Effect of genetic variants in FAS and let-7a on radiation-induced intestinal toxicity in the treatment of prostate cancer

Type
Research paper

Keywords
prostate cancer, radiotherapy, Fas, intestinal toxicity, let-7a, rs1800682, rs10739971

Abstract
Introduction
The present study aimed to explore the effects of pri-let-7a-1 rs10739971 and FAS-670 rs1800682 polymorphisms on the pathogenesis of radiation induced intestinal toxicity in prostate cancer (PC) patients.

Material and methods
380 PC patients with or without signs of intestinal toxicity were enrolled to study the effects of let-7a rs10739971 and FAS-670 rs1800682 polymorphisms on rectal volume and the risk of intestinal toxicity. In addition, real-time PCR, Western-blot analysis, immunohistochemistry, luciferase assays and computational analyses were performed to explore the mechanism underlying the role of let-7a rs10739971 polymorphism in radiation induced intestinal toxicity.

Results
The let-7a rs10739971 polymorphism but not the FAS-670 rs1800682 polymorphism was closely related to the risk of radiation induced intestinal toxicity featured by a high rectal volume. In addition, there was no obvious association between the rectal volume and the genotype and allele frequencies of FAS -670 rs1800682 and Pri-let-7a-1 rs10739971 polymorphisms. The GG genotype of let-7a rs10739971 polymorphism reduced let-7a expression but enhanced FAS expression. In addition, the intestinal toxicity (-) group showed a much higher level of let-7a and a much lower level of FAS than the intestinal toxicity (+) group. FAS was a virtual target gene of let-7a, which decreased FAS protein expression in a dose-dependent manner.

Conclusions
The GG genotype of pri-let-7a-1 rs10739971 polymorphism could increase the risk of radiation induced intestinal toxicity in PC patients. Therefore, the pri-let-7a-1 rs10739971 polymorphism could be used as a putative marker to predict the risk of intestinal toxicity in PC patients undergoing radiotherapy.
Effect of genetic variants in FAS and let-7a on radiation-induced intestinal toxicity in the treatment of prostate cancer

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Abstract

Background: The present study aimed to explore the effects of pri-let-7a-1 rs10739971 and FAS-670 rs1800682 polymorphisms on the pathogenesis of radiation induced intestinal toxicity in prostate cancer (PC) patients. Method: 380 PC patients with or without signs of intestinal toxicity were enrolled to study the effects of let-7a rs10739971 and FAS-670 rs1800682 polymorphisms on rectal volume and the risk of intestinal toxicity. In addition, real-time PCR, Western-blot analysis, immunohistochemistry, luciferase assays and computational analyses were performed to explore the mechanism underlying the role of let-7a rs10739971 polymorphism in radiation induced intestinal toxicity. Result: The let-7a rs10739971 polymorphism but not the FAS-670 rs1800682 polymorphism was closely related to the risk of radiation induced intestinal toxicity featured by a high rectal volume. In addition, there was no
obvious association between the rectal volume and the genotype and allele frequencies of FAS -670 rs1800682 and Pri-let-7a-1 rs10739971 polymorphisms. The GG genotype of let-7a rs10739971 polymorphism reduced let-7a expression but enhanced FAS expression. In addition, the intestinal toxicity (-) group showed a much higher level of let-7a and a much lower level of FAS than the intestinal toxicity (+) group. FAS was a virtual target gene of let-7a, which decreased FAS protein expression in a dose-dependent manner. **Conclusion:** The GG genotype of pri-let-7a-1 rs10739971 polymorphism could increase the risk of radiation induced intestinal toxicity in PC patients. Therefore, the pri-let-7a-1 rs10739971 polymorphism could be used as a putative marker to predict the risk of intestinal toxicity in PC patients undergoing radiotherapy.

**Running title:** Rs1800682 and rs10739971 are associated with prostate cancer

**Key word:** prostate cancer, intestinal toxicity, radiotherapy, let-7a, FAS, rs1800682, rs10739971

**Introduction**

At present, prostate cancer (PC) is regarded as a leading contributor of cancer-related mortality in males, while radiotherapy (RT) was applied as one of the treatment options [1]. However, the efficacy of RT in PC treatment is limited by its rectal toxicity, which exerts a negative effect on patients’ life quality [1]. Past studies showed that the prevalence and magnitude of RT-induced rectal toxicity varies significantly according to the characteristics of patients and radiation regimens, including the dose and volume of radiation [2]. In fact, as reported by a randomized study and a meta-analysis enrolling more than 2,000 patients, a higher delivered dose of total radioactivity to the prostate substantially elevated rectal toxicity [3, 4].

