Expression patterns analysis of the RNA biosynthesis, processing, transporting or catabolism-associated genes during rat liver regeneration

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Received January 22, 2008

Abstract

To study the roles of RNA biosynthesis, processing, transporting or catabolism in liver regeneration (LR) at transcriptional level, we collected RNA biosynthesis, processing, transporting or catabolism-associated genes from the database information and related records, and checked the gene expression changes in rat regenerating liver by Rat Genome 230 2.0 array. Then we confirmed the relevance between the genes and LR by comparing difference in gene expression changes between partial hepatectomy (PH) group and sham-operation (SO) group, and analyzed their actions by systems biology approach. At last, we found 92 genes were to be associated with LR. The number of initially and totally expressed genes occurring in initial phase of liver regeneration (0.5 – 4 h after PH), G0/G1 phase (4 – 6 h after PH), cell proliferating phase (6 – 66 h after PH), cell differentiation and structure-function reorganization phase (72 – 168 h after PH) was 19, 4, 70, 3 and 38, 17, 226, 67, respectively, illustrating that the associated genes mainly were triggered at the initial stage of LR, and worked at different phases. According to their expression similarity, these genes were categorized into 63 up-, 20 down-, and 9 up/down-regulated genes; and the total up- and down-expression times were 249 and 68, respectively, demonstrating that expression of most of the genes increased during LR, while that of a few ones decreased. Their expression patterns were classified into 21 types respectively, showing that the cellular physiological and biochemical activities during LR were diverse and complicated. RNA biosynthesis, processing, transporting or catabolism were tightly closed to LR. [Life Science Journal. 2008; 5(2): 1 – 8] (ISSN: 1097 – 8135).

Keywords: partial hepatectomy; Rat Genome 230 2.0 array; RNA biosynthesis, processing, transporting or catabolism; genes; liver regeneration

1 Introduction

RNA, playing an important role in biological evolution[1], can not only carry and transfer genetic information[2], but also catalyze biological reactions directly[3]. It plays a decisive part in translating the genetic information, and instructs the biosynthesis of protein directly[4–6]. For example, mRNA is the translator of the message of encodes the genetic information[7–9]; rRNA is the central DNA, component of ribosome, and the latter is a molecular machine that synthesizes proteins, in addition, rRNA acts as a catalyst[10]; tRNA is response for transport of amino acids[11]. RNA biosynthesis, processing, transporting or catabolism were inseparable from cell survival and cell growth.

The liver is an important organ to maintain life activities[12]. After partial hepatectomy (PH)[13] or liver injury, the remnant liver cells are activated rapidly to compensate the lost or injured liver tissue, and finally to rebuild tissue-structure and recovery function by dedifferentiation and redifferentiation, which is called liver regeneration

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(LR)[14,15]. Generally, the regeneration process is usually categorized based on the cellular physiological and biochemical activities into four stages[16]: initiation phase (0.5 h to 4 h after PH, G0/G1 transition (4 – 6 h after PH), cell proliferation (6 – 66 h after PH), cell differentiation and reorganization of the structure-function (66 – 168 h after PH). In this LR, RNA biosynthesis, processing, transporting or catabolism play important roles[17].

Sequence pattern analysis has been successfully utilized for predicting protein subcellular localization, membrane protein type, enzyme functional class, signal peptides, HIV-protease cleavage sites, tight turn type, protease type, GPCR type, protein structural class, as well as predicting 3-dimentional structures of proteins[18–22]. Using graphic approaches or diagrammatic expression to study various complicated biological systems can provide very useful insights, as demonstrated by many previous studies on a series of important biological topics, such as enzyme-catalyzed reactions, internal motions of biomacromolecules, protein folding kinetics, inhibition kinetics of processive nucleic acid polymerases and nucleases, analysis of codon usage, base frequencies in the anti-sense strands, hepatitis B viral infections, HBV virus gene missense mutation, and visual analysis of SARS-CoV[23–27].

The study indicates that more than 270 genes participate in RNA biosynthesis, processing, transporting or catabolism. In order to give insight into the relativity between RNA biosynthesis, processing, transporting, catabolism and LR at the transcriptional level[16,28], Rat Genome 230 2.0 array[29] containing 235 genes associated with RNA biosynthesis, processing, transporting or catabolism was used to check the gene expression changes in regenerating liver after 2/3 hepatectomy, and 92 of them were found to be associated with LR, and the expression changes, patterns and action of them during LR were primarily analyzed.

