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Decizie de indexare a faptei de plagiat la poziţia 00160 / 17.04.2015 şi pentru admitere la publicare în volum tipărit

care se bazează pe:

A. Nota de constatare şi confirmare a indiciilor de plagiat prin fişa suspiciunii inclusă în decizie.

Fişa suspiciunii de plagiat / Sheet of plagiarism's suspicion			
Opera suspicionată (OS)		**Opera autentică (OA)**	
Suspicious work		**Authentic work**	
OS	AFTENIE, Loredana Mariana, FRANCIUC , Irina, MARTINESCU, Alina, and HONCEA, Adina. Comparison Between Currently Used Blood Samples And New Saliva Dna Collection Method For Quality Of Genomic DNA And Genotyping. *ARS Medica Tomitana*. 2012 Dec 1. **18**(1). pp.19-23.		
OA	HANSEN, TV, SIMONSEN, MK, NIELSEN, FC, HUNDRUP, YA. Collection of blood, saliva, and buccal cell samples in a pilot study on the Danish nurse cohort: comparison of the response rate and quality of genomic DNA. *Cancer Epidemiology and Prevention Biomarkers*. 2007 Oct 1; **16**(10). pp.2072-2076.		
Incidenţa minimă a suspiciunii / Minimum incidence of suspicion			
P01:	p.19:12d – p.20:10s	P01.01:	p.2072:02s – p.2072:08s
		P01.02:	p.2072:11s – p.2072:06d
		P01.03:	p.2072:08d – p.2072:00d
P02:	p.20:13d – p.20:30d	P02:	p.2073:08d – p.2073:27d
Fişa întocmită pentru includerea suspiciunii în Indexul Operelor Plagiate în România de la Sheet drawn up for including the suspicion in the Index of Plagiarized Works in Romania at www.plagiate.ro			

Notă: Prin „p.72:00" se înţelege paragraful care se termină la finele pag.72. Notaţia „p.00:00" semnifică până la ultima pagină a capitolului curent, în întregime de la punctul iniţial al preluării.

Note: By „p.72:00" one understands the text ending with the end of the page 72. By „p.00:00" one understands the taking over from the initial point till the last page of the current chapter, entirely.

B. **Fişa de argumentare a calificării** de plagiat alăturată, fişă care la rândul său este parte a deciziei.

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Fişa de argumentare a calificării

Nr. crt.	Descrierea situaţiei care este încadrată drept plagiat	Se confirmă
1.	Preluarea identică a unor pasaje (piese de creaţie de tip text) dintr-o operă autentică publicată, fără precizarea întinderii şi menţionarea provenienţei şi însuşirea acestora într-o lucrare ulterioară celei autentice.	✓
2.	Preluarea a unor pasaje (piese de creaţie de tip text) dintr-o operă autentică publicată, care sunt rezumate ale unor opere anterioare operei autentice, fără precizarea întinderii şi menţionarea provenienţei şi însuşirea acestora într-o lucrare ulterioară celei autentice.	
3.	Preluarea identică a unor figuri (piese de creaţie de tip grafic) dintr-o operă autentică publicată, fără menţionarea provenienţei şi însuşirea acestora într-o lucrare ulterioară celei autentice.	
4.	Preluarea identică a unor tabele (piese de creaţie de tip structură de informaţie) dintr-o operă autentică publicată, fără menţionarea provenienţei şi însuşirea acestora într-o lucrare ulterioară celei autentice.	
5.	Republicarea unei opere anterioare publicate, prin includerea unui nou autor sau de noi autori fără contribuţie explicită în lista de autori	
6.	Republicarea unei opere anterioare publicate, prin excluderea unui autor sau a unor autori din lista iniţială de autori.	
7.	Preluarea identică de pasaje (piese de creaţie) dintr-o operă autentică publicată, fără precizarea întinderii şi menţionarea provenienţei, fără nici o intervenţie personală care să justifice exemplificarea sau critica prin aportul creator al autorului care preia şi însuşirea acestora într-o lucrare ulterioară celei autentice.	✓
8.	Preluarea identică de figuri sau reprezentări grafice (piese de creaţie de tip grafic) dintr-o operă autentică publicată, fără menţionarea provenienţei, fără nici o intervenţie care să justifice exemplificarea sau critica prin aportul creator al autorului care preia şi însuşirea acestora într-o lucrare ulterioară celei autentice.	
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10.	Preluarea identică a unor fragmente de demonstraţie sau de deducere a unor relaţii matematice care nu se justifică în regăsirea unei relaţii matematice finale necesare aplicării efective dintr-o operă autentică publicată, fără menţionarea provenienţei, fără nici o intervenţie care să justifice exemplificarea sau critica prin aportul creator al autorului care preia şi însuşirea acestora într-o lucrare ulterioară celei autentice.	
11.	Preluarea identică a textului (piese de creaţie de tip text) unei lucrări publicate anterior sau simultan, cu acelaşi titlu sau cu titlu similar, de un acelaşi autor / un acelaşi grup de autori în publicaţii sau edituri diferite.	
12.	Preluarea identică de pasaje (piese de creaţie de tip text) ale unui cuvânt înainte sau ale unei prefeţe care se referă la două opere, diferite, publicate în două momente diferite de timp.	