It was shown that single nucleotide polymorphism (SNP) located in the mRNAs of FASL and FAS increased the susceptibility to high-grade rectal and/or urinary toxicity in PC patients undergoing radiation therapies, indicating that the FASL −844 C>T SNP exerted a protective impact against the onset of high-grade toxicity during the RT of PC patients.
SNPs located in gene promoters were shown to affect the transcription of host genes, thus subsequently affecting the susceptibility to diseases [6]. Two SNPs located in FAS promoter, i.e., rs2234767 1377 G>A and rs1800682670 A>G, were reported to affect the expression of STAT1 and SP1 genes, respectively, which in turn dysregulates the expression of FAS [7, 8].

MicroRNA (miRNA) can affect the expression of its target genes by interacting with the 3’ UTRs of these genes and subsequently altering their translation. The complementarity formed between the 3’ UTR of target mRNA and miRNA results in mRNA degradation and translation inhibition in both plants and mammals [9]. The miRNAs act as either oncogenes [10] or tumour suppressors [10]. The miRNA let-7a was characterized as a tumour suppressor in several human cancers [11]. Dong et al reported that let-7a expression was reduced in resected PC samples [12]. In addition, PC-3 and DU145 cells (androgen-independent) express less let-7a than LNCaP cells (androgen-dependent). Target prediction algorithms indicated that let-7a1 could target a number of oncogenes, such as IGF1R. As a SNP located in the 559 bp position upstream of the coding sequence of let-7a-1, rs10739971 was shown to impact the susceptibility to gastric cancer. Furthermore, the rs10739971 SNP in pri-let-7a-1 could interact with the rs9471643 and rs6458238 SNPs in PGC to change the risk of atrophic gastritis [13].

FAS/FASL signaling pathway is functionally involved in the pathogenesis of radiation induced intestinal toxicity in prostate cancer [5, 14]. In addition, the rs1800682 SNP in the promoter region of FAS was shown to affect the expression of FAS, while the rs10739971 SNP in the flanking region of let-7a could alter the expression of let-7a, a negative regulator of FAS [15-17]. In this study, we collected samples from PC patients who have been treated with radiotherapy to investigate the role of the two SNPs in radiation induced intestinal toxicity.

Materials and Methods

Human sample collection
A total of 380 PC patients were enrolled in our research, which consisted of 122 PC patients diagnosed with radiation induced intestinal toxicity (the intestinal toxicity (+) group) and 258 PC patients free of intestinal toxicity (the intestinal toxicity (-) group). All subjects underwent RT prior to their enrollment in this study. The demographic and clinicopathological characteristics of all PC subjects, such as age at the initiation of RT, gender, PSA level upon the first diagnosis of PC, T1/T2 or T3/T4 stage of PC, grade 1-2 or 3 of PC, the history of any resection surgery prior to RT, the history of any adjuvant hormone therapy prior to RT, the administration of oral anticoagulants, the history of smoking (current smoker, non-smoker or past smoker), the presence of diabetes mellitus, the presence of hypertension, the levels of administrated median total dose (Gy), mean rectal dose (Gy) and mean V_{60} rectum dose (Gy), were collected and summarized. Student t test was utilized to perform the statistical comparison between the demographic and clinicopathological characteristics of the PC subjects in these two groups.

In addition, the peripheral blood samples of all subjects were collected during fasting to analyze their expression of various target genes. At the same time, PC tissue samples were collected from 72 subjects during their surgical operation and were used for subsequent genotyping and immunohistochemistry assays.

**Radiation therapy (RT)**

All of the subjects enrolled in this study were treated by RT prior to their enrollment. Among these subjects, 40% patients began their RT treatment in the prone position, while the remaining subjects began their RT treatment in the supine position. All subjects underwent periodic CT scans using an in-room CT system installed in the RT treatment room to follow up with their prognosis of PC. In addition, the position of prostate in each subject was determined before the dosing in each RT cycle via the in-room CT image system to ensure the accurate delivery of RT. During the CT scan, the position of each subject was initially adjusted with label marks on skin and lasers. In the next step, images were acquired using the in-room CT system. In case of any major
deviation in the position of a subject, the matching of pelvic bone location was performed using the in-room CT system, followed by the manual matching carried out by a RT therapist to make sure the location of the prostate in each subject was at the planned location of RT treatment. Subsequently, feces and gas in the rectum, changes in bladder volume, and deviation of adjacent intestines (large and small intestines) from the planning CT images were checked. When the presence of feces and gas was noted in the rectum, defecation or passage of gas was encouraged. Nevertheless, if the situation of the subject did not improve, deaeration was performed by inserting a catheter into the rectum via the anus. Moreover, patients were encouraged to drink water when they had insufficient bladder volumes. At this moment, CT images were acquired once again. In the next step, irradiation was performed after there was enough geometric verification.