2 Materials and Methods

2.1 Regenerating liver preparation

Healthy SD rats weighing 200 – 250 g were separated into groups at random and one group included 6 rats (Male: Female = 1 : 1). PH was performed according to Higgins and Anderson[30], the left and middle lobes of liver were removed. Rats were killed by cervical vertebra dislocation at 0.5, 1, 2, 4, 6, 8, 12, 16, 18, 24, 30, 36, 42, 48, 54, 60, 66, 72, 96, 120, 144 and 168 h after PH and the regenerating livers were observed at corresponding time point. The livers were rinsed three times in PBS at 4 °C, then 100 – 200 mg livers from middle parts of right lobe, and six samples of each group were gathered and mixed together to 1 – 2 g, i.e. (0.1 – 0.2 g) × 6 total liver tissue, then stored at – 80 °C. The sham-operation (SO) groups were the same with PH ones except the liver lobes unremoved. The laws of animal protection of China were enforced strictly.

2.2 RNA isolation and purification

Total RNA was isolated according to the manual of Trizol reagent (Invitrogen Corporation, Carlsbad, California, USA)[31] and then purified following the RNeasy protocol (Qiagen, Inc, Valencia, CA, USA)[32]. RNA concentration and purity was mensurated by 260/280 nm ratio[33]. The quality of total RNA samples was assessed by agarose electrophoresis (180 V, 0.5 h) with a 2 : 1 ratio of 28S rRNA to 18S rRNA intensities and selected for use.

2.3 cDNA, cRNA synthesis and purification

As template, 5 μg of total RNA was used for synthesizing the first strand of cDNA by using SuperScript II RT (Invitrogen Corporation, Carlsbad, CA), and T7-oligo dT(24) (W.M. Keck Foundation, New Haven, CT) as the primer. Second strand synthesis was performed following the Affymetrix cDNA single-Stranded cDNA Synthesis Kit. The resulting cDNA was purified following cDNA purify protocol. 12 μg purified cDNA subsequently served as template for production of biotin labeled cRNA transcript using the GeneChip *In Vitro* Transcript Labeling Kit (ENZO Biochemical, New York, NY). Labeled cRNA was purified according to the cRNA purify protocol[34]. The concentration, purity and quality of cDNA and cRNA were assessed as above.

2.4 cRNA fragmentation and microarray detection

15 μl cRNA (1 μg/μl) was incubated with 6 μl 5 × fragmentation buffer and 9 μl RNase free water for 35 min at 94 °C, and digested into 35 – 200 bp cRNA fragments. The hybridization buffer prepared according to Affymetrix protocol and added the prehybridized Rat Genome 230 2.0 microarray to it, then hybridization was carried out in a rotating chamber (60 rpm, 16 h, 45 °C). After absorbed superfluous hybridization buffer, arrays were washed and stained by GeneChip fluidics station 450 (Affymetrix Inc., Santa Clara, CA, USA). Subsequently, they were scanned with a GeneChip Scanner 3000 (Affymetrix Inc., Santa Clara, CA, USA) and obtained images[34].

2.5 Microarray data analysis

Images were converted to signal value by Affymetrix

GCOS 1.4 software[35]. The probe signal values were scaled to evaluate gene expression ($P < 0.05$), marginally expression ($0.05 < P < 0.065$), and no expression ($P > 0.065$). Then signal values of each chip were normalized, and evaluated whether a gene changed by the ratios that compared the normalized *P*-value of PH groups to that of control groups, e.g. if the ratios ≥ 3, as up-regulated expression genes; if the ratios ≤ 0.33, as down-regulated expression genes; otherwise as no-sense genes[36]. To minimize the technical error from the microarray analysis, regenerating liver of each time point was measured three times with Rat Genome 230 2.0 microarray. Their average value was calculated as corrective value use. Finally, these values were analyzed with GeneMath, GeneSpring (Silicon Genetics, San Carlos, CA) and Microsoft Excel Software (Microsoft, Redmond, WA)[37].

