0	688	41	10	0	0	0
		Thick descending tubule (s3)	347	81	17	2	0	0	292	0	0	0	0	0	639	81	17	2	0	0
		Thick ascending tubule	406	36	5	0	0	0	292	0	0	0	0	0	698	36	5	0	0	0
		Distal convoluted tubule	445	2	0	0	0	0	292	0	0	0	0	0	737	2	0	0	0	0
		Collecting duct	429	17	1	0	0	0	292	0	0	0	0	0	721	17	1	0	0	0
	Apoptosis	No precise localization possible	443	4	0	0	0	0	290	2	0	0	0	0	733	6	0	0	0	0
		Prox. convoluted tubule (PCT, s1-s2)	431	15	1	0	0	0	291	1	0	0	0	0	722	16	1	0	0	0
		Thick descending tubule (s3)	443	3	1	0	0	0	291	1	0	0	0	0	734	4	1	0	0	0
		Thick ascending tubule	446	1	0	0	0	0	292	0	0	0	0	0	738	1	0	0	0	0
		Collecting duct	436	10	1	0	0	0	292	0	0	0	0	0	728	10	1	0	0	0
Tubular Cell Regeneration	Basophilia	No precise localization possible	373	54	11	1	9	0	258	34	0	0	0	0	631	88	11	1	9	0
		Prox. convoluted tubule (PCT, s1-s2)	370	50	16	10	0	1	283	8	1	0	0	0	653	58	17	10	1	0
		Thick descending tubule (s3)	352	46	32	17	0	0	290	1	0	0	0	0	642	47	32	17	0	0
		Thick ascending tubule	373	50	15	9	0	0	290	2	0	0	0	0	663	52	15	9	0	0
		Distal convoluted tubule	431	13	3	0	0	0	290	2	0	0	0	0	721	15	3	0	0	0
		Collecting duct	420	22	5	0	0	0	291	1	0	0	0	0	711	22	6	0	0	0
	Mitosis increase	No precise localization possible	445	2	0	0	0	0	292	0	0	0	0	0	737	2	0	0	0	0
		Prox. convoluted tubule (PCT, s1-s2)	419	26	2	0	0	0	292	0	0	0	0	0	711	26	2	0	0	0
		Thick descending tubule (s3)	413	33	1	0	0	0	292	0	0	0	0	0	705	33	1	0	0	0
		Thick ascending tubule	434	13	0	0	0	0	292	0	0	0	0	0	726	13	0	0	0	0
		Distal convoluted tubule	441	3	3	0	0	0	292	0	0	0	0	0	733	3	3	0	0	0
Tubular Cell Alterations	Hyaline droplet formation	No precise localization possible	446	1	0	0	0	0	292	0	0	0	0	0	738	1	0	0	0	0
		Prox. convoluted tubule (PCT, s1-s2)	399	36	11	1	0	0	290	2	0	0	0	0	682	43	13	1	0	0
		Thick descending tubule (s3)	424	18	5	0	0	0	292	0	0	0	0	0	716	18	5	0	0	0
		Thick ascending tubule	436	11	0	0	0	0	292	0	0	0	0	0	728	11	0	0	0	0
	Hypertrophy/Enlargement	No precise localization possible	439	8	0	0	0	0	292	0	0	0	0	0	731	8	0	0	0	0
		Prox. convoluted tubule (PCT, s1-s2)	415	18	5	9	0	0	292	0	0	0	0	0	707	18	5	9	0	0
		Thick descending tubule (s3)	411	22	12	2	0	0	292	0	0	0	0	0	703	22	12	2	0	0
		Loop of Henle	446	1	0	0	0	0	292	0	0	0	0	0	738	1	0	0	0	0
		Thick ascending tubule	437	10	0	0	0	0	292	0	0	0	0	0	729	10	0	0	0	0
		Distal convoluted tubule	445	2	0	0	0	0	292	0	0	0	0	0	737	2	0	0	0	0
		Collecting duct	417	20	9	1	0	0	292	0	0	0	0	0	709	20	9	1	0	0
	Cellular sloughing	No precise localization possible	428	16	3	0	0	0	292	0	0	0	0	0	720	16	3	0	0	0
		Prox. convoluted tubule (PCT, s1-s2)	425	22	0	0	0	0	292	0	0	0	0	0	717	22	0	0	0	0
		Thick descending tubule (s3)	416	26	5	0	0	0	292	0	0	0	0	0	708	26	5	0	0	0
		Thick ascending tubule	443	2	2	0	0	0	292	0	0	0	0	0	735	2	2	0	0	0
		Distal convoluted tubule	446	1	0	0	0	0	292	0	0	0	0	0	738	1	0	0	0	0
	Vacuolation	Prox. convoluted tubule (PCT, s1-s2)	417	27	3	0	0	0	289	3	0	0	0	0	706	30	3	0	0	0
		Thick descending tubule (s3)	439	7	1	0	0	0	292	0	0	0	0	0	731	7	1	0	0	0
		Thick ascending tubule	445	2	0	0	0	0	292	0	0	0	0	0	737	2	0	0	0	0
		Collecting duct	440	6	1	0	0	0	292	0	0	0	0	0	732	6	1	0	0	0
	Granular	Thick descending tubule (s3)	443	4	0	0	0	0	292	0	0	0	0	0	735	4	0	0	0	0
Intratubular Casts	Hyaline (proteinaceous, pigmented)	No precise localization possible	407	34	6	0	0	0	290	2	0	0	0	0	697	36	6	0	0	0
		Prox. convoluted tubule (PCT, s1-s2)	412	14	18	3	0	0	291	1	0	0	0	0	703	15	18	3	0	0
		Thick descending tubule (s3)	413	9	13	12	0	0	291	1	0	0	0	0	704	10	13	12	0	0
		Loop of Henle	401	30	12	4	0	0	292	0	0	0	0	0	693	30	12	4	0	0
		Thick ascending tubule	394	33	15	5	0	0	292	0	0	0	0	0	686	33	15	5	0	0
		Distal convoluted tubule	431	9	7	0	0	0	292	0	0	0	0	0	723	9	7	0	0	0
		Collecting duct	429	16	2	0	0	0	291	1	0	0	0	0	720	17	2	0	0	0
	Leukocytic	No precise localization possible	435	12	0	0	0	0	292	0	0	0	0	0	727	12	0	0	0	0
		Thick descending tubule (s3)	446	1	0	0	0	0	292	0	0	0	0	0	738	1	0	0	0	0
	Mineralization	Thick descending tubule (s3)	427	13	7	0	0	0	292	0	0	0	0	0	719	13	7	0	0	0
		Loop of Henle	445	2	0	0	0	0	292	0	0	0	0	0	737	2	0	0	0	0
		Thick ascending tubule	437	6	4	0	0	0	292	0	0	0	0	0	729	6	4	0	0	0
Tubular Dilatation	Tubular Dilatation	Cortex	371	19	59	18	0	0	288	1	3	0	0	0	659	20	62	18	0	0
		Medulla	372	18	47	9	1	0	288	0	4	0	0	0	660	18	51	9	1	0
		Papilla	426	17	4	0	0	0	292	0	0	0	0	0	718	17	4	0	0	0
	Tubular Cystic Dilatation / Tubular Cyst(s)	Cortex	446	0	0	1	0	0	292	0	0	0	0	0	738	0	0	1	0	0
		Medulla	445	1	0	1	0	0	291	1	0	0	0	0	736	2	0	1	0	0
Glomerular Alteration	Mesangial proliferation/expan	Glomerulus	407	33	7	0	0	0	292	0	0	0	0	0	699	33	7	0	0	0
	Glomerular Vacuolation	Glomerulus	433	13	1	0	0	0	292	0	0	0	0	0	725	13	1	0	0	0
Juxtaglomerular Apparatus Hypertrophy		Juxtaglomerular	417	18	12	0	0	0	292	0	0	0	0	0	709	18	12	0	0	0
Pelvis Dilatation		Pelvis	435	7	4	0	0	0	278	11	3	0	0	0	713	18	7	1	0	0
Inflammation	Interstitial, acute	Pelvis	447	0	0	0	0	0	291	1	0	0	0	0	738	1	0	0	0	0
	Interstitial, chronic	Cortex	391	56	0	0	0	0	270	20	2	0	0	0	661	76	2	0	0	0
		Medulla	438	9	0	0	0	0	292	0	0	0	0	0	730	9	0	0	0	0
		Pelvis	447	0	0	0	0	0	291	1	0	0	0	0	738	1	0	0	0	0
Fibrosis	Interstitial	Cortex	444	3	0	0	0	0	291	1	0	0	0	0	735	4	0	0	0	0
		Medulla	447	0	0	0	0	0	290	2	0	0	0	0	737	2	0	0	0	0
	Interstitial Bowman's capsule	Glomerulus	433	14	0	0	0	0	291	1	0	0	0	0	724	15	0	0	0	0
Concentric Lamellar Bodies		Cortex	439	8	0	0	0	0	290	2	0	0	0	0	729	10	0	0	0	0
		Medulla	447	0	0	0	0	0	291	1	0	0	0	0	738	1	0	0	0	0
		Papilla	446	1	0	0	0	0	292	0	0	0	0	0	738	1	0	0	0	0
Urothelial hypertrophy-hyperplasia		Papilla	446	1	0	0	0	0	292	0	0	0	0	0	738	1	0	0	0	0

FIG. 3

HISTOPATHOLOGY KIDNEY LESIONS

FIG. 5

RENAL HISTOPATHOLOGY MATRIX FOR THE CISPLATIN STUDY

Histopathology Finding	Count
acute coagulative necrosis	9
acute hepatocellular necrosis	1
apoptosis / single cell necrosis	13
bile duct degeneration / necrosis	19
bile duct hyperplasia	67
bile duct proliferation	2
biliary epithelial mitotic figures	5
capsular fibrosis / focal	2
capsular inflammation	1
capsular thickening	1
centrilobular hepatocellular atrophy	2
coagulative necrosis	1
congestion	4
extramedullary hematopoiesis	8
focal necrosis	55
glycogen content	112
glycogen depletion	31
granuloma(s)	9
hemorrhage	1
hepatocellular atrophy	7
hepatocellular hemosiderosis	7
hepatocellular hemosiderosis / focal	1
hepatocellular hemosiderosis / left papillary process	2
hepatocellular microvacuolation	2
hepatocellular vacuolation	10
increased mitotic figures	41
inflammation / necrosis	22
inflammation / necrosis / focal	4
mononuclear cell aggregation	88
periportal hepatocellular vacuolation	27
periportal inflammatory cell infiltration	18
perivascular inflammation	1
pigmented-laden macrophages	6
pigment-laden macrophages	1
portal edema	3
portal fibrosis	10
portal granulocyte infiltration	29
portal mononuclear cell infiltration	107
prominent bile duct nuclei	3
prominent hepatocellular nucleoli	54
prominent Kupffer cell	1
single cell necrosis	53
sinusoidal ectesia	1
subcapsular fibrosis	1
subcapsular necrosis	1

