Unambiguous Detection of Multiple TP53 Gene Mutations in AAN-Associated Urothelial Cancer in Belgium Using Laser Capture Microdissection

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Abstract

In the Balkan and Taiwan, the relationship between exposure to aristolochic acid and risk of urothelial neoplasms was inferred from the A>T genetic hallmark in TP53 gene from malignant cells. This study aimed to characterize the TP53 mutational spectrum in urothelial cancers consecutive to Aristolochic Acid Nephropathy in Belgium. Serial frozen tumor sections from female patients (n = 5) exposed to aristolochic acid during weight-loss regimen were alternatively used either for p53 immunostaining or laser microdissection. Tissue areas with at least 60% p53-positive nuclei were selected for microdissecting sections according to p53-positive matching areas. All areas appeared to be carcinoma in situ. After DNA extraction, mutations in the TP53 hot spot region (exons 5–8) were identified using nested-PCR and sequencing. False-negative controls consisted in microdissecting fresh-frozen tumor tissues both from a patient with a Li-Fraumeni syndrome who carried a p53 constitutional mutation, and from negative controls consisted in microdissecting fresh-frozen tumor tissues both from a patient with a Li-Fraumeni syndrome who carried a p53 constitutional mutation, and from normal fresh ureteral tissues (n = 4) were processed with high laser power. No unexpected results being identified, molecular analysis was pursued on malignant tissues, showing at least one mutation in all (six different mutations in two) patients, with 13/16 exonic (nonsense, 2; missense, 11) and 3/16 intronic (one splice site) mutations. They were distributed as transitions (n = 7) or transversions (n = 9), with an equal prevalence of A>T and G>T (3/16 each). While current results are in line with A>T prevalence previously reported in Balkan and Taiwan studies, they also demonstrate that multiple mutations in the TP53 hot spot region and a high frequency of G>T transversion appear as a complementary signature reflecting the toxicity of a cumulative dose of aristolochic acid ingested over a short period of time.

Introduction

The Aristolochic Acid Nephropathy (AAN) was first reported in the early 1990’s in Belgian patients having undertaken a weight-loss regimen contaminated with aristolochic acid (AA) [1,2]. AAN is characterized by a rapidly progressive interstitial nephropathy with tubular proteinuria and glucosuria, early severe anemia, extensive hypocalcemic interstitial fibrosis decreasing from the outer to the inner cortical labyrinth, and a rapid development of urinary tract transitional cell carcinomas in 40–46% of the patients within 2–6 years after cessation of exposure [3–6]. AAN is now recognized as a devastating disease occurring worldwide with as many as 100 million people potentially at risk of AA exposure [7]. While the mechanism of AA nephrotoxicity remains to be thoroughly explored, the carcinogenic activity is currently attributed to genotoxicity of AL (aristolactam)-DNA adducts characterized by a high frequency of A>T transversion in the TP53 tumour suppressor gene of AA-associated tumors. This has been well documented in animal experiments [8,9] and, although not consistently, in patients showing clinical and histopathological similarities with the original Belgian AAN cases [10–14]. Whereas AL-DNA adducts demonstrating AA exposure have been well documented in kidney tissues from the Belgian cohort [6,13,16], the presence of A>T transversion witnessing the causal relationship between exposure and malignancy had yet to be investigated. The aim of the present work was therefore to characterize the TP53 mutational spectrum in frozen samples of malignant urothelial tissues from Belgian AAN patients using thoroughly validated genotyping methods.

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Patients and Methods

Ethics Statement

In 2001, a study on the genetic polymorphism of enzymes implicated in the metabolism of aristolochic acid among Belgian AAN patients was approved by Prof JM Maloteaux, Chairman of the Faculty of Medicine and Health Sciences Research Ethics Committee of the Université catholique de Louvain (Belgium). Following Ethics Committee approval, a written informed consent was provided by each patient from the Belgian AAN series. These study data remained unpublished.

In 2009, an amendment to the pilot study defined specifically the current TP53 research which was carried out on tissue samples from 5 AAN patients reported in this study, and was accepted as such by the Research Ethics Committee of the Université catholique de Louvain (Belgium) as a continuation of the study started in 2001. Tissue samples from patients 1–5 which were all part of the original study (2001) were anonymized prior to analysis.