**The definitions of target volumes**

In this study, CTV, i.e., clinical target volume, was determined in subjects with a low risk of RT induced toxicity by calculating the volume of their prostate plus the volume of the base of seminal vesicles. However, in subjects with a moderate to high risk of RT induced toxicity, CTV was determined by calculating the volume of their prostate plus the volume of 2/3 of seminal vesicles along the proximal direction. In addition, PTV, i.e., planning target volume, of each subject was calculated by adding 9 mm along the inferior direction, 9 mm along the left direction, 10 mm along the superior direction, 9 mm along the right direction, 6 mm along the posterior direction, and 6 mm along the posterior direction of the prostate with automatic expansion.

**LSE scoring**

The rectal LSE values were assessed by the LENT-SOMA scale.

**Level of soluble Fas in the serum**

After the collection of peripheral samples from each subject, the serum component in each sample was isolated via centrifugation and the level of soluble Fas was measured.
using a commercially kit of sandwich ELISA (Diaclone, Besancon, France) in accordance
to the instructions of the kit provider.

Genotyping by Taqman assays

Using the peripheral samples collected from each subject, the genotypes of rs1800682
SNP at -670 position of FAS and the rs10739971 SNP in pri-let-7a-1 were determined
using a TaqMan Gene Expression & Genotyping assay kit (Thermo Fisher Scientific,
Waltham, MA) following the instructions of the kit. Subsequently, based on the results
of rs10739971 genotyping, the subjects were allocated into three groups, i.e., AA, AG
and GG groups.

RNA isolation and real time PCR

Total RNA was first isolated from peripheral blood and tissue samples using Trizol
reagents (Invitrogen, Carlsbad, CA). After converting isolated RNA to cDNA, real time
PCR was performed according to routine methods using a SYBR Green Master mix kit
(ABI, Foster City, CA) on a PRISM 7900HT real time PCR machine (ABI, Foster City, CA), so
as to quantify the relative expression of let-7a and FAS. The expression of U6 and β-actin
was used as the internal control during the calculation of mRNA relative expression.

Cell culture and treatment

DU145 and PC-3 cells were maintained in DMEM (Invitrogen, Carlsbad, CA) added with
10% fetal calf serum and appropriate antibiotics. Subsequently, the cells were divided
into different groups and transfected with let-7a, let-7a inhibitor, or FAS siRNA,
respectively, using Lipofectamine 3000 (Invitrogen, Carlsbad, CA) following the
instructions of the manufacturer. The expression of target genes was measured at 48
hrs after transfection.

Vector construction and luciferase assays

The 3' UTR of FAS containing the let-7a binding site was sub-cloned into a pcDNA3.1
luciferase reporter vector to generate the plasmid for wild type FAS 3' UTR. In the next
step, the let-7a binding site located in the 3' UTR of FAS was subjected to site-directed
mutagenesis using a Stratagene gene mutagenesis kit (Stratagene, San Diego, CA)
according to kit recommendations. The mutant FAS 3' UTR was similarly sub-cloned into
another pcDNA3.1 luciferase reporter vector to generate the plasmid for mutant FAS
3'UTR. Then, DU145 and PC-3 cells were seeded into 96-wells plates and grown to 50%
confluence, followed by the co-transfection with let-7a and wild type or mutant FAS
3'UTR using Lipofectamine 3000. After 48 hrs of transfection, the luciferase activity of
transfected cells was determined using a Bright-Glo Luciferase Assay kit (Promega,
Madison, WI).

**Western blot analysis**

Western blot was carried out using a conventional method to determine the relative
protein expression of FAS in the peripheral blood and tissue samples collected from
each subject. The primary anti-FAS antibodies and HRP-labeled secondary antibodies
were purchased from Abcam (Cambridge, MA). The protein expression of β-actin was
used as the internal control to calculate the expression of Fas. In addition, the protein
bands on the PVDF membranes were developed using an ECL reagent kit (BD
Biosciences, San Jose, CA) according to kit manual. The gray values of protein blots were
analyzed using Image J software (NIH, Bethesda, MD).

**Immunohistochemistry assays**

Collected tissue samples were routinely paraffin embedded, sectioned to 5 μm in
thickness, deparaffinized, made transparent in xylene, rehydrated using gradient alcohol,
blocked at room temperature for 10 min in 3% H₂O₂, and incubated with 0.1% trypsin
for 30 min at 37 °C to retrieve antigens. Then, the tissue sections were immersed in a
solution of primary anti-FAS antibodies (1: 200, Abgent, San Diego, CA) at 4 °C overnight,
followed by another 1 hr of incubation at 37 °C for 30 min with biotin-labeled secondary
IgG antibodies (Invitrogen, Carlsbad, CA). After staining with 3,3-diaminobenzidine (VWR,
Waltham, MA) and hematoxylin, the sample sections were assessed using Image-Pro
Plus and a Leica image analyzer (Leica, Wetzlar, Germany) under a 400x magnification.
**Statistical analysis**

All experimental data was shown as means ± Standard Deviation. The comparisons among different groups were done using one-way ANOVA or Student’s t tests. A minimum of three repeated tests were done for each set of experiments. A *P* value of ≥ 0.05 was associated with statistical significance.