FIG. 5

HISTOPATHOLOGY LIVER LESIONS

Biomarker	Entitiy	Matrix	Pathology	AUC	Direct	N° Ctrls	N° Dis	Thr	Spec %	Sens %
Kim1	Protein	Urine	Proximal Tubular Damage	0.91 ± 0.02	+	283	132	1.87	95	79
Clusterin	Protein	Urine	Proximal Tubular Damage	0.88 ± 0.02	+	289	132	1.85	95	70
LCN2	Protein	Urine	Proximal Tubular Damage	0.75 ± 0.03	+	289	132	2.50	95	52
SPP1	Protein	Urine	Proximal Tubular Damage	0.71 ± 0.03	+	289	132	2.39	95	34
Timp1	Protein	Urine	Proximal Tubular Damage	0.73 ± 0.03	+	289	132	2.98	95	34
Calb1	Protein	Urine	Collecting Duct Damage / Regeneration	0.87 ± 0.03	+	291	52	1.93	95	46
Calb1	Protein	Urine	Juxtaglomerular Apparatus Hypertrophy	0.96 ± 0.02	-	292	30	0.35	95	87
B2-Microglob	Protein	Urine	Glomerular Alterations / Damage	0.89 ± 0.03	+	291	40	2.50	95	78
Total Protein	Protein	Urine	Glomerular Alterations / Damage	0.86 ± 0.04	+	291	40	1.50	95	78
Cystatin C	Protein	Urine	Glomerular Alterations / Damage	0.91 ± 0.03	+	291	40	2.00	95	80
NAG	Protein	Urine	Tubular Damage / Regeneration / Dilatation	0.79 ± 0.02	+	244	215	1.38	95	45
LDH	Protein	Urine	Tubular Damage / Regeneration / Dilatation	0.73 ± 0.02	+	244	215	2.10	95	38
Calcium	Protein	Urine	Tubular Mineralization	0.99 ± 0.01	+	292	20	1.59	95	100
Kim1	Protein	Blood	Proximal Tubular Damage	0.74 ± 0.03	+	266	119	2.27	95	13
LCN2	Protein	Blood	Proximal Tubular Damage	0.72 ± 0.03	+	289	132	2.54	95	31
SPP1	Protein	Blood	Intratubular Hayline Casts (proteinaceous, pigmented)	0.84 ± 0.03	+	290	82	1.24	95	63
SPP1	Protein	Blood	Thick Ascending Tubular Damage / Regeneration	0.83 ± 0.03	+	290	84	1.24	95	61
Cystatin C	Protein	Blood	Glomerular Alterations / Damage or Tubular Damage/ Regeneration / Dilatation	0.81 ± 0.02	+	244	224	1.22	95	54
Cystatin C	Protein	Blood	Proximal Tubular Damage	0.89 ± 0.02	+	289	132	1.23	95	64
Cystatin C	Protein	Blood	Glomerular Alterations / Damage	0.89 ± 0.03	+	291	40	1.23	95	75
B2-Microglob	Protein	Blood	Proximal Tubular Damage	0.81 ± 0.02	+	289	132	1.62	95	39
Total Protein	Protein	Blood	Glomerular Alterations / Damage	0.99 ± 0.01	-	291	40	0.93	95	95
Albumin	Protein	Blood	Glomerular Alterations / Damage	0.98 ± 0.02	-	291	40	0.91	95	88
ALP	Protein	Blood	Glomerular Alterations / Damage	0.95 ± 0.02	-	291	40	0.71	95	73
Natrium	Ion	Blood	Distal Tubular Damage / Regeneration	0.88 ± 0.05	-	290	22	0.98	95	64
Natrium	Ion	Blood	Tubular Mineralization	0.95 ± 0.04	-	292	20	0.98	95	75
Kim1	mRNA	Kidney	Proximal Tubular Damage	0.99 ± 0.01	+	289	132	3.34	95	98
Clusterin	mRNA	Kidney	Proximal Tubular Damage	0.93 ± 0.02	+	281	132	1.52	95	77
SPP1	mRNA	Kidney	Proximal Tubular Damage	0.93 ± 0.02	+	289	132	2.66	95	78
Timp1	mRNA	Kidney	Proximal Tubular Damage	0.91 ± 0.02	+	289	132	1.84	95	75
LCN2	mRNA	Kidney	Proximal Tubular Damage	0.87 ± 0.02	+	289	132	4.10	95	70
VEGF	mRNA	Kidney	Proximal Tubular Damage	0.82 ± 0.02	-	289	132	0.85	95	58
EGF	mRNA	Kidney	Proximal Tubular Damage	0.88 ± 0.02	-	289	132	0.80	95	70
CYR61	mRNA	Kidney	Tubular Damage / Regeneration / Dilatation	0.79 ± 0.02	+	244	215	1.82	95	52
Calb1	mRNA	Kidney	Juxtaglomerular Apparatus Hypertrophy	1.00 ± 0.00	-	292	30	0.62	95	100
Cystatin C	mRNA	Kidney	Glomerular Alterations / Damage	0.94 ± 0.03	+	291	40	1.29	95	75
KIM1	mRNA	Kidney	Tubular Damage / Regeneration / Dilatation	0.87 ± 0.02	+	244	215	2.90	95	78
Clusterin	mRNA	Kidney	Tubular Damage / Regeneration / Dilatation	0.82 ± 0.02	+	244	215	1.45	95	59
EGF	mRNA	Kidney	Tubular Damage / Regeneration / Dilatation	0.83 ± 0.02	-	244	215	0.80	95	59
Creatinine	Molecule	Blood	Proximal Tubular Damage	0.73 ± 0.03	+	289	132	1.15	95	40
Creatinine	Molecule	Blood	Glomerular Alterations / Damage	0.53 ± 0.05	-	291	40	0.95	95	33
Creatinine	Molecule	Blood	Tubular Damage / Regeneration / Dilatation	0.70 ± 0.02	+	244	215	1.15	95	31
Creatinine	Molecule	Blood	Glomerular Alterations / Damage or Tubular Damage/ Regeneration / Dilatation	0.71 ± 0.02	+	244	224	1.15	95	30
Creatinine	Molecule	Blood	Collecting Duct Damage / Regeneration	0.85 ± 0.03	+	291	52	1.15	95	52
Creatinine	Molecule	Blood	Distal Tubular Damage / Regeneration	0.83 ± 0.05	+	290	22	1.15	95	50
Creatinine	Molecule	Blood	Thick Ascending Tubular Damage / Regeneration	0.77 ± 0.03	+	290	84	1.15	95	43
Creatinine	Molecule	Blood	Juxtaglomerular Apparatus Hypertrophy	0.75 ± 0.05	+	292	30	1.15	95	13
Creatinine	Molecule	Blood	Tubular Mineralization	0.90 ± 0.05	+	292	20	1.15	95	30
Creatinine	Molecule	Blood	Intratubular Hayline Casts (proteinaceous, pigmented)	0.67 ± 0.04	+	290	82	1.15	95	43
BUN	Molecule	Blood	Proximal Tubular Damage	0.79 ± 0.03	+	289	132	1.20	95	51
BUN	Molecule	Blood	Glomerular Alterations / Damage	0.80 ± 0.04	+	291	40	1.20	95	55
BUN	Molecule	Blood	Tubular Damage / Regeneration / Dilatation	0.70 ± 0.02	+	244	215	1.20	95	40
BUN	Molecule	Blood	Glomerular Alterations / Damage or Tubular Damage/ Regeneration / Dilatation	0.70 ± 0.02	+	244	224	1.20	95	39
BUN	Molecule	Blood	Collecting Duct Damage / Regeneration	0.58 ± 0.04	+	291	52	1.20	95	38
BUN	Molecule	Blood	Distal Tubular Damage / Regeneration	0.73 ± 0.06	+	290	22	1.20	95	41
BUN	Molecule	Blood	Thick Ascending Tubular Damage / Regeneration	0.86 ± 0.03	+	290	84	1.20	95	60
BUN	Molecule	Blood	Juxtaglomerular Apparatus Hypertrophy	0.62 ± 0.06	+	292	30	1.20	95	10
BUN	Molecule	Blood	Tubular Mineralization	0.84 ± 0.06	+	292	20	1.20	95	45
BUN	Molecule	Blood	Intratubular Hayline Casts (proteinaceous, pigmented)	0.80 ± 0.03	+	290	82	1.20	95	55