2.6 Identification of genes associated with LR

Firstly, the nomenclature of RNA biosynthesis, processing, transporting or catabolism (e.g. RNA transcription initiation) was adopted from the GENEONTOLOGY database (www.geneontology.org), and inputted into the databases at NCBI (www.ncbi.nlm.nih.gov) and RGD (rgd.mcw.edu) to identify the rat, mouse and human genes associated with RNA biosynthesis, processing, transporting or catabolism. According to maps of biological pathways embodied by GENMAPP (www.genmapp.org), KEGG (www.genome.jp/kegg/pathway.html#amino) and BIOCARTA (www.biocarta.com/genes/index.asp), the genes associated with the above process were collated. The results of this analysis were codified, and compared with the results obtained for human and mouse searches in order to identify human and mouse genes which are different from those of rat. Comparing these genes with the analysis output of the Rat Genome 230 2.0 array, those genes which showed a greater than threefold change in expression level, observed as meaningful expression changes, were referred to as rat homologous genes or rat specific genes associated with above process under evaluation. Genes, which displayed reproducible results with three independent analyses with the chip and which showed a greater than threefold change in expression level in at least one time point during liver regeneration with significant difference ($0.01 \leq P < 0.05$) or extremely significant difference ($P \leq 0.01$) between PH and SO, were referred to as associated with LR.

3 Results

3.1 Expression changes of the RNA biosynthesis, processing, transporting or catabolism-associated genes during LR

According to the data of databases at NCBI, GENMAPP, KEGG, BIOCARTA, RGD etc, 276 genes were associated with RNA biosynthesis, processing, transporting or catabolism. In which, 235 genes were contained in the Rat Genome 230 2.0 array, 92 of them revealed meaningful expression changes at least at one time point after PH, showed significant or extremely significant differences in expression when comparing PH with SO, and repeated in three times of detection by Rat Genome 230 2.0 array, suggesting that the genes were associated with LR, the range of up regulation was 3 – 32 folds of control, and that of down- was 3 – 15 folds (Table 1).

3.2 Initial and total expression number of the RNA biosynthesis, processing, transporting or catabolism -associated genes during LR

At each time point of LR, the numbers of initially up-, down-regulated and totally up-, down-regulated genes were in sequence: both 6 and 2 at 0.5 h; 3, 0 and 8, 2 at 1 h; 1, 3 and 5, 5 at 2 h; 1, 3 and 6, 4 at 4 h; 0, 0 and 4, 3 at 6 h; 1, 0 and 6, 2 at 8 h; 0, 1 and 4, 1 at 12 h; 19, 3 and 24, 7 at 16 h; 7, 1 and 14, 4 at 18 h; 6, 0 and 21, 1 at 24 h; 11, 5 and 17, 9 at 30 h; 1, 1 and 20, 2 at 36 h; 6, 2 and 22, 4 at 42 h; 4, 1 and 16, 2 at 48 h; 1, 0 and 12, 3 at 54 h; 0, 0 and 11, 3 at 60 h; 0, 0 and 13, 1 at 66 h; 0, 1 and 5, 2 at 72 h; 2, 0 and 19, 5 at 96 h; 0, 0 and 7, 3 at 120 h; 0, 0 and 5, 2 at 144 h; 0, 0 and 4, 1 at 168 h (Figure 1). Wholly, gene expression changes span the whole LR. Total expression frequencies of the up- and down-regulated genes were 249 and 68, respectively. The initially up-regulated genes were predominant at 0.5 – 1 and 16 – 54 h, whereas very few were initially expressed at other time points (Figure 2).

3.3 Expression patterns of the RNA biosynthesis, processing, transporting or catabolism-associated genes during LR

21 patterns of the above 92 genes could be obtained according to gene expression changes: 63 genes were up-regulation, 20 genes were down-, and 9 genes were up- at some time points and down- at others (up/down-genes). The total expression was 249 up- and 68 down-(Figure 2): (1) up-regulation at one time point, at 16, 24, 30, 36, 42, 48, 54, 96 h, 20 genes involved; (2) up-regulation at two time points, at 16 and 30 h, 16 and 42 h, 16 and 96 h, 18 and 120 h, 24 and 66 h, 30 and 42 h, 30 and 54 h, 30 and 96 h, 42 and 96 h, 16 genes involved; (3) up-regulation at three time points, 6 genes involved; (4) up-regulation at multiple time points, 4 genes involved; (5) up-regulation in one phase, at 18 – 24 h, 2 genes in-