**Results**

Demographic, clinicopathological and genotypic parameters of the participants recruited in this study

A total of 380 PC patients were enrolled in our research, which consisted of 122 PC patients diagnosed with radiation induced intestinal toxicity (the intestinal toxicity (+) group) and 258 PC patients free of intestinal toxicity (the intestinal toxicity (-) group). All subjects underwent RT prior to their enrollment in this study. The demographic and clinicopathological characteristics of all PC subjects were summarized in table I. Student t tests were utilized to perform the statistical comparison and the results revealed no obvious differences between the two groups in terms of above demographic, clinicopathological and genotypic parameters.

Pri-let-7a-1 rs10739971 was associated with radiation induced intestinal toxicity in PC

Multivariate logistic regression analysis was used to evaluate the role of the pri-let-7a-1 rs10739971 SNP and FAS -670 rs1800682 SNP in the risk of radiation induced intestinal toxicity in PC. The results showed that the FAS-670 rs1800682 SNP was not associated with the risk of radiation induced intestinal toxicity in PC, while the pri-let-7a-1 rs10739971 SNP was closely associated with the risk of radiation induced intestinal toxicity in PC (Table 2).

Pri-let-7a-1 rs10739971 was associated with a high rectal volume

Rectal volume of radiotherapy was determined for all participants. Among all subjects, 190 PC patients had a high rectal volume and 190 patients had a low rectal volume.
Then, the role of the genotype and allele frequencies of the pri-let-7a-1 rs10739971 SNP and FAS -670 rs1800682 SNP in the risk of radiation induced intestinal toxicity was evaluated. As shown in Table 3, we observed a significant association between the genotype distribution of the Pri-let-7a-1 rs10739971 SNP and a high rectal volume. Both the heterozygous GA (P = 0.011, OR = 2.24, 95% CI = 1.15-4.37) and homozygous AA (P = 0.0062, OR = 4.92, 95% CI = 1.57-15.38) variants were more frequent among patients with a high rectal volume. The A allele (P = 0.0005, OR = 2.37, 95% CI = 1.45-3.88) was also significantly more frequent in patients with a high rectal volume. However, there were no significant associations between the genotype and allele frequencies of the FAS -670 rs1800682 SNP and a high rectal volume. As shown in Table 4, there was no obvious association between a low rectal volume and the genotype and allele frequencies of the FAS -670 rs1800682 and Pri-let-7a-1 rs10739971 SNPs.

**Pri-let-7a-1 rs10739971 was involved in radiation induced intestinal toxicity by affecting let-7a and FAS expression**

Real-time PCR and IHC were performed to compare the expression of let-7a and FAS in prostate tissue and peripheral blood samples collected from the PC patients in the intestinal toxicity (+) and intestinal toxicity (-) group, as well as in patients carrying different genotypes (AA, AG and GG). The expression of let-7a was much higher in the prostate tissue (Fig. 1A) and peripheral blood (Fig. 2A) samples collected from the intestinal toxicity (-) group compared with the intestinal toxicity (+) group. In addition, the prostate tissue (Fig. 1B) and peripheral blood (Fig. 2B) samples collected from subjects carrying the GG genotype exhibited a lower level of let-7a compared to the samples in the AA and AG groups (Fig. 1B). Meanwhile, the mRNA (Fig. 1C and 2C) and protein (Fig. 1E and 2E) expression of FAS in the prostate tissue (Fig. 1C and 1E) and peripheral blood (Fig. 2C and 2E) samples collected from the intestinal toxicity (+) group was much higher than those in the intestinal toxicity (-) group, while the FAS mRNA expression in the prostate tissue (Fig. 1D) and peripheral blood (Fig. 2D) samples collected from the GG group was higher than that in the AA and AG groups. We also evaluated the effect of FAS -670 rs1800682 SNP on the expression of let-7a and FAS, and
no difference was noted among patients carrying different genotypes of rs1800682 SNP (data not shown).