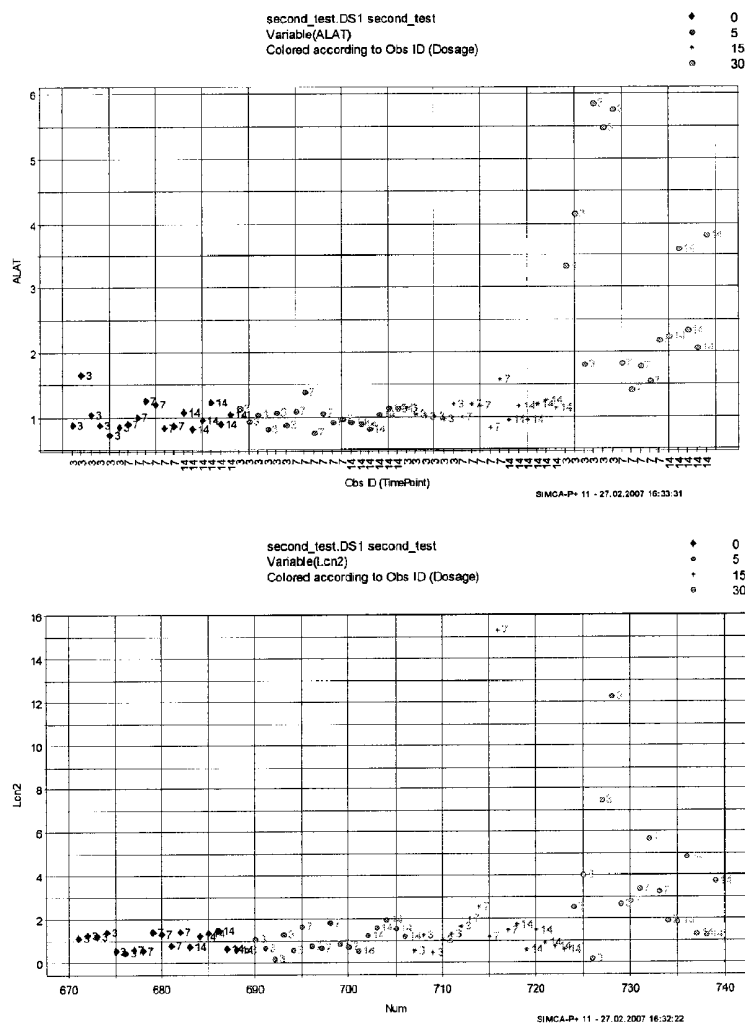## FIG. 6

RESULTS OF THE ROC ANALYSIS FOR BIOMARKERS

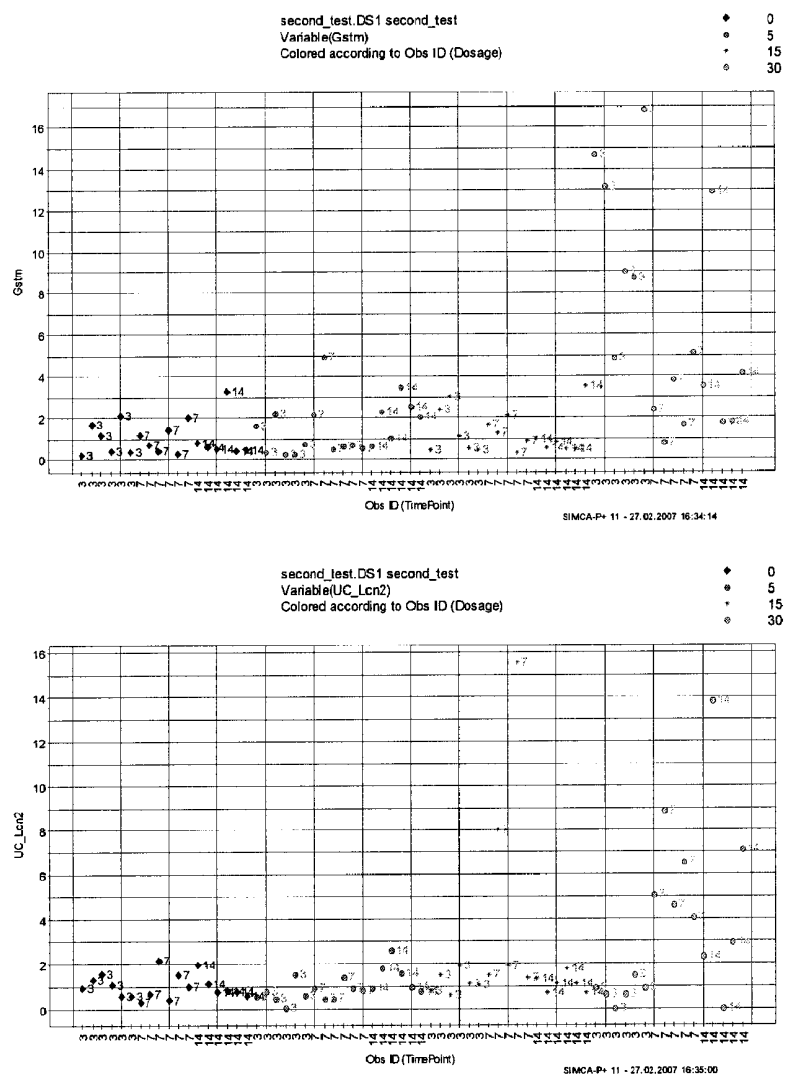FIG. 7A

HEPTATOXICITY BY DIFFERENT PROTEIN BIOMARKERS

FIG. 7B
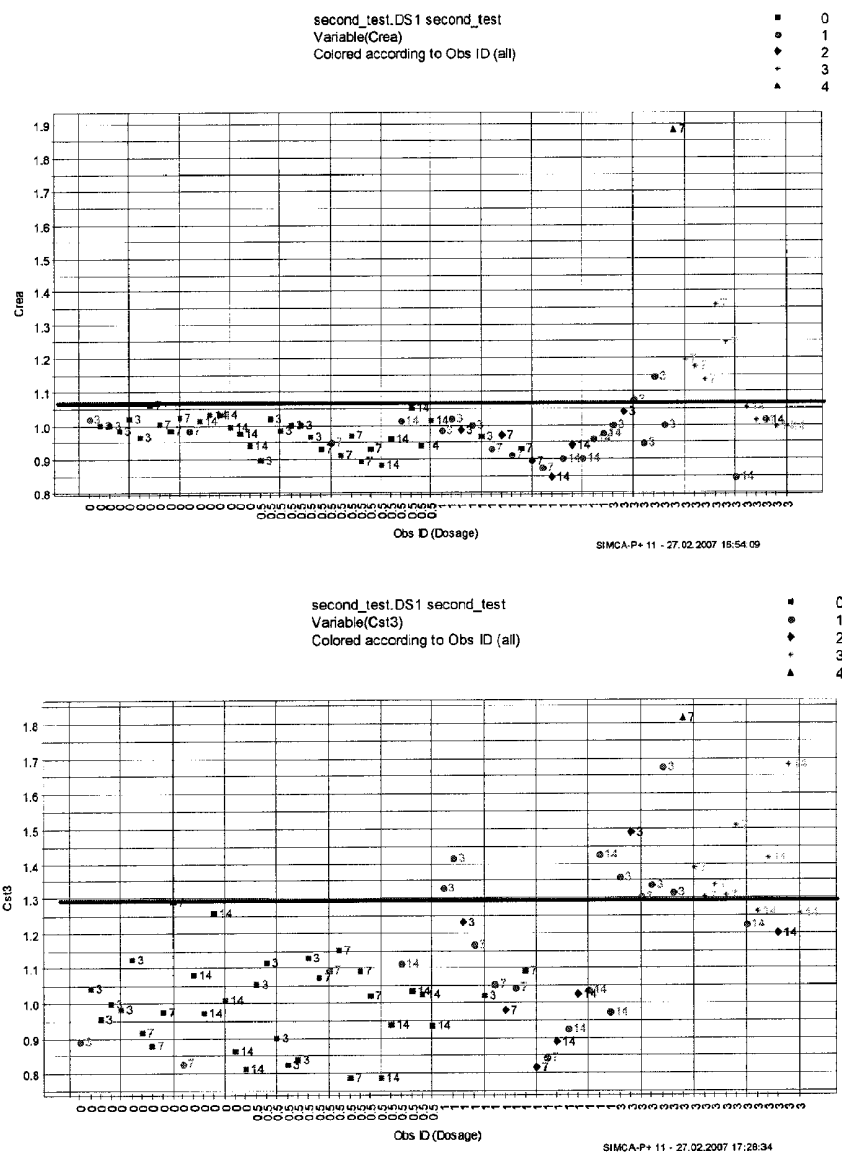
HEPTATOXICITY BY DIFFERENT PROTEIN BIOMARKERS

second_test.DS1 second_test
Variable(Crea)
Colored according to Obs ID (all)

■ 0
o 1
♦ 2
+ 3
▲ 4

Crea

Obs ID (Dosage)

SIMCA-P+ 11 - 27.02.2007 16:54 09

second_test.DS1 second_test
Variable(Cst3)
Colored according to Obs ID (all)

■ 0
● 1
♦ 2
+ 3
▲ 4

Cst3

Obs ID (Dosage)

SIMCA-P+ 11 - 27.02.2007 17:28:34

FIG. 8A

KIDNEY INJURY BY DIFFERENT PROTEIN BIOMARKERS AND

CLINICAL CHEMISTRY PARAMETERS

second_test.DS1 second_test
Variable(UC_Kim1)
Colored according to Obs ID (all)

■	0
●	1
◆	2
٭	3
▲	4

Obs ID (Dosage)

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Variable(UC_Lcn2)
Colored according to Obs ID (all)

■	0
●	1
◆	2
٭	3
▲	4

Obs ID (Dosage)

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FIG. 8B

KIDNEY INJURY BY DIFFERENT PROTEIN BIOMARKERS AND CLINICAL CHEMISTRY PARAMETERS
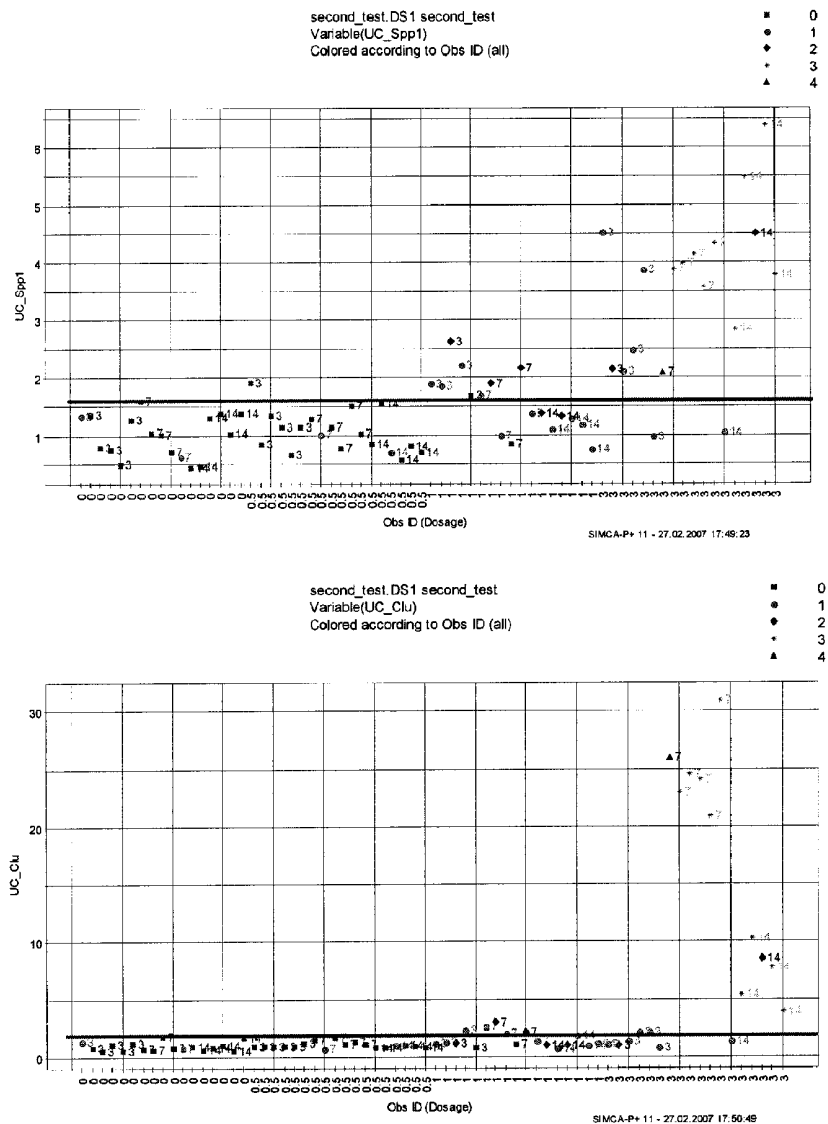
FIG. 8C