Blood samples were part of a previous study (UCL Ethics Committee approval reference no. 2003/05/03/08) [17]. Adenocarcinoma and surgical ureteric samples were collected from AA-unrelated patients as part of their medical treatment and were anonymized prior to analysis. After written information, adenocarcinoma tissues were stored in UCL Biological library (http://www.centreducancer.be/fr/show/index/section/8/page/34). Non AA-related ureteric samples taken from nephroureterectomies removed at the time of renal transplantation were used as controls in this study with a codification after pathological analysis in accordance with the Belgian laws on tissue banking (2008).

The snap-frozen granulosa-cell tumour specimen from the Li-Fraumeni patient was obtained from the UCL biological library (same as above). After written consent from the parents, this sample was anonymized prior to use.

Previous reported data include AL-DNA adducts identified in kidney tissue from patients 1, 3, 4 [15,16,18] and TP53 gene sequencing performed in a bladder TCC from patient 1 [10].

AAN patients

Five AAN patients referred to Cliniques Universitaires Saint-Luc (Brussels, Belgium) were studied (Table 1). All were women with a mean age of 42.8 years (range: 27–53) at presentation. One patient was a smoker. None had a history of analgesic abuse or tobacco smoking. None had a history of analgesic abuse or tobacco smoking. None had a history of analgesic abuse or tobacco smoking. None had a history of analgesic abuse or tobacco smoking. None had a history of analgesic abuse or tobacco smoking.

Surgical specimens

Tissues from five pelvi-ureterectomies and a single cystectomy were selected on the basis of the availability of frozen material. Carcinoma in situ (CiS) and papillary TCC were diagnosed accordingly to the 2004 WHO classification of urothelial tumours [21,22]. Unilateral multifocal CiS developed in the right upper urinary tract (pelvis, upper, mid and lower ureter) in two patients (patient 1 and 5). While ureteral CiS invaded focally the lamina propria in patient 1, she also developed bladder papillary TCC. Bilateral multifocal CiS developed in the upper urinary tract of the remaining patients. Delay between end of exposure and surgery averaged 44.75 months (range 15–96) in patients 1, 2, 3, 5 and was unavailable in patient 4. In the former four patients, unilateral and bilateral TCC were diagnosed an average of 61 months (range: 27–96) and 41 months (range: 18–64) after end of known exposure, respectively.

p53 immunohistochemistry (IHC)

CiS was identified by light microscopy on hematoxylin eosin stained sections from frozen pelvi-ureteric samples. Out of serial frozen sections (7 μm-thick), sections n’1, n’3 and n’5 were used for p53 immunohistochemistry (IHC) and kept overnight at 37°C whereas sections n’2, n’4 and n’6 were used for laser microdissection. The latter three sections were placed on biochemically inert Polyethylene naphlate (PEN) membrane covered slides and kept at -20°C until use. For p53 IHC, the sections kept at 37°C were subsequently fixed in formaldehyde 4% for 3 hours. Endogenous peroxydase was blocked with 0.3 % hydrogen peroxide in deionized water for 30 min. The slides were incubated at 97°C for 75 min and rinsed in a solution containing deionized water and Triton 0.05%. The sections were then covered for 30 min with 10% normal goat serum (NGS) containing 1% bovine serum albumin (BSA), diluted in tris-triton. They were incubated overnight at room temperature with the anti-p53 mouse monoclonal antibody DO-7 (Biocarta, Europe Gmbh) at a dilution of 1:1000. After washing with tris-triton 0.05%, the slides were incubated at room temperature for 75 min with a ready-for-use anti-mouse EnVision-Peroxidase system (Dako, Glostrup, Denmark) according to the manufacturer’s protocol and counter-stained with hematoxylin. A normal goat serum was used as negative control.

Overexpression of p53 was defined as nuclear staining irrespective of IHC intensity. Extensive p53 staining by IHC was selected for microdissection. Exactly matching areas from yet unprocessed serial sections (n’2, n’4 and n’6) underwent microdissection as detailed hereafter.