FAS was confirmed as a direct target of let-7a

Based on the computational analysis, we identified let-7a as a direct target of FAS (Fig. 3A). To further confirm whether let-7a and FAS can interact with each other, we conducted a luciferase assay to show that FAS is a direct target of let-7a, since the luciferase activity of wild-type FAS 3’ UTR in DU145 and PC-3 cells over-expressing let-7a was significantly lower compared with that in cells expressing mutant FAS 3’ UTR or the scramble control (Fig. 2B). Real-time PCR and Western-blot analysis were carried out to investigate the effect of let-7a on FAS expression. In DU145 and PC-3 cells, the transfection with let-7a dose-dependently increased let-7a expression, while the transfection with FAS siRNA had no effect on let-7a expression (Fig. 3C). In addition, the transfection of DU145 and PC-3 cells with let-7a reduced the levels of FAS mRNA (Fig. 3D) and protein (Fig. 3E) in a dose-dependent manner. On the contrary, the transfection with let-7a inhibitor dose-dependently decreased let-7a expression (Fig. 3F) upregulated mRNA (Fig. 3G) and protein (Fig. 3H) expression of FAS.

Discussion

In this study, we enrolled 380 PC patients with or without signs of radiation induced intestinal toxicity to investigate the association between the risk of radiation induced intestinal toxicity and the let-7a rs10739971 and FAS-670 rs1800682 SNPs using a multivariate logistic regression analysis. The results showed that the let-7a rs10739971 SNP but not the FAS-670 rs1800682 SNP was closely related to the risk of radiation induced intestinal toxicity. In addition, based on their rectal volume, we stratified the subjects into a high rectal volume group and a low rectal volume group, and showed an obvious association between the genotype distribution of the let-7a rs10739971 SNP and high rectal volume. In contrary, in the low rectal volume group, neither of the two SNPs was associated with radiation induced intestinal toxicity.
As a family member of let-7 containing 12 different miRNAs, including miR-98 and let-7a-1, -7a-2, -7a-3, -7b, -7e, -7f-1, -7f-2, -7g, and -7i, let-7a was demonstrated in previous studies on clinical specimens to affect the development of human cancers, such as lung cancer, medulloblastoma, breast cancer, ovarian cancer, and ES [18, 19]. Nevertheless, it was also demonstrated that miRNAs could act as oncogenes according to different cellular contexts. Under certain conditions, miRNAs could switch from their repressive role to an activating role via upregulating their targets, including let-7a [20]. Lu et al. (2007, 2011) found that ectopic expression of let-7a substantially activated the expression of IGF-II, which plays an essential role in the onset of ES [21-24]. Let-7a could also be used as a marker for the diagnosis and treatment of PC [25]. A recent study (Wang et al.2) demonstrated that let-7a1 could suppress the levels of IGF1R by targeting the 3’ UTR of its mRNA [26]. Moreover, let-7a1-induced downregulation of IGF1R resulted in reduced expression of c-fos and Elk1 activity, thus leading to inhibited proliferation of PC-3 cells and enhanced apoptosis, while the suppression of let-7a1 expression up-regulated IGF1R expression and increased Elk1 activity to promote cell proliferation [26]. It was proven that let-7a, one of the most conserved and abundant miRNAs in BMSCs, targets both Fas and Fasl mRNAs to suppress their expression [27]. Let-7a is also enriched in BMSCs and can suppress both Fas and Fasl expression [27]. Therefore, let-7a is a crucial regulator of immunoregulatory properties in BMSCs. In this study, we carried out computational analyses, luciferase assays, real-time PCR and Western-blot analyses to explore the interaction between let-7a and FAS. Our results identified FAS as a virtual target gene of let-7a, which inhibited the expression of FAS.

As a receptor of tumor necrosis factor, Fas could induce apoptosis and prevent the onset of autoimmune diseases and cancer [28, 29]. In addition, Fas could enhance cancer metastasis and growth by regulating the proliferation and survival of cancer cells [30]. Therefore, Fas is deemed essential for the development of cancer and has demonstrated some potential in clinical application, although the detailed mechanism underlying the role of Fas in cancer and cell apoptosis remains elusive [31, 32]. In addition, the subjects carrying the −844CC allele of FASL showed much higher levels of
FASL expression than the carriers of homozygous −844T genotype, which can significantly affect the toxicity induced by radiation [33]. Therefore, the −844T allele of FASL may protect its carriers against RT-induced urinary and/or rectal toxicity [5]. In this study, we performed real-time PCR and IHC to explore the mechanism underlying the role of let-7a rs10739971 SNP in radiation induced intestinal toxicity. The results showed that the GG genotype of let-7a rs10739971 SNP reduced let-7a expression while enhancing FAS expression. In addition, the intestinal toxicity (−) group showed a much higher level of let-7a and a much lower level of FAS than the intestinal toxicity (+) group.