KIDNEY INJURY BY DIFFERENT PROTEIN BIOMARKERS AND
CLINICAL CHEMISTRY PARAMETERS
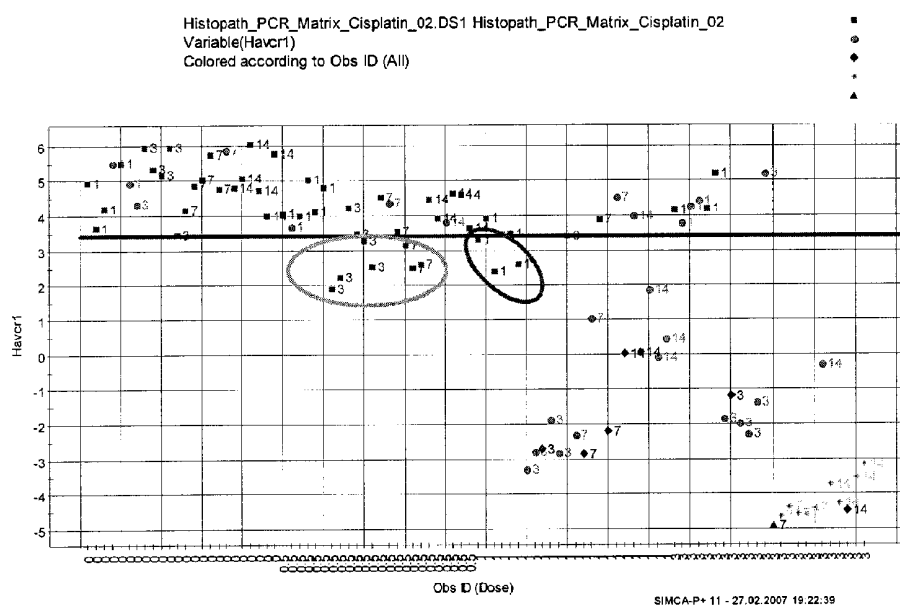
FIG. 9A

KIDNEY INJURY BY TRANSCRIPTION OF DIFFERENT GENES -

ASSAY OF mRNA FROM KIDNEY
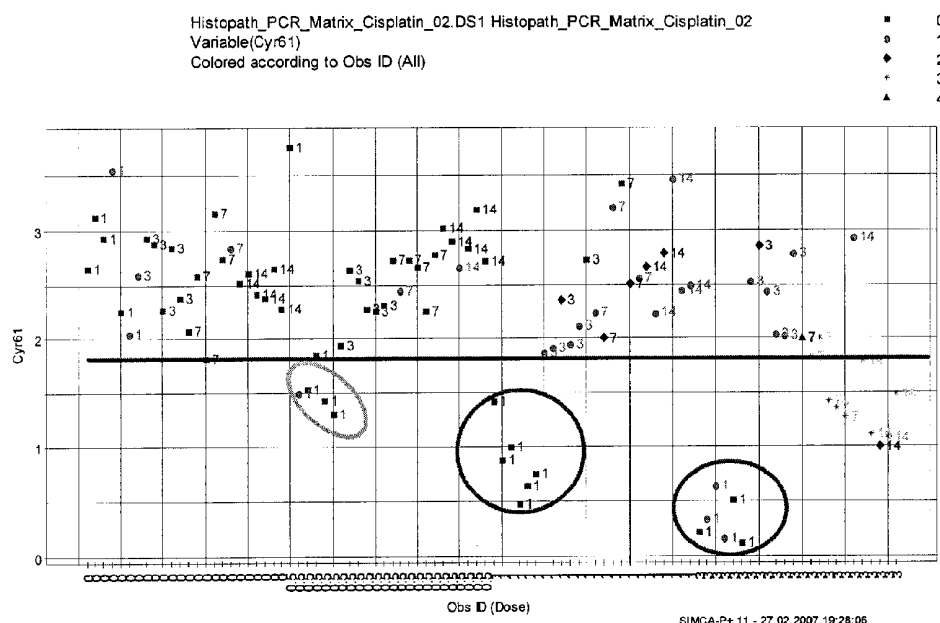
FIG. 9B

KIDNEY INJURY BY TRANSCRIPTION OF DIFFERENT GENES -

ASSAY OF mRNA FROM KIDNEY

PREDICTIVE RENAL SAFETY BIOMARKERS AND BIOMARKER SIGNATURES TO MONITOR KIDNEY FUNCTION

FIELD OF THE INVENTION

[0001] The invention relates to biomarker signatures and their use in methods and devices for the monitoring, prognosis, diagnosis, and/or treatment of kidney or liver toxicity, and more specifically renal tubular toxicity as a consequence of disease or drug treatment.

BACKGROUND OF THE INVENTION

[0002] Progression to end-stage renal failure is the final common pathway of various proteinuric nephropathies. The degree of proteinuria is associated with the rate of progression of renal disease.

[0003] In human proteinuric diseases, tubulointerstitial injury is a better predictor of renal function decline than is glomerular damage. Filtered tubulotoxic plasma proteins are believed to be responsible for this association, although the nature of these proteins is uncertain. Filtered proteins partly exert their detrimental effects via activation of proximal tubular cells (PTC), which excrete chemokines and cytokines, resulting in inflammation, myotransformation of interstitial fibroblasts, fibrosis, and apoptosis. This ultimately leads to end-stage renal failure. Renal tubular epithelial cells are therefore considered to be crucial in the progression of interstitial damage. Proteinuria has been proposed to cause tubular injury and interstitial fibrosis.

[0004] There is a continuing need in the art for determining and monitoring the kidney and liver function in animals and man after drug treatment or when kidney function is impaired due to a disease.

SUMMARY OF THE INVENTION

[0005] The invention provides tests and devices to diagnose or predict the state, function and integrity of kidney and liver. The biomarkers of the invention, other clinical chemistry parameters or combinations thereof can be converted into an assay, test or device to diagnose the status of kidney or liver, to monitor adverse events such as drug-induced nephrotoxicity or hepatotoxicty, to adapt treatment regimens of drugs on the basis of the status of kidney or liver, or to develop a clinical test for the diagnosis of disease in kidney or liver or the prevalence of it.

[0006] The invention makes possible the prediction, classification, correlation and diagnosis of kidney or liver toxicity based on the data presented herein.

[0007] Also described herein are animal studies, in which different model nephrotoxicants and hepatotoxicants were administered to the animals using different dosing regimens. Different biological samples were sampled from the animals at different time points. Urine, blood, organ tissues, mRNA from organ tissues and blood were sampled at different time points and in different treatment groups. The animals were assessed during the in vivo period and afterwards using different methods, in particular using clinical observations, in vivo data (such as body weight, food consumption, macroscopic and microscopic examinations of organs (in particular, kidney and liver).

BRIEF DESCRIPTION OF THE DRAWINGS

[0008] The drawing figures depict preferred embodiments by way of example, not by way of limitations.

[0009] FIG. 1 is a list of the compounds administered to the animals in the in vivo studies.

[0010] FIG. 2 shows the number of kidney lesions, which were reported in all 10 studies. The numbers are sub-divided by grade and by treatment groups (nephrotoxicant-treated animals versus vehicle- and hepatotoxicant-treated animals).

[0011] FIG. 3 is a table showing the histopathology kidney lesions that were reported in the 10 in vivo studies. The number of occurrences are listed categorized by grade and by treatment groups (nephrotoxicant-treated versus vehicle- and hepatotoxicant-treated).

[0012] FIG. 4 is a renal histopathology matrix for the cisplatin study. Each column represents a localized lesion. Each row corresponds to an animal, whereby the animals are ordered by dose-group (controls, low-dosed, mid-dosed, and high-dosed) and within each dose-group by termination time-point. If a lesion was reported, the grade is represented by an orange box with the corresponding grade in it (grade 1, grade 2-5, no report/grade 0). Dominating processes are labeled.

[0013] FIG. 5 is a table showing the histopathology liver lesions that were reported in the 10 in vivo studies. The number of occurrences is listed.

[0014] FIG. 6 is a table showing the results of the receiver operator characteristic (ROC) analysis for biomarkers and current standards for certain pathologies. Column 1 represents the biomarker, column 2 the molecular entity, column three the medium, in which the biomarker was measured and column 4 the pathology for which the ROC analysis was performed. Column 5 represents the AUCs and the standard error thereof. Column 6 indicates if a biomarker value increases with the presence of the corresponding pathology (+) or decreases (–). Columns 7 and 8 display the numbers of animals used for the corresponding analyses. Column 11 shows the corresponding sensitivity for 95% specificity (column 10) and column 9 the corresponding threshold of the biomarker. Besides of the biomarkers of interest, also the results for the current standards BUN and serum creatinine are shown for the 10 pathologies of interest. This table demonstrates the use and performance of implementations of devices, assays, diagnostic test or diagnostic kits of the listed specific biomarkers to monitor the listed specific renal pathologies.

[0015] FIG. 7 is a set of scatter plots showing an assessment of hepatotoxicity by different protein biomarkers. The biomarkers were obtained from animals to which vehicle or different doses of the hepatotoxicant ANIT (alpha-naphtyl-isothiocyanate) was administered. In this study dose-related histopathology findings in the liver but not in the kidney were observed. In the plots the relative concentration levels (fold changes versus controls) are shown. The dose-levels are represented by the different color shadings, the time points of sampling are represented by the labels. The biomarker levels correlate well with the dose and thus with the dose-related hepatotoxicity. The biomarkers represented in these plots are ALAT measured in plasma (FIG. 7A top), lipocalin-2 mea-

sured in plasma (FIG. 7A bottom), GST-mu measured in plasma (FIG. 7B top) and lipocalin-2 measured in urine (FIG. 7B bottom).