Table 1. Expression abundance of 92 RNA biosynthesis, processing, transporting or catabolism-associated genes during rat LR

Name	Gene abbr.	Fold difference	Name	Gene abbr.	Fold difference	Name	Gene abbr.	Fold difference
1. Transcription initiation			Cycli-dependent kinase 8	Cdk8	6.8	Small nuclear ribonucleoprotein polypeptide A	Snrpa	9.8
Brf1 homolog, subunit of RNA polymerase III transcription initiation factor IIIB	Brf1	4.6	Elongation factor RNA polymerase II	Ell	4.0	Small nuclear ribonucleoprotein B	Snrpb	3.6
			High mobility group nucleosomal binging domain 1	*Hmgn1	3.0	Small nuclear ribonucleoprotein D1	*Snrpd1	4.3
BRF2, subunit of RNA polymerase III transcription initiation factor, BRF1-like	Brf2	5.5	Menage a trois 1	Mnat1	0.2	Serine/arginine repetitive matrix	Sarm1	7.6
			Transcription elongation factor A, 3	Tcea3	11.2	Splicing factor proline/glutamine-rich	Sfpq	5.6
Cofactor required for Sp1 transcriptional activation, sununit 3	Crsp3	0.3, 6.8	Transcription elongation factor B, polypiptide 1	Tceb1	0.2	THO complex 4	Thoc4[7]	8.4
			Transcription elongation factor B, polypiptide 1	Tceb3	0.3	U2 small nuclear ribonucleoprotein auxiliary factor 2	U2af2	6.0
E2F transcription factor 2	E2f2	6.8	**3. mRNA 7-methylguanosine**			WD repeat domain 57	Wdr57	4.3
General transcription factor 2a, 1	Gtf2a1	3.7	RNA guanylytransferase and 5'-phosphatase	Rngtt	3.7	**6. mRNA editing**		
General transcription factor IIF, polypeptide 1	Gtf2f1	3.3	**4. mRNA poly-A tail-adding**			Apobec-1 complementation factor	Acf	5.7
General transcription factor IIF, polypeptide 2	Gtf2f2	10.3	Cleavage stimulation factor, 3' pre-RNA sununit 2	Cstf2[5]	4.7	Apolipoprotein B editing complex 1	Apobec1	0.2
General transcription factor IIH, polypeptide 1	*Gtf2h1	3.3	Cleavage stimulation factor, 3' pre-RNA sununit 2, tau	Cstf2t	0.3	**7. mRNA export from nucleus**		
Myelocytomatosis viral oncogene homolog	*Myc	19.7	Cleavage stimulation factor, 3' pre-RNA sununit 3	Cstf3[5]	5.4	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19b	Ddx19b	4.2
MYC-associated zinc finger protein	Maz	6.8	Stem-loop binding protein	Slbp	0.3, 10.6	Nucleoporin 107	Nup107	8.0
Mediator of RNA polymerase II transcription sununit 6 homolog	Med6	0.3	**5. mRNA splicing**			Nucleoporin 133	Nup133	29.9
			Cell division cycle 5-like	Cdc5l	3.9	RNA, member RAS oncogene family	*Ran	3.2
Nuclear receptor coactivator 3	Ncoa3	4.3	DEAD (Asp-Glu-Asp) box polypeptide 10	Ddx10	3.0	Similar to RNA protein	Rgd13.6195	0.3, 7.0
Peroxisome proliferative activeated receptor gamma,coactivated receptor 1 alpha	Ppargc1a	0.2	DEAD (Asp-Glu-Asp) box polypeptide 21	Ddx21	7.8	UPF3 regulator of nonsense transcripts homolog A	Upf3a[8]	0.2