An A to G SNP has been found at the −670 position of Fas promoter and may affect the expression of STAT-1 [34]. In addition, this SNP was linked to the onset of PC, hepatocellular cancer, breast cancer, and esophageal cancer [35]. Recent studies also revealed that the SNPs located in some members of the let-7 family can affect the susceptibility to cancer. In particular, the interaction between the rs1917799 SNP in ERCC6 and the rs10739971 SNP in pri-let-7a-1 could substantially change the susceptibility to GC [13]. Moreover, the rs10877887 SNP in let-7 promoter was associated with a substantially increased risk of hepatocellular cancer, while the rs629367 SNP located in pri-let-7a-2 could result in a poor prognosis of GC [36, 37]. However, few researchers have studied the correlation between the SNPs in pri-let-7a-1 and the prognosis of cancer, although a SNP in pri-let-7a-1 could alter the binding affinity between let-7a-1 and GATA to affect the expression of pri-miR-34 b/c [38]. It was also speculated that the rs10739971 SNP in pri-let-7a-1 could significantly affect GC prognosis by regulating the expression of mature let-7a. Moreover, there are limitations of this study. All subjects included in this study were Chinese population. And the signaling pathway established in this study should be verified not only in cell lines, but also in vivo in animal models.

**Conclusion**

In conclusion, the FAS rs1800682 and let-7a rs10739971 SNPs were involved in radiation-induced intestinal toxicity in PC patients. In addition, the rs1800682 SNP in the
promoter region of FAS changed the expression of FAS, while the rs10739971 SNP in the 
flanking region of let-7a altered the expression of let-7a, a negative regulator of FAS. 
Therefore, the pri-let-7a-1 rs10739971 polymorphism could be introduced into the clinic 
as a putative marker for the prognosis of intestinal toxicity in PC patients undergoing 
radiotherapy.

Conflict of interest

None

Figure legends

Fig. 1

Differential expression of let-7a and FAS in the prostate tissues collected from different 
groups

A: let-7a level in the intestinal toxicity (+) group was decreased compared with that in 
the intestinal toxicity (-) group

B: The GG genotype of let-7a rs10739971 SNP reduced let-7a expression compared with 
the AA or AG genotype

C: FAS mRNA expression in the intestinal toxicity (+) group was increased compared with 
that in the intestinal toxicity (-) group

D: The GG genotype of let-7a rs10739971 SNP enhanced FAS mRNA expression 
compared with the AA or AG genotype

E: FAS protein in the intestinal toxicity (+) group was much higher than that in the 
intestinal toxicity (-) group

Fig. 2

Differential expression of let-7a and FAS in the peripheral blood collected from different 
groups
A: let-7a expression in the intestinal toxicity (+) group was decreased compared with that in the intestinal toxicity (-) group

B: The GG genotype of let-7a rs10739971 SNP reduced let-7a expression compared with the AA or AG genotype

C: FAS mRNA expression in the intestinal toxicity (+) group was increased compared with that in the intestinal toxicity (-) group

D: The GG genotype of let-7a rs10739971 SNP enhanced FAS mRNA expression compared with the AA or AG genotype

Fig. 3

FAS was confirmed as a direct target of let-7a

A: A putative target of let-7a site was present on FAS 3’UTR

B: let-7a mimics obviously reduced the luciferase activity of wild-type FAS 3’UTR but not that of mutant FAS 3’UTR in DU145 and PC-3 cells

C: let-7a mimic dose-dependently increased let-7a expression in DU145 and PC-3 cells, while FAS siRNA had no effect on let-7a expression

D: let-7a mimics decreased FAS mRNA expression in DU145 and PC-3 cells in a dose-dependent manner

E: let-7a mimics decreased FAS protein expression in DU145 and PC-3 cells in a dose-dependent manner

F: let-7a inhibitors dose-dependently decreased let-7a expression in DU145 and PC-3 cells

G: let-7a inhibitors up-regulated FAS mRNA expression in DU145 and PC-3 cells in a dose-dependent manner

H: let-7a inhibitors up-regulated FAS protein expression in DU145 and PC-3 cells in a dose-dependent manner
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<th>Intestinal toxicity (-) (N=258)</th>
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</tr>
<tr>
<td>Yes</td>
<td>31 (25.4)</td>
<td>69 (26.7)</td>
<td></td>
</tr>
<tr>
<td>No</td>
<td>91 (74.6)</td>
<td>189 (73.3)</td>
<td></td>
</tr>
<tr>
<td>Hypertension</td>
<td></td>
<td></td>
<td>0.721</td>
</tr>
<tr>
<td>Yes</td>
<td>71 (58.2)</td>
<td>159 (61.6)</td>
<td></td>
</tr>
<tr>
<td>No</td>
<td>51 (41.8)</td>
<td>99 (38.4)</td>
<td></td>
</tr>
<tr>
<td>Mean rectal dose (range)</td>
<td>73 Gy (64-78 gy)</td>
<td>75 Gy (63-78 gy)</td>
<td></td>
</tr>
<tr>
<td>Mean rectal dose (Gy) ± SD</td>
<td>38.8 ± 7.2</td>
<td>39.7 ± 6.7</td>
<td>0.842</td>
</tr>
<tr>
<td>Mean V60 rectum (ccm) ± SD</td>
<td>21.6 ± 4.2</td>
<td>22.5 ± 6.4</td>
<td>0.781</td>
</tr>
</tbody>
</table>

Table 1. Demographic and clinicopathological characteristics of the participants of this study
Table 2. Comparison of genotype and allele of rs10739971 and rs1800682 between radiation induced intestinal toxicity (+) and radiation induced intestinal toxicity (-) groups.