Laser capture microdissection

After toluidine blue staining, each unfixed frozen tissue area which exactly matched the area of interest defined according to p53 IHC slides was isolated using a PALM microlaser system (Bernried, Germany) equipped with a pulsed UV nitrogen laser (wavelength: 337 nm; Pulse energy >270 μJ, pulse duration 3ns, pulse frequency 1–30/sec) and the PALM Robot Software Version 2.2. The system was coupled to an Axiovert 200 microscope and a Plan Neofluar 20× (Zeiss, Oberkochen, Germany). Microdissected foci were catapulted into a microtube cap and frozen at −20°C until DNA extraction (Figure 1).
| AAN Patients (Age/Sex) | Duration of formula 2 regimen (month) | Smoking status (pack-years) | Months from end of AA exposure and Surgery | RAL in renal tissue (mean ± SD/10exp7 nucleotides)* | p53 positive areas analysed for TP53 mutations | Localisation of tissue | Multifocal TCC | IHC | Genomic position | Mutated codon | Effect of the mutation |
|------------------------|-------------------------------------|-----------------------------|---------------------------------------------|-------------------------------------------------|-------------------------------------------------|----------------------|----------------|----|-----------------|---------------|----------------------|
| 1 (27/F) 20 5 15 (Left Nux) 4.1±2.7 | - | ND | ND | ND | ND | ND | ND | ND | ND | ND | ND | ND |
| 27 (Right Nux) 3.0±1.8 | Pelvis | Cis | + | - | 7 | g. A13325C | T230P | Missense |
| 111 (Cxi)* | Bladder | Cis and papillary | + | - | g.G13380A | R248Q | Missense |
| 2 (41/F) 15 0 50 (Left Nux) ND Pelvis Cis + | - | 5 | g.A12478T | K164X | Nonsense |
| 53 (Right Nux) ND Pelvis Cis + | - | - | - | - | - |
| 3 (42/F) 21 0 18 (Right Nux) 2.5±2.1 Ureter Cis ND | - | - | ND | ND | ND | ND |
| 64 (Left Nux) ND Pelvis Cis + | 7 | - | g.A13757C | Intrinsic |
| 4 (53/F) NA 0 NA (Bilateral Nx) 2.9±2.0 in right cortex | - | ND | ND | ND | ND | ND | ND | ND |
| NA (Right subtotal Ux) ND Upper ureter Cis | + | - | 5 | g.C12401T | A138V | Missense |
| NA (Left Ux and remnant right Ux) ND Left upper ureter Cis | + | - | 5 | g.T12722C | V218A | Missense |
| Left mid ureter Cis | + | - | 5 | g.G12461T | R158L | Missense |
| + | 6 | - | g.G12759A | Intrinsic |
| + | - | 7 | g.G13323T | C229F | Missense |
| Left lower ureter Cis | + | - | 8 | g.C13824T | R282W | Missense |
| 5 (51/F) 20 0 96 (Right and left Nux) ND Right pelvis Cis | + | - | 6 | g.A12728G | Y220C | Missense |
| 8 | g.G13791C | E271Q | Missense |
| 8 | g.A13837T | E286V | Missense |
| Right mid ureter Cis | + | 5 | - | g.A12627T | Donor splice site |
| - | 6 | g.A12683G | Y205C | Missense |
| - | 8 | g.G13836T | E286X | Nonsense |

Abbreviations: RAL: Relative adduct labelling, Nx: Nephrectomy, Nux: Nephroureterectomy, Ux: Ureterectomy, Cx:Cystectomy, ND: not done, NA: not available.

* No Cis found.

No mean of at least three determinations in reported separate experiments [15,16,18].

Mutations previously reported [10] and confirmed by the FASAY method [25] in the Center for Applied Molecular Technology of the Université Catholique de Louvain.

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DNA extraction

In each cap, 10 μl of a solution containing EDTA 0.001 M (pH 8), Tris HCl 0.02 M (pH 8), 0.5% Tween 20, proteinase K (2 mg/ml) and ultrapure water was included. After mixing and centrifugation, each reaction tube was overlaid with one drop of mineral oil to prevent evaporation and incubated overnight at 55°C with continuous agitation (600 rpm). Ultrapure water (5 μl) was then added to the reaction tube to increase the final volume of the solution. After centrifugation, the solution was heated at 99°C for 10 min to inactivate the proteinase K. Finally the extract was transferred to another microtube.