			DEAD (Asp-Glu-Asp) box polypeptide 39	Ddx39[7]	0.3, 3.5	**8. mRNA catabolism**		
PPAR binding protein	*Pparbp	5.0	DEAD (Asp-Glu-Asp) box polypeptide 46	Ddx46	0.2	Heat shock 70kD protein 1B	*Hspa1b	0.3, 3.6
Proteasome 28 sununit, beta	*Psme2	4.0	DEAD (Asp-Glu-Asp) box polypeptide 51	Ddx51	0.3	Polyribonucleotide nucleotidyl transferase 1	Pnpt1	4.0
Small nuclear RNA activating complex, polypeptide 5	Snapc5	0.3	DEAD (Asp-Glu-Ala-His) box polypeptide 38	Dhx38	15.5	Zinc finger protein 36	*Zfp36	0.1, 4.6
Small nuclear ribonucleoprotein N	*Snrpn	7.3	LSM3 homolog, U6 small nuclear RNA associated	Lsm3	3.2	**These genes can't be classified definitely.**		
TAF11 RNA polymerase II, TATA box binding protein-associated factor	Taf11	7.2	LSM6 homolog, U6 small nuclear RNA associated	Lsm6	0.3	ElaC homolog 2	Elac2	22.4
			LSM7 homolog, U6 small nuclear RNA associated	Lsm7	15.5	GTP binding protein 3	*Gtpbp3	5.2
TAF13 RNA polymerase II, TATA box binding protein-associated factor	Taf13	3.2	Myeloblastosis oncogene-like 1	Mybl1	9.2	High mobility group 20B	Hmg20b	8.3
			NHP2 non-histone chromosome protein 2-like 1	Nhp2l1	3.2	Methyltransferase-like 3	Mettl3	0.3
TAF15 RNA polymerase II, TATA box binding protein-associated factor	Taf15	9.0	Pleiotropic regulator 1 homolog	Plrg1	3.4	Nucleolar and coiled-body phosphoprotein 1	*Nolc1	3.7
			PRP 18 pre-mRNA processing factor 18 homolog	Pprf18	6.8	Programmed cell death protein 11	Pdcd11	3.7
TAF6-like RNA polymerase II, p300/CBP-associated factor-associated factor	Taf6l	0.1	RNA binding motifprotein 25	Rbm25	4.0	Period homolog 1	*Per1	0.3, 4.3
			Ribonuclease, RNase A family 4	Rnase4	0.1	Polymerase (RNA) II (DNA directed) polypeptide B	Polr2b	3.0
Transforming growth factor, beta 1	*Tgfb1	4.0	Scaffold attavhment factor B	*Safb	0.2	Polymerase (RNA) II (DNA directed) polypeptide C	Polr2c	0.2
TAF9-like RNA polymerase II, TATA box binding protein-associated factor	Taf9l	0.1, 3.2	Splicing factor 3a, subunit 1	Sf3a1	8.6	Processing of precursor 4, ribonuclease P/MRP family	Pop4	3.7
			Splicing factor 3a, subuni 2	Sf3a2	4.3	Pituitary tumor-transforming 1	Pttg1	0.3, 32.0
Thyroid homone receptor associated protein 3	Thrap3	4.8	Splicing factor 3b, subuni 2	Sf3b2	0.2	Ribonuclease P 25 subunit	Rpp25	4.3
Thyroid homone receptor associated protein 4	Thrap4	0.2	Splicing factor,arginine/serine-rich 2, interacting protein	Sfrs2ip	4.2	Ribonuclease P/MRP 38kDa subunit	Rpp38	0.2
2. Single stranded RNA elongation			Splicing factor, arginine/serine rich 9	Sfrs9	4.2	Exportin 1, CRM1 homolog	*Xpo1	3.2