[0016] FIG. 8 is a set of scatter plots showing an assessment of kidney injury by different protein biomarkers and clinical chemistry parameters. The biomarkers were obtained from animals to which vehicle or different doses of the nephrotoxicant cisplatin were administered. In the plots the relative concentration levels (fold changes versus controls) are shown. The dose-levels are represented as labels of the x-axis, the time points of sampling are represented by as labels of the samples. The samples are color shaded by the highest grade of histopathology finding observed in kidney. The horizontal bar indicates the highest biomarker level observed for case control animals (vehicle dosed animals without histopathology finding in kidney). Protein levels higher than the bar are significantly increased (100% specificity for case controls). The different clinical parameters and proteins detect kidney injury with different sensitivity. Creatinine measured in serum, which is the current standard peripheral test for kidney injury and kidney function, is the least sensitive method (FIG. 8A top). Cystatin C measured in plasma (FIG. 8A bottom), Kim-1 measured in urine (FIG. 8B top), lipocalin-2 measured in urine (FIG. 8B bottom), osteopontin measured in urine (FIG. 8C top) and clusterin measured in urine (FIG. 8C bottom) identify more animals with significant kidney findings.

[0017] FIG. 9 is a set of scatter plots showing an assessment of kidney injury by transcription of different genes in mRNA from kidney. The biomarkers were obtained from animals to which vehicle or different doses of the nephrotoxicant cisplatin were administered. In the plots the expression values (Ct values referenced to Polr2g) are shown. The dose-levels are represented as labels of the x-Axis, the time points of sampling are represented by as labels of the samples. The samples are color shaded by the highest grade of histopathology finding observed in kidney. The horizontal bar indicates the highest expression (lowest value in the plot) observed for control animals. Values below the bar correspond to significantly increased expression levels (100% specificity for non-dosed animals). Both Kim-1 (FIG. 9A) and Cyr61 (FIG. 9B) can detect kidney injury earlier (at earlier time points) and in a more sensitive way (at lower dose levels) than histopathological examination.

DETAILED DESCRIPTION OF THE INVENTION

[0018] Definitions. As used herein the expression "renal toxicity" or "renal injury" or similarly "kidney disorder" shall all mean a renal or kidney failure or dysfunction either sudden (acute) or slowly declining over time (chronic), that may be triggered by a number of disease or; disorder processes, including (but not limited to) for acute renal toxicity: sepsis I (infection), shock, trauma, kidney stones, kidney infection, drug toxicity, poisons or toxins, or after injection with an iodinated contrast dye (adverse effect); and for chronic renal toxicity: long-standing hypertension, diabetes, congestive heart failure, lupus, or sickle cell anemia. Both forms of renal failure result in a life-threatening metabolic derangement.

[0019] The expression "body samples" shall include but is not limited to biopsies, preferably of the kidney, and body fluids such as blood, plasma, serum, lymph, cerebrospinal fluid, cystic fluid, ascites, urine, stool and bile. One advantage of the invention is that one marker can be particularly well

monitored in body fluids, such as plasma or urine. For instance, level of expression of clusterin can be particularly well determined in plasma.

[0020] As used herein the term "individual" shall mean a human person, an animal, such as mouse or rat, or a population or pool of individuals.

[0021] As used herein, the term "candidate agent" or "drug candidate" can be natural or synthetic molecules such as proteins or fragments thereof, antibodies, small molecule inhibitors or agonists, nucleic acid molecules, organic and inorganic compounds and the like.

[0022] General methods. In practicing the invention, many conventional techniques in molecular biology, microbiology, and recombinant DNA are used. These techniques are well known and are explained in, for example, *Current Protocols in Molecular Biology, Volumes I, II, and III*, 1997 (F. M. Ausubel ed.); Sambrook et al., *Molecular Cloning: A Laboratory Manual, Second Edition* (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989); *DNA Cloning: A Practical Approach, Volumes I and II*, D. N. Glover ed. (1985); *Oligonucleotide Synthesis*, M. L. Gait ed. (1984); Hames & Higgins, *Nucleic Acid Hybridization*, (1985); *Transcription and Translation*, Hames & Higgins eds. (1984); *Animal Cell Culture*, R. I. Freshney ed. (1986); *Immobilized Cells and Enzymes*, (IRL Press, 1986); Perbal, *A Practical Guide to Molecular Cloning*; the series, *Methods in Enzymology* (Academic Press, Inc., 1984); *Gene Transfer Vectors for Mammalian Cells*, J. H. Miller & M. P. Calos eds. (Cold Spring Harbor Laboratory, 1987); and *Methods in Enzymology* Vol. 154 and Vol. 155 (Wu & Grossman, and Wu, eds., respectively).

[0023] All references cited herein are incorporated herein by reference in their entirety and for all purposes to the same extent as if each individual publication or patent or patent application was specifically and individually indicated to be incorporated by reference in its entirety for all purposes. In addition, all GenBank accession numbers, Unigene Cluster numbers and protein accession numbers cited herein are incorporated herein by reference in their entirety and for all purposes to the same extent as if each such number was specifically and individually indicated to be incorporated by reference in its entirety for all purposes.

[0024] Biomarkers of the invention. The genomic and protein expressions of several biomarkers (listed in TABLES 1 and 2) in kidney tissues was measured. The course of the related protein in urine and plasma was also measured. A correlation of genomic or protein expression in tissue, urine and plasma concentration was made with histopathology and with urinalysis parameters such as proteinuria (TABLE 2) and plasma clinical chemistry parameters (see TABLE 2) such as creatinine, blood urea nitrogen (BUN) and creative clearance. The question that was investigated was whether urinary renal biomarkers reflect renal tissue damage and possibly kidney function.

[0025] TABLE 1 provides a list of biomarkers assessed on a transcription level (mRNA from kidney and liver) and on a protein level (in urine and blood). The measurements of these biomarkers in TABLE 1, described further below.

TABLE 1

List of Biomarkers Assessed on a Transcription Level and on a Protein Level

Name	mRNA	Protein	Swissprot Nbr	Gene Symbol
β-2-microglobulin	no	yes	P07151	B2m
N-acetyl-beta-glucosaminidase, Beta-hexosaminidase alpha chain, NAG	no	yes	Q641X3	Hexa
Alpha Glutathione-S-transferase (alpha-GST)/ Glutathione S-transferase alpha 5	yes	yes	P46418	Gsta5
Calbindin d28	yes	yes	P07171	Calb1
Clusterin	yes	yes	P05371	Clu
Cystatin C	yes	yes	P14841	Cst3
Cysteine-rich protein-61 (CYR61)	yes	yes	Q9ES72	Cyr61
Epidermal growth factor (EGF)	yes	yes	P07522	Egf
Glutathione S-transferase Mu 1, GST Yb1, mu GST	yes	yes	P04905	Gstm1
Kidney Injury Molecule-1, Hepatitis A virus cellular receptor 1 homolog, Kim-1	yes	yes	O54947	Havcr1 or Kim1
Neutrophil gelatinase-associated lipocalin, HNL, Lipocalin 2	yes	yes	P30152	Lcn2
Osteopontin, Secreted phosphoprotein 1	yes	yes	P08721	Spp1 or 2b7
Podocin	yes	yes	Q8K4G9	Nphs2
Metalloproteinase inhibitor 1, TIMP-1	yes	yes	P30120	Timp1
VEGF/Vascular endothelial growth factor A	yes	yes	P16612	VEGF of VEGF-A

[0026] Among the biomarkers of the invention are the following:

[0027] Calbindin D-28k is a calcium-binding protein member of the large EF-hand family. Calbindin D-28k is present in all classes of vertebrates and in a wide range of tissues. Several researchers have shown that in the kidney highest amounts of Calbindin D-28k are localized in the distal tubule, which correlates with the role of the distal tubule as the site of calcium absorption. Rhoten W B et al., *Anat. Rec.* 227:145-151; Borke J L et al., *Am. J. Physiol. (Renal Fluid Electrolyte Physiol)* 257: F842-F849 26 (1989). Furthermore, it has been shown that the decreased expression of calbindin D-28k with age may contribute to the age-related decrease in Ca^{++} transport in intestine and kidney. Armbrecht H J et al., *Endocrinology* 125: 2950-2956 (1989). Cyclosporine A-induced decrease in rat renal calbindin-D 28k protein is a consequence of a decrease in its mRNA. Grenet O et al., *Biochem. Pharmacol.* 55(7): 1131-1133 (1998); Grenet O et al., *Biochem. Pharmacol.* 59(3): 267-272 (2000).

[0028] Clusterin, also known as testosterone-repressed prostate message 2 (TRPM-2) is an ubiquitous, secreted glycoprotein induced in many organs, including the kidney, at times of tissue injury and/or remodeling, and it has been found in the tubular lumen of epithelial ducts. Jenne D E & Tschopp J, *Trends Biochem. Sci.* 14: 154-159 (1992). Clusterin may preserve cell interactions that are otherwise perturbed by renal insults. Silkensen J R et al., *J. Am. Soc. Nephrol.* 8(2): 302-305 (1997). Furthermore, cyclosporine A (CsA) increases clusterin mRNA levels in the rat kidney. Darby I A et al., *Exp. Nephrol.* 3(4): 234-239 (1995).

[0029] Epidermal growth factor (EGF) is a small polypeptide belonging to a class of molecules that can mediate cell growth, differentiation, and acute phase responses. EGF mRNA is transcribed primarily in cells of the kidney. In a variety of experimentally induced forms of acute renal failure, the mRNA and protein levels for kidney EGF fall markedly and remain low for a prolonged period. Price P M et al., *Am J Physiol.* 268(4 Pt 2): F664-670 (1995). Furthermore, EGF is believed to play a major role in renal tubular regen-

eration after ischemic injury to the kidney (Di Paolo S, et al., *Nephrol Dial Transplant* 2: 2687-2693 (1997)) and in renal tissue repair after drug-induced nephrotoxicity (Morin N J et al., *Am. J. Physiol.* 263: F806-F811 (1992). EGF expression levels have been shown to be markedly reduced in renal transplantation patients suffering from chronic rejection or drug-induced nephrotoxicity. In addition, decreases in EGF expression in the kidney following cyclosporine A (CsA) treatment have been reported. Deng J T et al., *Transplant Proc.* 26(5): 2842-2844; Yang C W, et al., *Kindey Int.* 60: 847-857 (2001).