Alte argumente particulare: a) Deşi nu citează Tabelul 1 scrierea plagiată îi schimbă sursa faţă de scrierea autentică. b) Piesa P01 cuprinde un citat menţionat în scrierea autentică pe care scrierea plagiată nu-l mai identifică.

Notă:

a) Prin „provenienţă" se înţelege informaţia din care se pot identifica cel puţin numele autorului / autorilor, titlul operei, anul apariţiei.

b) Plagiatul este definit prin textul legii[1].

> *„ …plagiatul – expunerea într-o operă scrisă sau o comunicare orală, inclusiv în format electronic, a unor texte, idei, demonstraţii, date, ipoteze, teorii, rezultate ori metode ştiinţifice extrase din opere scrise, inclusiv în format electronic, ale altor autori, fără a menţiona acest lucru şi fără a face trimitere la operele originale…".*

Tehnic, plagiatul are la bază conceptul de **piesă de creaţie** care[2]:

> *„…este un element de comunicare prezentat în formă scrisă, ca text, imagine sau combinat, care posedă un subiect, o organizare sau o construcţie logică şi de argumentare care presupune nişte premise, un raţionament şi o concluzie. Piesa de creaţie presupune în mod necesar o formă de exprimare specifică unei persoane. Piesa de creaţie se poate asocia cu întreaga operă autentică sau cu o parte a acesteia…"*

cu care se poate face identificarea operei plagiate sau suspicionate de plagiat[3]:

> *„…O operă de creaţie se găseşte în poziţia de operă plagiată sau operă suspicionată de plagiat în raport cu o altă operă considerată autentică dacă:*
> *i) Cele două opere tratează acelaşi subiect sau subiecte înrudite.*
> *ii) Opera autentică a fost făcută publică anterior operei suspicionate.*
> *iii) Cele două opere conţin piese de creaţie identificabile comune care posedă, fiecare în parte, un subiect şi o formă de prezentare bine definită.*
> *iv) Pentru piesele de creaţie comune, adică prezente în opera autentică şi în opera suspicionată, nu există o menţionare explicită a provenienţei. Menţionarea provenienţei se face printr-o citare care permite identificarea piesei de creaţie preluate din opera autentică.*
> *v) Simpla menţionare a titlului unei opere autentice într-un capitol de bibliografie sau similar acestuia fără delimitarea întinderii preluării nu este de natură să evite punerea în discuţie a suspiciunii de plagiat.*
> *vi) Piesele de creaţie preluate din opera autentică se utilizează la construcţii realizate prin juxtapunere fără ca acestea să fie tratate de autorul operei suspicionate prin poziţia sa explicită.*
> *vii) In opera suspicionată se identifică un fir sau mai multe fire logice de argumentare şi tratare care leagă aceleaşi premise cu aceleaşi concluzii ca în opera autentică…"*

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[1] Legea nr. 206/2004 privind buna conduită în cercetarea ştiinţifică, dezvoltarea tehnologică şi inovare, publicată în Monitorul Oficial al României, Partea I, nr. 505 din 4 iunie 2004
[2] ISOC, D. *Ghid de acţiune împotriva plagiatului: bună-conduită, prevenire, combatere*. Cluj-Napoca: Ecou Transilvan, 2012.
[3] ISOC, D. *Prevenitor de plagiat*. Cluj-Napoca: Ecou Transilvan, 2014.

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ARS Medica Tomitana - 2017; 2(23): 106
10.1515/arsm-2017-0097

Retraction of:
Aftenie Loredana Mariana[1], Franciuc Irina[1], Martinescu Alina[2], Honcea Adina[2]
Comparison between currently used blood samples and new saliva DNA Collection Method for quality of Genomic DNA and Genotyping
ARS Medica Tomitana - 2012; 1(68); Pages 19-23. Feb 2012

(DOI 10.2478/v10307-012-0003-0)

The article is emphasizing the original results of the authors within the Molecular Genetic Laboratory, using specific extraction methods and common international protocols. Due to these procedures, similarities between syntax and expressions may appear with literature. Thus, in order to avoid any confusion, the authors have requested that their article be withdrawn.