Nested-PCR

Exons 5 to 8, corresponding to the p53 DNA binding domain, a so-called “hot spot” for TP53 gene mutations [24], were amplified by nested-PCR. For the first PCR round, 3 μl of DNA extracted from each microdissected sample was added to a final 50 μl PCR mix including 2.25 mM MgCl2, 0.2 U/μl Taq Gold polymerase (Ampli Taq Gold, Applied Biosystems, Roche), 0.2 mM dNTP and 0.2 pm/μl primers (Eurogentec, Liège, Belgium) (Table 2). An initial incubation at 95°C for 4 min was followed by 25 cycles (95°C for 30 sec, 60°C except for exon 7 where annealing temperature was 55°C for 30 sec and 72°C for 1 min) and a final elongation for 7 min at 72°C. The second PCR round was carried out with 2.5 μl of the first PCR product using the same conditions as for the first round, except that 1.5 mM of MgCl2 and 0.4 U/μL of Taq Gold polymerase were used for exon 6. Ultrapure water was used as negative control whereas DNA extracted from unrelated blood samples was used as control for TP53 amplification.

Sequence analysis

Amplified products were purified using the MSB Spin PCRapace kit (STRATEC Molecular GmbH, Berlin, Germany) according to the manufacturer’s instructions. Sequence analysis was carried out on an automated ABI 377 A apparatus (Applied Biosystems, Foster City, CA), using the Taq Dye Deoxy Terminator Cycle Sequencing kit from the same manufacturer and according to its instructions. The TP53 reference sequence from Genbank was NC_000017.10.

Assessment of potential TP53 -artifactual alterations in tissue samples

To assess the ability of the current microdissection procedure to identify DNA mutations, four colorectal adenocarcinomas previously investigated for KRas mutation by routine clinical testing on FFPE (Formalin-fixed paraffin-embedded) tissue specimens were selected. Two of them carried a mutation and two were wild-type. These four samples were chosen because a snap-frozen counterpart was kept stored at −70°C in the Cancer Human Bio-bank of the Université catholique de Louvain (https://www.uclouvain.be/416846.html). Laser microdissection and DNA extraction of snap-frozen adenocarcinoma specimens were carried out using the procedure described above and the results of KRas testing were compared. Additionally, a snap frozen granulosa-cell tumour specimen from a 15 year-old young girl with a Li-Fraumeni syndrome was analysed using the same microdissection procedure. While the constitutional mutation had already been identified by FASAY (functional analysis of separated alleles in yeast) of the TP53 mRNA extracted from peripheral mononuclear cells of the patient [25], the tumour specimen was studied to further confirm the ability of the current microdissection.
procedure to identify correctly this TP53 mutation in frozen sections of the tumour.

(b) Whether snap-frozen tissue sections could be affected by a laser-induced effect is not known and this could even be worsened by additional interfering factors such as a deleterious effect of the fixation, staining and/or nested-PCR procedures. To exclude such technological bias, surgical ureter specimens were collected after nephroureterectomies (n = 4) taken from kidney transplanted patients for terminal uremia due to polycystic kidney disease and Taiwanese (n = 151) clinical series [11,12,14], and to compare the results of this analysis with those from patients with renal pelvis) (n = 1111) as reported in the IARC database results.

TP53 Mutations in Belgian AAN-Associated Cancer

Table 2. Primers used in the nested polymerase chain reaction.