[0030] Kidney injury molecule-1 (Kim-1) is a type 1 membrane protein containing an extracellular, six-cysteine immunoglobulin domain. Kim-1 mRNA and protein are expressed at a low, almost undetectable, level in normal kidney but are increased dramatically in proximal tubules in the postischemic kidney Kim-1 is implicated in the restoration of the morphological integrity and function to post-ischemic kidneys. Ichimura T et al., *J. Biol. Chem.* 273: 4135-4142 (1998). Kim-1 is sometimes described as "Havcr1". The early and abundant tubular expression following different types of injury makes Kim-1 a specific marker of tubular cell injury that may be linked to recuperative or damaging mechanisms that directs the process of interstitial damage. See WO 2004/005544, incorporated herein by reference.

[0031] Alpha-2u globulin related-protein (Alpha-2u), also known as lipocalin 2 (LCN2) or neutrophil gelatinase-associated lipocalin (NGAL) in humans, is stored in granules of neutrophils. It binds to small lipophilic substances and is believed to have a role in inflammation. Bundgaard J R et al., *Biochem. Biophys. Res. Commun.* 202: 1468-1475 (1994); Cowland J B & Borregaard N, *Genomics* 45: 17-23 (1997); Zerega B et al., *Eur. J. Cell Biol.* 79, 165-172 (2000).

[0032] Osteopontin (OPN), also known as secreted phosphoprotein 1 (SPP1), is a secreted, highly acidic and glycosylated phosphoprotein containing an arginine-glycine-aspartic acid (RGD) cell adhesion motif. OPN up-regulation has been demonstrated in several models of renal injury, suggesting a possible role in tissue remodeling and repair.

Persy V P et al., *Kidney Int.* 56(2): 601-611 (1999). Osteopontin was also found to be a major component of urinary calcium oxalate stones. Kohri K et al., *Biochem. Biophys. Res. Commun.* 84: 859-864 (1992). Furthermore, OPN is highly expressed in distal tubular cells in rats prone to urinary stone formation. Kohri K et al., *J. Biol. Chem.* 268: 15180-15184 (1993).

[0033] Podocin, also known as PDCN, SRN1, nephrosis 2, idiopathic, is a protein expressed in renal podocytes and plays a role in the regulation of glomerular permeability. It is almost exclusively expressed in the podocytes of fetal and mature kidney glomeruli. Mutations of podocyte proteins, e.g. podocin, result in congenital focal segmental glomerulosclerosis. Komatsuda A et al., *Ren. Fail.* 25(1): 87-93 (2003)) and is mainly implicated in steroid-resistant nephrotic syndrome.

[0034] Vascular Endothelial Growth Factor (VEGF) is known to promote angiogenesis, increase vascular permeability, serve as a chemotactic for monocytes, and has a role in diabetes, wound healing, inflammatory responses, and tissue remodeling. Benjamin L E, *Am J Pathol.* 158: 1181-1184 (2001).

[0035] As each marker can be linked to different renal pathological findings, it is possible to identify gene expression products of such markers that are particularly linked to a renal pathology. For instance, the calbindin-D28k level is used as an early marker for calcium disturbance predictor for mineralization. The Kim-1 level is a marker for general kidney insult. The OPN level is an early marker for macrophage infiltration often associated with kidney toxicity and a marker for tissue remodeling upon renal injury. The EGF level is an early marker for general kidney toxicity. The clusterin level is an early marker for immune-mediated kidney toxicity.

[0036] TABLE 2 provides a list of parameters from clinical chemistry determined in urine and in blood. The measurements of these biomarkers in TABLE 2, described further below.

TABLE 2

List of Parameters from Clinical Chemistry

Urine Parameters	Blood Parameters
Calcium (Ca++)	Albumin (ALB)
Chloride (Cl–)	Albumin/globulin ratio (A/G)
Creatinine (CREAT)	Alkaline phosphatase (ALP)
Creatinine clearance (CLEAR)	Alanine Aminotransferase (ALAT)
Inorganic phosphorus (I. PHOS)	Aspartate Aminotransferase (ASAT)
Lactate dehydrogenase (LDH)	Calcium (Ca++)
Magnesium (Mg++)	Chloride (Cl–)
Potassium (K+)	Creatinine (CREAT)
Sodium (Na+)	Glucose (GLUC)
Specific gravity (SP. GRAV)	Inorganic phosphorus (I. PHOS)
Total proteins (PROT)	Lactate dehydrogenase (LDH)
Urea (UREA)	Magnesium (MAGN)
Volume (VOLUME)	Potassium (K+)
Color (COLOR)	Sodium (Na+)
Appearance (APP)	Total bilirubin (TOT. BIL)
	Total cholesterol (CHOL)
	Total proteins (PROT)
	Triglycerides (TRIG)
	Urea (UREA)

[0037] Results of in vivo studies and histopathology. All 10 rat in vivo studies were successfully conducted. Sufficient urine could be collected from nearly all animals terminated at day 3, 7, 14, 21 and 22. Only animals, for which complete datasets (histopathology of kidney, urinary clinical chemistry, urinary protein biomarkers, clinical chemistry of blood,

plasma protein biomarkers, mRNA biomarkers in kidney) were available were analyzed and are reported here. In total, data from 739 animals were analyzed, including 447 animals treated with nephrotoxicants, 188 animals treated with vehicles and 104 animals treated with hepatotoxicants. For nine samples, no urinary Kim-1 measurements were available; for 84 samples no blood Kim-1 measurements were available. Those samples were excluded for the Kim-1 analyses but were included for the analyses of other parameters and biomarkers.

[0038] In FIG. 2, the distributions of grades of the histopathology assessment are shown. The predominance of grade 1 and grade 2 findings and the absence of grade 5 lesions indicate that the goal of inducing mainly mild nephrotoxicity has been achieved. The considerable number of grade 1 and some grade 2 findings in the vehicle-dosed and the hepatotoxicant-dosed animals indicates the level of sensitivity of the histopathology assessment performed in this project. No significant dose-dependent nephrotoxicity was induced by the hepatotoxicants. In FIG. 3 a detailed list of all reported localized lesions, including the number of occurrences for each grade, separated by nephrotoxicant-dosed animals and the control animals (vehicle-dosed and hepatotoxicant-dosed) is shown. Seventy-five different localized finding were observed.

[0039] The different types of lesions were usually not observed in an isolated fashion, but typically in a highly correlated manner representing different molecular processes. In FIG. 4, all histopathology findings are shown for the cisplatin study. The processes do not affect single isolated segments of the nephron, but several segments in a correlated way (e.g. proximal tubules and descending straight tubules). In addition, a logical sequence of molecular processes along the dose- and time-ordered animals can be observed. Necrosis as a consequence of damage is seen, and then regeneration processes such as basophilia and mitosis are seen, whereas secondary processes occur in parallel (e.g., enlargement of tubules, tubular dilatation, cellular sloughing, etc.).

[0040] For the qualification of biomarkers there are two consequences: First, an appropriate level of localization detail should be found that corresponds best to the expression of a biomarker. Second, single histopathology descriptions should be integrated into molecular processes, which correspond to the molecular events triggering the expression of the biomarkers. Thus, the localized lesions were here integrated into 10 different processes, whereby for each sample the highest grade of the corresponding localized lesions was assigned to the integrated pathology. In particular following 10 pathology processes are investigated:

[0041] 1. Proximal tubular damage: Lesions with a grade 1 ("minimal", "very few", "very small") or higher of the types "necrosis", "apoptosis" or "tubular cell sloughing" localized in any of the tubular segments S1, S2 or S3 or in non-localizable.

[0042] 2. Glomerular alterations/damage: Lesions with a grade 1 ("minimal", "very few", "very small") or higher of the types "mesangial cell proliferation", "mesangial cell enlargement", "glomerular vacuolization" or "interstitial Bowman's capsule fibrosis".

[0043] 3. Tubular damage/regeneration/dilatation: Lesions with a grade 1 ("minimal", "very few", "very small") or higher of the types "necrosis", "apoptosis", "tubular cell sloughing", "basophilia", or "mitosis increase" localized in any of the tubular segments S1, S2, S3, loop of Henle, thick

5

ascending tubules, distal tubules, or collecting ducts or non-localizable or "tubular dilatation" in cortex, medulla or papilla.

[0044] 4. Glomerular alterations/damage or tubular damage/regeneration/dilatation: Lesions with a grade 1 ("minimal", "very few", "very small") or higher of the types "mesangial cell proliferation", "mesangial cell enlargement", "glomerular vacuolization" or "interstitial Bowman's capsule fibrosis" or of the types "necrosis", "apoptosis", "tubular cell sloughing", "basophilia", or "mitosis increase" localized in any of the tubular segments S1, S2, S3, loop of Henle, thick ascending tubules, distal tubules, or collecting ducts or non-localizable or "tubular dilatation" in cortex, medulla or papilla.

[0045] 5. Thick ascending tubular damage/regeneration: Lesions with a grade 1 ("minimal", "very few", "very small") or higher of the types "necrosis", "apoptosis", "basophilia", or "mitosis increase" localized in the thick ascending tubules.

[0046] 6. Distal tubular damage/regeneration: Lesions with a grade 1 ("minimal", "very few", "very small") or higher of the types "necrosis", "basophilia", or "mitosis increase" localized in the distal tubules.

[0047] 7. Collecting Duct damage/regeneration: Lesions with a grade 1 ("minimal", "very few", "very small") or higher of the types "necrosis", "apoptosis", "tubular cell sloughing", or "basophilia", in the collecting ducts.

[0048] 8. Tubular Mineralization: Lesions with a grade 1 ("minimal", "very few", "very small") or higher of the type "intratubular casts—mineralization" localized in any of the tubular segments S1, S2, S3, loop of Henle, thick ascending tubules, distal tubules, or collecting ducts.

[0049] 9. Intratubular Hyaline Casts: Lesions with a grade 1 ("minimal", "very few", "very small") or higher of the type "intratubular Casts—Hyaline (proteinaceous, pigmented)" localized in any of the tubular segments S1, S2, S3, loop of Henle, thick ascending tubules, distal tubules, or collecting ducts.

[0050] 10. Juxtaglomerular Apparatus Hypertrophy: The pathologies observed in the liver of the animals of the 10 studies are listed in FIG. 5.

[0051] Description of analytics. Protein biomarkers were measured by validated multiplexed protein assays developed by and available from RulesBasedMedicine (Texas, USA). Clinical chemistry parameters (e.g. BUN, NAG, Creatinine, and LDH) were measured with standard clinical chemistry assays (ADVIA 1650 device). mRNA biomarkers were measured with TaqMan Gene Expression Assays from Applied Biosystems on Low Density Arrays on an Applied Biosystems 7900HT real-time PCR instrument. The mRNA had been extracted from half a kidney using standard procedures.