<table>
<thead>
<tr>
<th>Genotype</th>
<th>radiation induced intestinal toxicity (+) (N=122)</th>
<th>radiation induced intestinal toxicity (-) (N=258)</th>
<th>OR (95%CI)</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>FAS -670 rs1800682</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>AA</td>
<td>34 (0.28)</td>
<td>67 (0.26)</td>
<td>Reference (1.00)</td>
<td></td>
</tr>
<tr>
<td>AG</td>
<td>62 (0.51)</td>
<td>129 (0.50)</td>
<td>1.05 (0.63-1.76)</td>
<td>0.835</td>
</tr>
<tr>
<td>GG</td>
<td>26 (0.21)</td>
<td>62 (0.24)</td>
<td>1.21 (0.65-2.24)</td>
<td>0.544</td>
</tr>
<tr>
<td>AA vs. AG+GG</td>
<td>88</td>
<td>191</td>
<td>1.10 (0.67-1.78)</td>
<td>0.695</td>
</tr>
<tr>
<td>AA+AG vs. GG</td>
<td>96</td>
<td>196</td>
<td>1.16 (0.69-1.96)</td>
<td>0.557</td>
</tr>
<tr>
<td>A</td>
<td>130</td>
<td>263</td>
<td>Reference (1.00)</td>
<td></td>
</tr>
<tr>
<td>G</td>
<td>114</td>
<td>253</td>
<td>1.09 (0.80-1.48)</td>
<td>0.552</td>
</tr>
<tr>
<td>Pri-let-7a-1 rs10739971</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GG</td>
<td>58 (0.43)</td>
<td>95 (0.37)</td>
<td>Reference (1.00)</td>
<td></td>
</tr>
<tr>
<td>GA</td>
<td>46 (0.41)</td>
<td>113 (0.44)</td>
<td>1.50 (0.93-1.98)</td>
<td>0.093</td>
</tr>
<tr>
<td>AA</td>
<td>16 (0.16)</td>
<td>50 (0.19)</td>
<td>1.99 (0.99-3.65)</td>
<td>0.051</td>
</tr>
<tr>
<td>AA+AG vs. GG</td>
<td>62</td>
<td>163</td>
<td>1.58 (0.99-2.48)</td>
<td>0.054</td>
</tr>
<tr>
<td>AA vs. AG+GG</td>
<td>104</td>
<td>208</td>
<td>1.56 (0.84-2.87)</td>
<td>0.151</td>
</tr>
<tr>
<td>G</td>
<td>162</td>
<td>303</td>
<td>Reference (1.00)</td>
<td></td>
</tr>
<tr>
<td>A</td>
<td>82</td>
<td>213</td>
<td>1.38 (1.01-1.90)</td>
<td>0.047</td>
</tr>
</tbody>
</table>

Table 2. Comparison of genotype and allele of rs10739971 and rs1800682 between radiation induced intestinal toxicity (+) and radiation induced intestinal toxicity (-) groups.
<table>
<thead>
<tr>
<th>Genotype</th>
<th>radiation induced intestinal toxicity (+) (N=61)</th>
<th>radiation induced intestinal toxicity (-) (N=129)</th>
<th>OR (95%CI)</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>FAS -670 rs1800682</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>AA</td>
<td>17 (0.28)</td>
<td>33 (0.26)</td>
<td>Reference (1.00)</td>
<td></td>
</tr>
<tr>
<td>AG</td>
<td>31 (0.51)</td>
<td>65 (0.50)</td>
<td>1.21 (0.66-1.86)</td>
<td>0.765</td>
</tr>
<tr>
<td>GG</td>
<td>13 (0.21)</td>
<td>31 (0.24)</td>
<td>1.28 (0.76-2.34)</td>
<td>0.612</td>
</tr>
<tr>
<td>AA vs. AG+GG</td>
<td>44</td>
<td>96</td>
<td>1.65 (0.68-1.98)</td>
<td>0.712</td>
</tr>
<tr>
<td>AA+AG vs. GG</td>
<td>48</td>
<td>98</td>
<td>1.32 (0.79-2.12)</td>
<td>0.627</td>
</tr>
<tr>
<td>A</td>
<td>65</td>
<td>131</td>
<td></td>
<td></td>
</tr>
<tr>
<td>G</td>
<td>57</td>
<td>127</td>
<td>1.54 (0.91-1.76)</td>
<td>0.671</td>
</tr>
<tr>
<td>Pri-let-7a-1 rs10739971</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GG</td>
<td>37 (0.43)</td>
<td>47 (0.37)</td>
<td>Reference (1.00)</td>
<td></td>
</tr>
<tr>
<td>GA</td>
<td>20 (0.41)</td>
<td>57 (0.44)</td>
<td>2.24 (1.15-4.37)</td>
<td>0.011</td>
</tr>
<tr>
<td>AA</td>
<td>4 (0.16)</td>
<td>25 (0.19)</td>
<td>4.92 (1.57-15.38)</td>
<td>0.0062</td>
</tr>
<tr>
<td>AA+AG vs. GG</td>
<td>24</td>
<td>82</td>
<td>2.68 (1.43-5.03)</td>
<td>0.002</td>
</tr>
<tr>
<td>AA vs. AG+GG</td>
<td>57</td>
<td>104</td>
<td>3.42 (1.13-10.33)</td>
<td>0.028</td>
</tr>
<tr>
<td>G</td>
<td>94</td>
<td>151</td>
<td>Reference (1.00)</td>
<td></td>
</tr>
<tr>
<td>A</td>
<td>28</td>
<td>107</td>
<td>2.37 (1.45-3.88)</td>
<td>0.0005</td>
</tr>
</tbody>
</table>