| Exons | Primers | Sequence (5'-3') | Exon Position | Target size (bp) | Concentration (nm) |
|-------|---------|-----------------|---------------|-----------------|-------------------|
| 5     | E-S     | TGGTCACCCGTGACCCTGACTT | 12334 - | 21 | 60.7 |
|       | I-S     | TTCACTTCGTTCGTCTTCCTTCCTC | 12357 - | 24 | 128.55 |
|       | E-AS    | AGAGCAATCTGATGGAGAATCAG | 12604 - | 22 | 60.87 |
|       | I-AS    | AGGCTGGTCTGCCTCCTCCA | 12563 - | 18 | 113.69 |
| 6     | E-S     | TTGCACACCCTTCTCCCTCCCAG | 12599 - | 17 | 78.38 |
|       | I-S     | GGCTCTTACGCATCTCACTGA | 12618 - | 20 | 40.04 |
|       | E-AS    | GAGGGCCACTGACAACCA | 12784 - | 18 | 77.91 |
|       | I-AS    | TTAACCCCTCCTCCCTCAGAGA | 12761 - | 20 | 51.3 |
| 7     | E-S     | GCCACAGGTCTCCCCAA | 13270 - | 17 | 72.1 |
|       | I-S     | GCCACTTGCTCTCATCT | 13288 - | 17 | 104.67 |
|       | E-AS    | GGTACCCGCGCAAGCAGA | 13468 - | 17 | 48.13 |
|       | I-AS    | TCCAGGGTGGCAAAGTG | 13428 - | 17 | 102.96 |
| 8     | E-S     | GGTGGGGAGTATGAGGAGCCT | 13690 - | 21 | 29.54 |
|       | I-S     | TTTCCCTACTGCTTCTCCCTC | 13743 - | 23 | 106.47 |
|       | E-AS    | CATTTGAGGTATAGCTGGAACCTT | 14097 - | 27 | 53.77 |
|       | I-AS    | TGAGGACTACGTTGACCCCTT | 13935 - | 20 | 74.94 |

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Assessment of potential artifactual TP53 alterations in tissue samples

Using the microdissection procedure enabled a correct identification of known DNA mutations characterized by previous routine testing. Regarding the identification of K Ras mutations on
snap-frozen adenocarcinomas, results were strictly identical to those previously obtained on FFPE samples (i.e., identification of G12S and G12D mutations in the KRas mutated tissues and wild-type status in the other two tumours). Regarding identification of a constitutional g.13380 G>A, p.R156H mutation identified by FASAY assay in peripheral blood cells of a patient with Li-Fraumeni syndrome, this mutation was also found in malignant cells from the granulosa cell tumor using DNA extraction, microdissection, nested-PCR and sequencing procedures as used in the present study.

Conversely, no artificial TP53 alterations were found in the various controls carried out to test the occurrence of TP53 DNA-induced damage related to DNA extraction, microdissection, nested-PCR and sequencing procedures. No mutations were found in three out of four ureter samples used to test a TP53 iatrogenic damage. The only exception was the ureter sample from a type 2 diabetic patient with a G>A transition (g.12455, p.R156H) in exon 5 of the TP53 gene after microdissection under high laser power. No mutations were found in the p53 DNA binding domain (exons 5 to 6) when analyzing DNA extracted from a phenacetin-induced urothelial carcinoma.

Assessment of limit of detection for Sanger sequencing

The limit of detection for Sanger sequencing was identified at 6.25% of mutant to wild-type DNA ratio with both TP53 mutated cell lines, irrespective of the mutation or deletion assessed. At this DNA ratio, the heterozygous A/G peak with serial DNA dilutions from SC173/HN30 mixed DNAs was still visible as also was the heterozygous G and C peak combined with a 32-bp deletion in exon 7 with serial DNA dilutions from SC263/HN30 mixed DNAs.

Morphology

All p53 positive areas corresponded to papillary TCC or to CIS containing anaplastic and dysplastic cells (Table 1). Intra-urothelial and lamina propria inflammation, hyperplasia and reactive atypia were absent. In patient 2, neoplastic and dysplastic cells were clinging to the basement membrane (clinging CIS).

TP53 gene mutations

Including two previously reported results [10], a total of 16 totally different exonic (n = 13) or intronic (n = 3) mutations of the TP53 gene were found in malignant urothelial tissues from the Belgian AAN cohort (Table 1). In patient 1, two mutations were found in the same exon (exon 7) whereas a single mutation was found in patient 2 (exon 5) and 3 (intron 7). Patients 4 and 5 harbored 5 different exonic and 1 intronic mutations. Among the 13 exonic mutations, two were nonsense (patients 2 and 5) and 11 missense mutations (patients 1, 4, and 5). They were located in exon 5 (3 mutations), exon 6 (3 mutations), exon 7 (3 mutations) or exon 8 (4 mutations). One of the three intronic mutations (g.12627A>T, patient 5) was located at the AG acceptor splice site. Globally, mutations affected A:T pairs (7/16) and G:C pairs (9/16). There was a nearly equal number of transitions (7/16) and transversions (9/16). Transitions (7/16) occurred indeed with a similar frequency at A:T pairs (3/16) and G:C pairs (4/16). A>G, G>A and C>T (2/16) occurred with a similar frequency as T>C (1/16). Similarly, transversions (9/16) were found at A:T pairs (4/16) and G:C pairs (5/16) distributed as follows: A>T (3/16), G>T (3/16), G>C (2/16) and A>C (1/16).