[0052] Description of data pre-processing. The concentration values of the biomarkers obtained from the analytical devices were pre-processed according to following steps: (1) concentration values, which were above the upper limit of quantitation, were replaced by the upper limit of quantitation; (2) concentration values, which were below the lower limit of quantitation, were replaced by the lower limit of quantitation; (3) urinary biomarkers were normalized to the concentration of urinary creatinine by dividing each sample by the corresponding urinary creatinine value; and (4) to express the data as fold-changes, each value was divided by the arithmetic average of the time-matched and study-matched control group (usually 6 animals).

[0053] Description of data analysis. The quantitative analyses of the data were all based on receiver operator characteristic analyses (ROC). In a ROC analysis the decision threshold is systematically varied for a binary decision problem (e.g. controls versus diseased animals) and the true positives (sensitivity) are plotted versus the true negatives (1-specificity). The area under the curve (AUC) is a measure of the diagnostic power combining sensitivity and specificity into one value, whereby a random discriminator corresponds to an AUC of 0.5 and a perfect discriminator to 1. The calculation of the AUC was performed by using trapezoidal integration as described by Bradley A P, *Pat. Recogn.* 30(7):1145-1159 (1997). The standard error of the AUC was calculated from the standard error of the Wilcoxon statistic as described by Bradley (1997).

[0054] As an application example out of the ROC analysis for a given biomarker and pathology, a threshold for the biomarker/pathology was established for a predefined minimum specificity following way:

[0055] For a given minimum specificity (e.g. 95%) first of all the lowest possible exact specificity above or at the minimum specificity was determined. For that exact specificity, the threshold with the highest corresponding sensitivity was selected. The algorithm does not look, if higher specificities for this sensitivity are possible by further varying the threshold. For this threshold, the corresponding specificity and sensitivity are reported herein.

[0056] For the analysis of the data, following definitions of control animals and diseased animals were used: (a) Control group: Animals dosed with vehicles or hepatotoxicants, and which do not show the lesion investigated. (b) Diseased group: Animals dosed with nephrotoxicants, and which were assigned a grade of 1 or higher for the lesion of interest at the histopathology assessment.

[0057] Hepatotoxicant-dosed animals are included into the control group to test the specificity of the markers versus other hepatotoxic changes and due to the fact that no dose-related nephrotoxicity was observed in these studies.

[0058] Animals that were dosed but did not show any lesion or only other lesions (other than the specific histopathology context of interest) were left out for the ROC considering that these animals are not "clean". This group of animals represents an undefined state especially when a molecular response is earlier and faster than a histopathological manifestation. In that case it cannot be decided, if (1) a single histopathology slide of one kidney is not representative for the overall state of the kidney (false negative histopathology); (2) the molecular response is earlier/more sensitive than histopathology, a so-called prodromal state; or (3) the animals are false positives if histopathology would be the only truth (false positive biomarker). The most conservative way of treating these animals is to exclude these animals from any analysis as no definitive assignment to any group can be made.

[0059] Results for biomarkers and pathologies of interest to monitor renal injury. The results of the ROC analysis combining histopathology, study information and biomarker values are shown for the most interesting renal pathologies and biomarkers in FIG. 6.

[0060] Proteins and clinical chemistry parameters to monitor and identify liver injury. The biomarkers were obtained from animals to which vehicle or different doses of the hepatotoxicant ANIT (alpha-Naphtylisothiocyanate) was administered. See, FIG. 7. Dose-related histopathology findings in

the liver but not in the kidney were observed. In the plots the relative concentration levels (fold changes versus controls) are shown. The dose-levels are represented by the different color shadings, the time points of sampling are represented by the labels. The biomarker levels correlate well with the dose and thus with the dose-related hepatotoxicity. The biomarkers represented in these plots are the current standard ALAT measured in plasma (FIG. **7A** top) and the new markers Lipocalin-2 measured in plasma (FIG. **7A** bottom), GST-mu measured in plasma (FIG. **7B** top) and Lipocalin-2 measured in urine (FIG. **7B** bottom).

[0061] Proteins and clinical chemistry parameters to monitor and identify kidney injury. The biomarkers were obtained from animals to which vehicle or different doses of the nephrotoxicant Cisplatin was administered. See, FIG. **7**. In the plots the relative concentration levels (fold changes versus controls) are shown. The dose-levels are represented as labels of the x-Axis, the time points of sampling are represented by as labels of the samples. The samples are color shaded by the highest grade of histopathology finding observed in kidney. The horizontal bar indicates the highest biomarker level observed for case control animals (vehicle dosed animals without histopathology finding in kidney). Protein levels higher than the bar are significantly increased (100% specificity for case controls). Also, other thresholds are possible. Specific thresholds for 95% specificity are given in FIG. **6**. The different clinical parameters and proteins detect kidney injury with different sensitivity. Creatinine measured in serum, which is the current standard peripheral test for kidney injury and kidney function, is the least sensitive method (FIG. **8A** top). Cystatin C measured in plasma (FIG. **8A** bottom), Kim-1 measured in urine (FIG. **8B** top), lipocalin-2 measured in urine (FIG. **8B** bottom), osteopontin measured in urine (FIG. **8C** top) and clusterin measured in urine (FIG. **8C** bottom) identify more animals with significant kidney findings.

[0062] Gene transcription to monitor and idents kidney injury. The biomarkers were obtained from animals to which either vehicle or the nephrotoxicant cisplatin was administered. See, FIG. **9**. In the plots the expression values (Ct values referenced to Polr2g) are shown. The dose-levels are represented as labels of the x-Axis, the time points of sampling are represented by as labels of the samples. The samples are color shaded by the highest grade of histopathology finding observed in kidney. The horizontal bar indicates the highest expression (lowest value in the plot) observed for control animals. Values below the bar correspond to significantly increased expression levels (100% specificity for non-dosed animals). Also, other thresholds are possible. Specific thresholds for 95% specificity are proposed in FIG. **6**. Both Kim-1 (FIG. **9A**) and Cyr61 (FIG. **9B**) can be used to detect kidney injury earlier (at earlier time points) and in a more sensitive way (at lower dose levels) than histopathological examination.

[0063] Embodiments and aspects of the invention. Using mathematical operations and data described herein, the invention provides the following embodiments:

[0064] The invention provides methods for diagnosing, predicting and classifying renal toxicity and/or liver toxicity by the use of single biomarkers of the invention or combinations of biomarkers (clinical chemistry parameters, proteins, mRNA transcription) in biological matrices (urine, blood, mRNA from kidney and blood). The invention also provides methods for diagnosing, predicting and classifying histopathology findings, combinations of histopathology findings

and mechanisms manifested by histopathology findings in kidney, in liver or in kidney and liver with the help of measurements of single biomarkers or combinations of biomarkers (clinical chemistry parameters, proteins, mRNA transcriptions) in single biological matrices or in different biological matrices. In the use of the invention, a histopathological finding in the kidney corresponds to a renal toxicity or renal disease symptom and a histopathological finding in the liver corresponds to a liver toxicity or liver disease symptom.

[0065] Thus, the level of expression, or the level of function, of a marker in an individual can be determined to thereby select appropriate agent for therapeutic or prophylactic treatment of the individual. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure, and thus enhance therapeutic or prophylactic efficiency when treating a subject with a modulator of expression of a marker. See WO 2004/005544, incorporated herein by reference.

[0066] The invention further provides methods for diagnosing, predicting and classifying single biomarkers or combinations of biomarkers in biological matrices with the help of single biomarkers or combinations of biomarkers in the biological matrices.

[0067] The invention still further provides methods for predicting the fate of individuals (e.g. survival rate) with the help of measurements of the biomarkers of the invention in biological matrices.

[0068] In one aspect, the invention shows that the biomarkers of the invention can be used to predict, classify, and diagnose histopathology findings, combinations of histopathology findings, and mechanisms manifested by histopathology findings in kidney, in liver or in kidney and liver, with higher sensitivity and specificity, at earlier time point and at lower dose levels than other biomarkers.

[0069] In another aspect, the invention shows that the biomarkers of the invention can be used to predict, classify, and diagnose histopathology findings, combinations of histopathology findings, and mechanisms manifested by histopathology findings in kidney, in liver or in kidney and liver in the course of the study earlier than the assessment of histopathology of liver and kidney at that time point of the study. This means that the modeling, diagnosis, classification and prediction of histopathology with the help of biomarkers are earlier, more sensitive and more specific than the assessment of histopathology itself.

[0070] The methods of the invention can be used not only with the described biomarkers of the invention, but also with degradation products thereof or combinations of the described biomarkers and degradations products. The degradation products could be peptides or peptide fragments of described proteins or mRNA fragments and degradation products of described mRNA transcriptions. Moreover, the methods of the invention can use not only the described biomarkers, but also substantially similar biomarkers, such as different isoforms, splicing variants or fragments. In some embodiments, the methods of the invention can use polymorphisms in a gene of described biomarkers of the invention.

[0071] The invention also provides for the implementation of these markers, combination of these biomarkers and the models, correlations, predictions, classification and diagnostics of the biomarkers with histopathology and other biomarkers into a device. In particular, the invention provides a test, device, assay, biomarker test, clinical test kit or diagnostic device to monitor or diagnose the state and function of the

kidney or the state and function of the liver. In another embodiment, the invention provides a test, device, assay, biomarker test, clinical test kit or diagnostic device to monitor or diagnose adverse effects of drugs on the kidney or on the liver. In still another embodiment, the invention provides a test, device, assay, biomarker test, clinical test kit or diagnostic device to identify candidate agents (drugs) that do not provoke or induce adverse effects in the kidney or in the liver. In yet another embodiment, the invention provides a test, device, assay, biomarker test, clinical test kit or diagnostic device to determine if an individual responds to therapy with respect to kidney toxicity, liver toxicity or kidney and liver toxicity.

[0072] The components of the kit may be for the measurement of gene expression by Northern blot analysis, reverse transcription PCR or real time quantitative PCR, branched DNA, nucleic acid sequence based amplification (NASBA), transcription-mediated amplification, ribonuclease protection assay, or microarrays. Another particular embodiment provides a kit, wherein the means for determining the level of gene expression or gene expression product comprise at least one antibody specific for a protein encoded by the marker gene selected among the biomarkers of the invention. The antibody is preferably selected among polyclonal antibodies, monoclonal antibodies, humanized or chimeric antibodies, and biologically functional antibody fragments sufficient for binding of the antibody fragment to the marker. Particularly preferred are immunoassay methods for determining the level of gene expression.