*shows reported genes associated with liver regeneration; the number on the top right of gene represents gene is associated with another course.

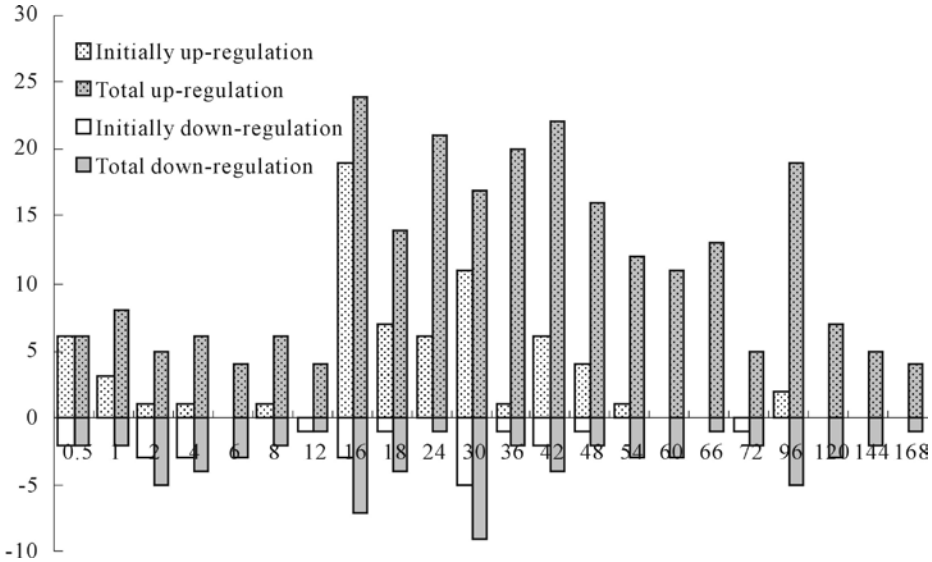

Figure 1. The initial and total expression complexion of 92 RNA biosynthesis, processing, transporting or catabolism-associated genes at each time point of LR. X-axis represents recovery time after PH (h); Y-axis shows the number of initial and total genes at each time point.

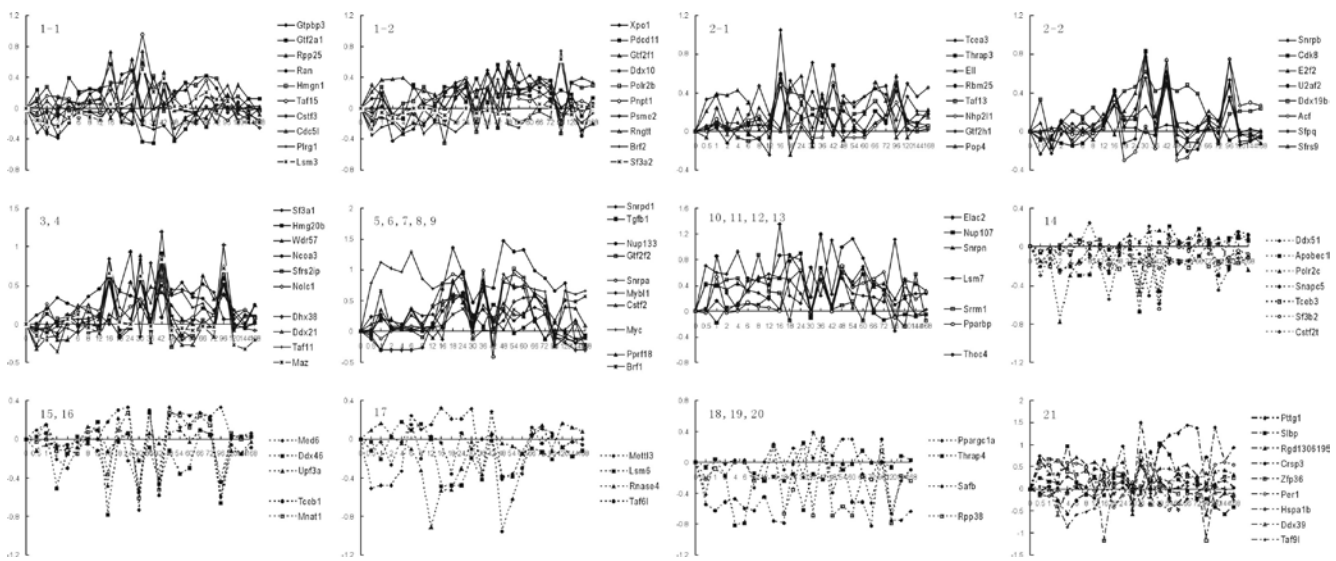

Figure 2. Expression patterns of 92 RNA biosynthesis, processing, transporting or catabolism-associated genes during LR. 21 expression patterns were obtained by the analysis of detection data of Rat Genome 230 2.0 array with Microsoft Excel. 1 – 13: 63 up-regulation genes; 14 – 20: 20 down-regulation genes; 21: 9 up/down-regulation genes. X-axis represents recovery time after PH (h); Y-axis shows logarithm ratio of the signal values of genes at each time point to control.