Comparative statistical analysis of number and type of mutations in current and previous data

The Poisson regression model showed a highly significant (p<0.001) relative increase of the TP53 mutation prevalence in p53 hotspot codons from the current clinical series, compared with IARC database results (Table 3). In contrast, a significant relative decrease was found both in the BEN (n = 97) [12] and the Taiwanese (n = 151) [14] clinical series compared with IARC and current clinical data (Table 3). A non-significant (p>0.05) relative decrease/increase was found in BEN (n = 11) [11] compared with IARC and current clinical data (Table 3).

Regarding the number of A>T transversion per patient, a significant relative increase was found in the current, both BEN [11,12], and the Taiwanese [14] clinical series, compared with IARC database results (Table 4). Non-significant (p>0.05) results were obtained when previous AAN and current clinical series were compared (Table 4).

Compared with the IARC database results, a significant 5.85 increase of G>T prevalence was found in the current clinical series (Table 5). No G>T transversion was found in both BEN series. Regarding the Taiwanese series, there was a non-significant relative decrease in G>T prevalence compared with IARC data whereas such decrease was highly significant when compared with current results (Table 5).

Discussion

This is the first report of the mutational spectrum of TP53 tumor suppressor gene in a series of Belgian patients (n = 5) with documented AAN and subsequent development of TCC in the upper urinary tract together with bladder involvement in one of them. Four of them had followed AA-contaminated weight-loss diet and one denied exposure to AA while presenting a typical renal histology of interstitial fibrosis [20] with AL-DNA adducts [18].

Using exclusively frozen samples was an absolute prerequisite to allow adequate comparison with reported data. Except for five out of 11 patients for whom formalin-fixed paraffin embedded tissues were used [11], all major TP53 genetic investigations in cases presenting with AA-induced genotoxicity and urothelial malignancies were indeed led using fresh frozen tissues [11,12,14]. Conversely, the aim was to avoid the well-known deleterious effect of formalin fixation in terms of DNA quality and characterization of tissue mutational status [28]. To prove that TP53 mutations did not result from technological artifacts when using frozen section, a special attention was paid to thorough validation procedures. The current TP53 testing included successive steps (i.e., laser capture microdissection of tumor cells after toluidine blue staining, DNA extraction, nested-PCR amplification and sequencing). This method did not produce false-negative results. It enabled indeed a correct identification of known KRas oncogenic mutations in adenocarcinomas. It also enabled a correct identification of a previously characterized TP53 constitutional mutation associated with a Li-Fraumeni syndrome. This mutation was found in tumor cells whereas the previous characterization was carried out by a functional assay on peripheral mononuclear cells.

Likewise, the current procedure did not create false-positive results when analyzing normal ureter specimens collected after nephroureterectomy in patients with AA-unrelated diseases or a phenacetin-induced carcinoma, and taking current conventional genotyping as gold standard. This also applied when performing laser capture microdissection with high intensity. The sole mutation found was a single G>A transition (g.12455, p.R156H) in the tissue specimen from a type 2 diabetic patient
Table 3. Relative increased/decreased prevalence of mutation.

| Reference database | Compared database |
|--------------------|-------------------|
| BEN (n = 111) [11]  | BEN (n = 97) [12]  |
| Taiwan (n = 151) [14] | BELGIAN (n = 5) |
| IARC (n = 1111) | 1.54 [0.98–2.42], p = 0.062 |
| BELGIAN (n = 5) | 0.54 [0.28–1.05], p = 0.069 |
| 0.46 [0.35–0.61], p < 0.001 | 0.16 [0.09–0.28], p < 0.001 |
| 0.50 [0.40–0.62], p < 0.001 | 0.17 [0.10–0.30], p < 0.001 |
| 2.85 [1.74–4.67], p < 0.001 |