Table 3. Comparison of genotype and allele of rs10739971 and rs1800682 between radiation induced intestinal toxicity (+) and radiation induced intestinal toxicity (-) groups stratified by rectal volume exposed to radiation (high volume)
<table>
<thead>
<tr>
<th>Genotype</th>
<th>Radiation induced intestinal toxicity (+) (N=61)</th>
<th>Radiation induced intestinal toxicity (-) (N=129)</th>
<th>OR (95%CI)</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>FAS -670 rs1800682</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>AA</td>
<td>18 (0.28)</td>
<td>35 (0.26)</td>
<td>Reference (1.00)</td>
<td></td>
</tr>
<tr>
<td>AG</td>
<td>33 (0.51)</td>
<td>65 (0.50)</td>
<td>1.32 (0.74-1.99)</td>
<td>0.642</td>
</tr>
<tr>
<td>GG</td>
<td>10 (0.21)</td>
<td>29 (0.24)</td>
<td>1.32 (0.79-2.83)</td>
<td>0.423</td>
</tr>
<tr>
<td>AA vs. AG+GG</td>
<td>43</td>
<td>94</td>
<td>1.76 (0.72-2.18)</td>
<td>0.802</td>
</tr>
<tr>
<td>AA+AG vs. GG</td>
<td>51</td>
<td>100</td>
<td>1.42 (0.82-2.63)</td>
<td>0.512</td>
</tr>
<tr>
<td>A</td>
<td>69</td>
<td>135</td>
<td>Reference (1.00)</td>
<td></td>
</tr>
<tr>
<td>G</td>
<td>53</td>
<td>123</td>
<td>1.61 (0.82-1.90)</td>
<td>0.712</td>
</tr>
<tr>
<td>Pri-let-7a-1</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>rs10739971</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GG</td>
<td>21 (0.43)</td>
<td>48 (0.37)</td>
<td>Reference (1.00)</td>
<td></td>
</tr>
<tr>
<td>GA</td>
<td>26 (0.41)</td>
<td>56 (0.44)</td>
<td>0.94 (0.47-1.88)</td>
<td>0.886</td>
</tr>
<tr>
<td>AA</td>
<td>12 (0.16)</td>
<td>25 (0.19)</td>
<td>0.91 (0.38-2.15)</td>
<td>0.832</td>
</tr>
<tr>
<td>AA+AG vs. GG</td>
<td>38</td>
<td>81</td>
<td>0.93 (0.49-1.77)</td>
<td>0.831</td>
</tr>
<tr>
<td>AA vs. AG+GG</td>
<td>47</td>
<td>104</td>
<td>0.94 (0.43-2.03)</td>
<td>0.878</td>
</tr>
<tr>
<td>G</td>
<td>68</td>
<td>152</td>
<td>Reference (1.00)</td>
<td></td>
</tr>
<tr>
<td>A</td>
<td>50</td>
<td>106</td>
<td>1.05 (0.67-1.63)</td>
<td>0.814</td>
</tr>
</tbody>
</table>

Table 4. Comparison of genotype and allele of rs10739971 and rs1800682 between radiation induced intestinal toxicity (+) and radiation induced intestinal toxicity (-) groups stratified by rectal volume exposed to radiation (low volume)
Fig. 1
Differential expression of let-7a and FAS in the prostate tissues collected from different groups
Fig. 2
Differential expression of let-7a and FAS in the peripheral blood collected from different groups
Fig. 3
FAS was confirmed as a direct target of let-7a