volved; (6) up-regulation in two phases, at 16 – 24 and 36 – 120 h, 18 – 24 and 54 – 60 h, 2 genes involved; (7) up-regulation at one time point/two phases, 3 genes involved; (8) up-regulation at one time point/three phases, 1 gene involved; (9) up-regulation at two time points/one phase, 2 genes involved; (10) up-regulation at three time points/one phase, 3 genes involved; (11) up-regulation at three time points/two phases, 1 gene involved; (12) up-regulation at multiple time points/one phase, 2 genes involved; (13) up-regulation at multiple time points/two phases, 1 gene involved; (14) down-regulation at one time point, at 2, 16, 30, 36, 42 h, 7 genes involved; (15) down-regulation at two time points, at 2 and 16 h, 16 and 30 h, 30 and 96 h, 3 genes involved; (16) down-regulation at three time points, 2 genes involved; (17) down-regulation in one phase, at 0.5 – 2 h, 12 – 18 h, 16 – 24 h,

48 – 54 h, 4 genes involved; (18) down-regulation at one time point/one phase, at 30 and 4 – 6 h, 72 and 120 – 168 h, 2 genes involved; (19) down-regulation at one time point/three phases, 1 gene involved; (20) down-regulation at three time points/one phase, 1 gene involved; (21) up/down-regulation mixed, 9 genes involved.

3.4 Expression dynamic and interrelations of RNA biosynthesis, processing, transporting or catabolism-associated genes during LR

To seek after the interrelation among the related genes of RNA biosynthesis, processing, transporting or catabolism, we constructed the web regulated picture used the ResnetCore1.2 database of the Pathway Studio 5.0. In which, one node shows one gene, and every link expresses the interelation between the genes. And there were 231 genes and 425 links contained in this picture (Figure 3).

4 Discussion

Information stream from DNA to protein, RNA not only take and transfer the information, but also play an important roles in gene expression and cellular physiological and biochemical activities. Finding from our research, there are 25 genes such as subunit of RNA polymerase III transcription initiation factor IIIB BRF1/BRF2 homolog (BRF1/BRF2)[38,39] promote the initiation of RNA transcription. The genes encoding the above proteins have the identical or similar expression profiles at some time points while different at others, inferring that they may co-regulate the initiation of RNA transcription in regenerating hepatocyte. There are 7 genes such as elongation factor RNA polymerase II (ELL)[40] speed up the process of elongation. The meaningful expression profiles of the genes encoding the proteins are same or similar at some points while different at others, indicating that they may co-regulate RNA elongation in regenerating hepatocyte. Among them, myc was up- at 0.5 – 24, 36, 48 – 72, and 120 – 168 h, and reached a peak at 6 h which is 19.7 times higher than the control, presuming that it played a key role in RNA transcipt initiation in the regenerating liver. Tcea3 was up- at 16, and 30 h, and reached a peak at 16 h which was 11.2 times higher than