Table 4. Relative increased/decreased prevalence of A>T mutation.

| Reference database | Compared database |
|--------------------|-------------------|
| BEN (n = 11) [11]  | BEN (n = 97) [12]  |
| Taiwan (n = 151) [14] | BELGIAN (n = 5) |
| IARC (n = 1111) | 40.40 [21.74–75.09], p < 0.001 |
| BELGIAN (n = 5) | 2.12 [0.61–7.38], p = 0.23 |
| 10.80 [6.71–17.38], p < 0.001 | 0.57 [0.17–1.85], p = 0.34 |
| 9.67 [6.23–15.01], p < 0.001 | 0.51 [0.16–1.63], p = 0.26 |
| 19.05 [5.86–61.93], p < 0.001 |
differences between previous studies [11,12,14] and the current work. Firstly, a limited number of patients (n=5) was assessed in this study compared with previous studies which included 11 to ~100 patients exposed to AA. Secondly, male and female patients were almost equally distributed in BEN and Taiwanese cohorts whereas the current cohort consisted only of women. Furthermore, there were substantial differences between both former and current cohorts in terms of mean age (66 versus 43 years old, respectively), and exposure duration and intensity. For the latter two features, no precise data could unfortunately be retrieved from the Taiwanese series as patient exposure resulted from intermittent ingestion of herbal remedies containing or likely to contain AA [14,37]. In contrast, repeated intake of contaminated bread over time was estimated to expose BEN patients to a toxic dietary exposure which is equivalent to that documented for Belgian patients with AAN [11,38]. While cumulative doses are a known significant risk factor for developing urothelial carcinoma [6], repeated AA exposure over a short period of time (mean 19 months) in the Belgian series may already have led to the cumulative toxic dose which, comparatively, was only achieved after several decades in BEN patients. Considering the higher daily intake of AA in Belgian compared to the BEN series and the susceptibility of hotspot codons to carcinogen-induced alterations, differences in the mutation profile would not be surprising. One of the major phenotypic difference observed in the Belgian cohort was the substantially quicker development of nephrotoxicity (within few months) and of cancer (within 2–6 years) after cessation of AA exposure [10]. Additional differences between studies laid in the current methodology for TP53 genotyping. This was indeed carried out only on fresh tissues using tissue microdissection followed by nested-PCR and conventional sequencing, which differs significantly from the AmpliChip p53 microarray on fresh [11,12,14] and on few formalin-fixed tissues [11] as previously reported. In that respect, it is interesting to note that the spectrum of TP53 genetic alterations in Taiwan and BEN patients whom tumors were assessed using identical TP53 genotyping, was notably similar [11,12,14].

In conclusion, our documentation of expected A > T transversions attributable to AA exposure in the TP53 gene of the Belgian AAN associated TCC is the first demonstration of a clear causal relationship between AA exposure and the development of urothelial malignancy in this cohort. Interestingly, and although assessed on small series of female patients, there are two striking highly significant observations characterizing the current series: the addition of poly- or multicolour TP53 alterations to the otherwise well-known AA mutational fingerprint and the unusually high prevalence of G>T transversion in the p53 binding site, two new features appearing as a complementary signature possibly reflecting the toxicity of a cumulative dose of AA over a short period of time.

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Author Contributions

Conceived and designed the experiments: SA AFD YG JPC JLG. Performed the experiments: SA AFD MH YG JPC JLG. Analyzed the data: SA MH YG JPC. Contributed reagents/materials/analysis tools: SA MH JPC JLG. Contributed to the writing of the manuscript: SA AFD JPC JLG. Designed the software for statistical analysis: JA.

Table 5. Relative increased/decreased prevalence of G>T mutation.

| Reference database | Compared database | BEN (n = 11) [11] | BEN (n = 97) [12] | Taiwan (n = 151) [14] | BELGIAN (n = 5) |
|--------------------|-------------------|------------------|------------------|----------------------|----------------|
| IARC (n = 1111)    | 0 *               | 0.65 [0.34–1.23], p = 0.18 | 5.85 [1.86–18.40], p = 0.002 |
| BELGIAN (n = 5)    | 0 *               | 0.11 [0.03–0.40], p < 0.001 |

* No record of GT mutation in BEN series [11,12].

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