[0073] In another preferred embodiment of the invention a kit is provided which further comprises means for obtaining a body sample of the individual, particularly plasma or urine. A particularly preferred embodiment further comprises a container suitable for containing the means for determining the level of gene expression and the body sample of the individual. In another preferred embodiment the kit further comprises instructions for use and interpretation of the kit results.

[0074] In several embodiments, the invention provides tests, devices, assays, biomarker tests, clinical test kits or diagnostic devices (i) to identify candidate agents (drugs) that ameliorate one or several symptoms of kidney toxicity; (ii) to identify candidate agents (drugs) that ameliorate one or several symptoms of liver toxicity; (iii) to compare the renal toxicity potential of two agents (drugs); and (iv) to compare the liver toxicity potential of two agents (drugs).

[0075] For example, the effectiveness of an agent to affect marker expression can be monitored in clinical trials of subjects receiving treatment for renal disease or toxicity. In a preferred embodiment, the invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (e.g., an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) comprising the steps of: (i) obtaining a pre-administration sample from a subject prior to administration of the agent; (ii) detecting the level of expression of one or more selected markers of the invention in the pre-administration sample; (iii) obtaining one or more post-administration samples from the subject; (iv) detecting the level of expression of the markers in the post-administration samples; (v) comparing the level of expression of the markers in the pre-administration sample with the level of expression of the markers in the post-administration sample or samples; and (vi) altering the administration of the agent to the subject accordingly. For example, modified administration of the agent can be desirable to increase expression of the markers to I higher levels than detected, i.e., to increase the effectiveness of the agent. Alternatively, increased/decreased administration of the agent can be desirable to increase/decrease the effectiveness of the agent, respectively.

[0076] In a particular embodiment, the invention provides a method for identifying candidate agents for use in the treatment of renal toxicity comprising the steps of (a) contacting a sample of a kidney tissue subject to toxicity with a candidate agent; (b) determining from the kidney tissue the level of gene expression or gene expression product, particularly protein, corresponding to one or more genes selected among of the biomarkers of the invention, to obtain a first set of value; and (c) comparing the first set of value with a second set of value corresponding to the level of gene expression or gene expression product, particularly protein, assessed for the same genes and under identical condition as for step (b) in a kidney tissue subject to toxicity not induced by the candidate agent.

[0077] In another particular embodiment, the invention provides a method for identifying candidate agents that do not provoke or induce renal toxicity comprising the steps of: (a) contacting a sample of a kidney tissue not subject to toxicity with a candidate agent; (b) determining from the kidney tissue the level of gene expression or gene expression product, particularly protein, corresponding to one or more genes selected among the biomarkers of the invention, to obtain a first set of value; and (c) comparing the first set of value with a second set of value corresponding to the level of gene expression or gene expression product, particularly protein, assessed for the same genes and under identical condition as for step (b) in a kidney tissue not subject to toxicity.

[0078] In another particular embodiment, the invention provides a method for comparing renal cytotoxic potentials of two drug candidates comprising the steps of (a) contacting a sample of a kidney tissue not subject to toxicity with a first drug candidate, and determining from the kidney tissue levels of gene expression or gene expression product, particularly protein, corresponding to one or more genes selected among the biomarkers of the invention to obtain a first value; and (b) contacting a sample of a kidney tissue not subject to toxicity with a second drug candidate, and determining from the kidney tissue level of gene expression corresponding to one or more genes selected among the biomarkers of the invention to obtain a second value; and (c) comparing the first value with the second value.

[0079] In other embodiments, the invention provides a therapeutic method for treating renal and/or liver toxicity in an individual patient by administrating a therapeutically effective amount of a modulating compound that modulates in the liver and/or kidney the synthesis, expression or activity of one or several genes, gene expression products or proteins listed in TABLE 1 so that at least one symptom or renal and/or liver toxicity is ameliorated.

[0080] In a particular aspect of the invention, a method is provided for both prophylactic and therapeutic methods of treating a subject having, or at risk of having, a kidney disorder or renal toxicity. Administration of a prophylactic agent can occur prior to the manifestation of symptoms characteristic of the kidney disorder, such that development of the kidney disorder is prevented or delayed in its progression.

[0081] In another particular embodiment, the invention provides a method for treating or preventing renal toxicity in an individual comprising the step of administering to said individual a therapeutically effective amount of a modulating

compound that modulates in the kidney the synthesis, expression or activity of one or more of the genes or gene expression products, particularly protein, of the group of genes of the biomarkers of the invention, so that at least one symptom of renal toxicity is ameliorated.

[0082] In yet another particular embodiment, the invention provides a method for treating renal toxicity in an individual comprising the step of administering to said individual a therapeutically effective amount of a modulating compound that modulates in the kidney the synthesis, expression or activity of one or more of the genes or gene expression products, particularly protein, of the group of genes of the biomarkers of the invention, so that at least one symptom of renal toxicity is ameliorated.

[0083] In a further embodiment, the invention provides a method for treating renal toxicity in an individual under treatment with a cytotoxic agent is provided, comprising the step of administering to said individual a therapeutically effective amount of a modulating compound that modulates in the kidney the synthesis, expression or activity of one or more of the genes or gene expression products, particularly protein, of the group of genes of the biomarkers of the invention, so that at least one symptom of renal toxicity is ameliorated.

[0084] The invention provides a method for identifying other new biomarkers for diagnosing, predicting, classifying or monitoring liver toxicity and/or kidney toxicity or symptoms thereof with the help of the markers, combination of the biomarkers and models, correlations, predictions, classifications and diagnostics of this invention.

[0085] One particular advantage of the above methods, i.e., methods (i) for identifying candidate agents, (ii) for comparing renal cytotoxic potentials of two drug candidates and (iii) for identifying candidate agents that do not provoke or induce renal toxicity, is that they an be performed in vitro. The kidney tissues that are used are preferably obtained from a cultured kidney tissue or cells that have been contacted with a cytotoxic agent. The kidney tissue can also be a kidney sample of an individual subject to renal toxicity, but this may limit broad in-vitro applications of such methods.

[0086] Thus, the invention provides a test which measures the above mentioned biomarkers in cultured kidney tissue or cells to predict, classify or diagnose kidney toxicity and/or liver toxicity in vivo. This may be a single or collection of kidney or liver cells such as the human kidney epithelial 293Tcells HK2 cell lines, human embryonic kidney cell lines, or human embryonic liver cell lines for instance. Changes in the expression profile from a baseline profile while the cells are exposed to various modifying conditions, such as contact with a drug or other active molecules can be used as an indication of such effects.

[0087] Cultured kidney tissue or cells may be advantageously based on an in vivo animal model that mimics human cellular and tissues disorders, preferably of the kidney. It may also be a single or collection of kidney cells such as the human kidney epithelial 293Tcells or a human embryonic kidney cell line, for instance. The kidney is particularly susceptible to the nephrotoxic action of drugs, because of its functional properties, including (a) the high volume of renal blood flow, which brings large amounts of toxin; (b) the large area in contact with the drug, either in the glomerulus or the tubule epithelium, which enables toxin interaction or uptake; (c) the kidney's ability to transfer active substances, which provides specific transfer mechanisms that mediate cellular uptake; (d) drug breakdown, which may occur in renal tubules and lead to the formation of toxic metabolites from non-toxic parent substances; e) the kidney's concentrating mechanisms, which can increase urinary and interstitial concentrations of non-absorbed products; the high metabolic rate of tubule cells required for normal function, which is subject to perturbation.

EQUIVALENTS

[0088] The invention is not to be limited in terms of the particular embodiments described in this application, which are intended as single illustrations of individual aspects of the invention. Many modifications and variations of this invention can be made without departing from its spirit and scope, as will be apparent to those skilled in the art. Functionally equivalent methods and apparatuses within the scope of the invention, in addition to those enumerated herein, will be apparent to those skilled in the art from the foregoing descriptions. Such modifications and variations are intended to fall within the scope of the appended claims. The invention is to be limited only by the terms of the appended claims along with the full scope of equivalents to which such claims are entitled.

We claim:

1. A method for assessing renal toxicity or liver toxicity in an individual following administration of compound suspected of causing renal toxicity or liver toxicity, wherein the renal toxicity or liver toxicity is identified by measurement of a set of biomarkers in a sample from the individual and comparison of the measured biomarker amount with the corresponding amount in a healthy individual, wherein the biomarkers are selected from the group consisting of the biomarkers listed in TABLE 1.

2. The method of claim 1, wherein the assessment of liver toxicity is by measurement of the set of protein biomarkers comprising:

(a) lipocalin-2 measured in a blood, plasma or serum sample from the individual,

(b) glutathione S-transferase mu 1(GST-mu) measured in a blood, plasma or serum sample from the individual; and

(c) lipocalin-2 measured in a urine sample from the individual.

3. The method of claim 1, wherein the assessment of renal toxicity is by measurement of the set of protein biomarkers comprising:

(a) cystatin C measured in a blood, plasma or serum sample from the individual,

(b) Kidney Injury Molecule-1 (Kim-1) measured in a urine sample from the individual; and

(c) lipocalin-2 measured in a urine sample from the individual.

4. The method of claim 1, wherein the assessment of renal toxicity is by measurement of a set of gene transcription biomarkers comprising:.

(a) Kidney Injury Molecule-1 (Kim-1); and

(c) cysteine-rich protein-61 (CYR61).

* * * * *

专利名称(译)	用于监测肾功能的预测性肾安全生物标志物和生物标志物特征

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摘要(译)

鉴定了生物标志物特征，其可用于诊断或预测肾脏或肝脏毒性，更具体地，由于疾病或药物治疗而导致的肾小管毒性。

Nephrotoxicants

Compound	Tubul.	Glom.	Coll. D.	Mode of Toxicity
Gentamycin	x			Lysosomal phospholipidosis
Puromycin	x (2nd)	x		Damage to podocytes
Vancomycin	x	x		Oxidative stress (free radicals)
Doxorubicin	x (2nd)	x		Oxidative stress to glom. filtr. membrane
Furosemide	x			Mineralization
Lithium carbonate	x	(x)	(x)	Influences formation of intracellular cyclic adenosine monophosphate
Cisplatin	x	(x)	(x)	Direct DNA alkylation of DNA, Ox. stress
FK506	x	(x)		Complex (vasoconstrict., calcification...)

Hepatotoxicants

α-Naphthyisothiocyanate (ANIT)	Cholangitis
Methapyrilene	Hepatocarcinogen (upon chronic treatment)

FIG. 1

COMPOUNDS ADMINISTERED IN THE *IN VIVO* STUDIES