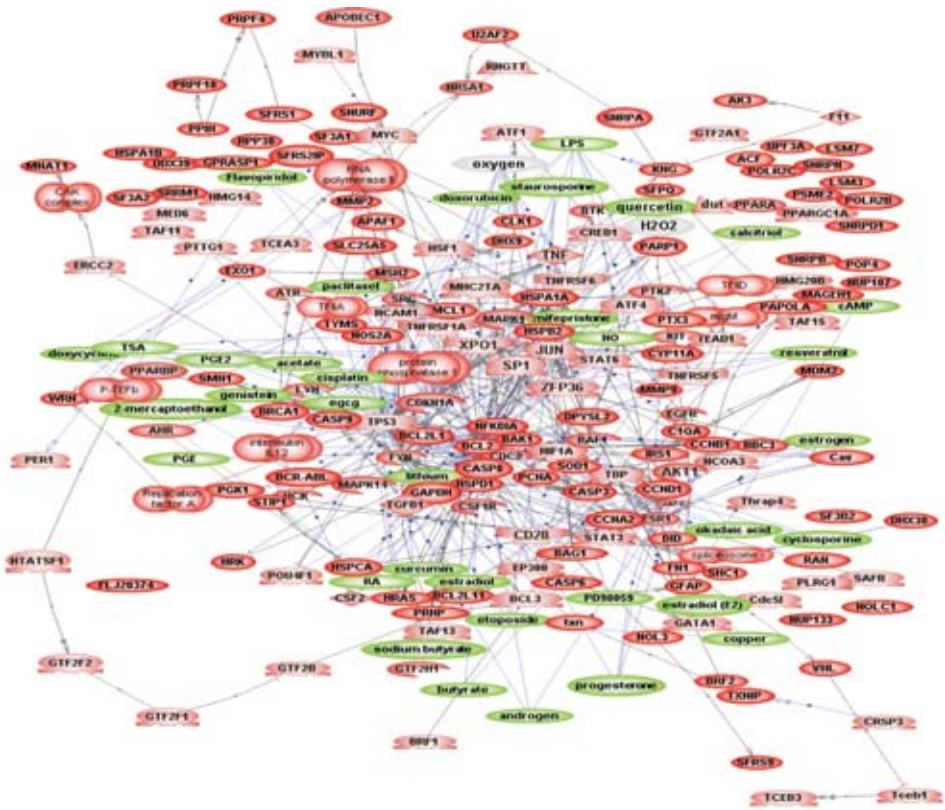

Figure 3. Expression changes and web interrelations of 92 RNA biosynthesis, processing, transporting or catabolism-associated genes during rat LR. Expression changes and web interrelations were obtained by using software called Pathway Studio 5.0. Red shows protein, green shows little molecule.

the control, presuming that it played an important role in RNA strand elongation in the regenerating liver.

RNA guanylyltransferase and 5'-phosphatase (RNGTT)[41] catalyzes 7-methylguanosine to be added to 5' end of mRNA. 4 genes including cleavage stimulation factor 3' pre-RNA subunit 2 (CSTF2)[42] promote the addition of poly (A) tail to the 3' end of mRNA. 32 genes have the roles in Pre-mRNA splicing apobec-1, for example, DEAH box polypeptide 38 (DHX38)[43]. Two genes called apobec-1 complementation factor (ACF)[34] and apolipoprotein B editing complex 1 (APOBEC1)[44] participate in mRNA editing. The meaningful expression profiles of these genes tend to be same or similar at some time points while different at others, indicating that they may co-regulate the addition of 7-methylguanosine cap to the 5' end of mRNA, poly A tail to the 3' end of mRNA, pre-mRNA splicing or mRNA editing in regenerating hepatocyte. Among them, dhx38[31] was up-regulated at 16, 30, 42 and 96 h, and reached a peak at 42 h which was 15.5 times higher than the control, presuming that it played a key role in pre-mRNA splicing in regenerating liver.

8 genes, for example, nucleoporin 133 (NUP133)[45] catalize the mRNA export from nucleus, which are same or similar at some time points while different at others, indicating that they may co-regulate the export of mRNA from nucleus. Among them, nup133 was up-regulated at 16 – 24 and 32 – 120 h, and reached a peak at 48 h which was 29.9 times higher than the control, presuming that it played a key role in this process in regenerating liver.

Heat shock 70 kD protein 1B (HSPA1B)[46], polyribonucleotide nucleotidyltransferase 1 (PNPT1), UPF3A regulator of nonsense transcripts homolog (UPF3A)[47] and zinc finger protein 36 (ZFP36)[48] modulate RNA catabolism, and they are same or similar at some time points while different at others, indicating that they may co-regulate the RNA cataboliam. In which, pnpt1 was up-regulated and reached the peak.at 48h, which was 4 times higher than the control, presuming that it played an important role in RNA catabolism in regenerating liver.

5 Conclusion

In conclusion, the expression changes of the genes associated with RNA biosynthesis, processing, transporting, catabolism after rat PH were investigated using high-throughput gene expression analysis. It was primarily confirmed that RNA transcription is enhanced in prophase, metaphase and early-anaphase; RNA catabolism is enhanced at prophase and metaphase, which were closely related with LR. Rat Genome 230 2.0 array was a useful tool analyzing the activities mentioned above at the transcriptional level. However, DNA→mRNA→protein were influenced by many factors including proteins interaction. Therefore, the above results will be further analyzed by the techniques, such as Northern blotting, protein chip, RNA interference, protein-interaction etc.

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