DOI: 10.1515/arsm-2017-0097

Collection of Blood, Saliva, and Buccal Cell Samples in a Pilot Study on the Danish Nurse Cohort: Comparison of the Response Rate and Quality of Genomic DNA

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Abstract

In this study, we compared the response rates of blood, saliva, and buccal cell samples in a pilot study on the Danish nurse cohort and examined the quantity and quality of the purified genomic DNA. Our data show that only 31% of the requested participants delivered a blood sample, whereas 72%, 80%, and 76% delivered a saliva sample, buccal cell sample via mouth swabs, or buccal cell sample on FTA card, respectively. Analysis of purified genomic DNA by NanoDrop and agarose gel electrophoresis revealed that blood and saliva samples resulted in DNA with the best quality, whereas the DNA quality from buccal cells was low. Genotype and PCR analysis showed that DNA from 100% of the blood samples and 72% to 84% of the saliva samples could be genotyped or amplified, whereas none of the DNA from FTA cards and only 23% of the DNA from mouth swabs could be amplified and none of the DNA from swabs and 94% of the DNA from FTA cards could be genotyped. Our study shows that the response rate of self-collection saliva samples and buccal cell samples were much higher than the response rate of blood samples in our group of Danish nurses. However, only the quality of genomic DNA from saliva samples was comparable with blood samples as accessed by purity, genotyping, and PCR amplification. We conclude that the use of saliva samples is a good alternative to blood samples to obtain genomic DNA of high quality and it will increase the response rate considerably in epidemiologic studies. (Cancer Epidemiol Biomarkers Prev 2007;16(10):2072–6)

Introduction

P01.01

Large population-based studies involving thousands of participants are needed in the search for genetic determinants underlying common diseases such as cardiovascular diseases, cancer diseases, osteoporosis, and diabetes. Therefore, increasingly epidemiologic studies are trying to supplement survey data with genomic DNA. Thus far, the preferred choice of genetic material has been blood samples because they provide large amounts of cells containing not only DNA but also a range of physiologic agents (1). However,

P01.02

collection of blood samples may not be feasible in large epidemiologic studies where participants are dispersed all over the country or because the method requires venepuncture done by trained staff, making collection of blood samples prohibitively expensive. Furthermore, study subjects may be reluctant to provide blood samples, thereby reducing participation rates. Therefore, less invasive and more cost-efficient procedures for collecting DNA are needed. Several studies have found that exfoliated buccal epithelial cells are promising alternative sources of DNA (1-11). Different protocols to obtain genomic DNA have been evaluated. Some studies have found that mouthwash samples yield high amounts of high-quality genomic DNA (3, 7, 12). Other studies have compared mouthwash samples with cytobrush samples and have found that mouthwash specimens are superior to cytobrushes for obtaining high molecular weight DNA (1, 4, 6). However, the disadvantage with mouthwash samples are that donors need to swish and spit an alcohol-containing mouthwash solution, which is distasteful (9) and has been reported to cause a burning sensation in the mouth (4). Alternatively, cytobrushes have been used to brush oral mucosa, and then transferred to a card treated to inhibit bacterial growth (5). However, a review of current practices note that quantities of DNA collected on these cards have not been sufficient for spectrophotometric detection (13). Recently, a Swedish study has tested a new method for self-collection of saliva, Oragene, and has found that Oragene saliva samples from men is of high quality and can be used as an alternative to blood DNA in epidemiologic studies (14). The purpose of this pilot study was to evaluate the DNA quantity and quality by using different methods of DNA collection and to assess to what extent the collection of DNA material affects the survey response rates in a group of Danish nurses.

P01.03

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Materials and Methods

Participants. The Danish Nurse Cohort was established in 1993, when all female members of the Danish Nurses Organization above 44 years old received a questionnaire. In 1999, the cohort was reinvestigated with additional inclusion of nurses, who had passed the age of 44 years between 1993 and 1999. In June 2006, the cohort comprised 30,508 nurses 51 years old or above. From this database, we randomly selected 300 nurses for this pilot study, all of which were representative of the cohort in terms of age (median age 61 years, range 51-91 years). Two hundred nurses were geographically representative of the cohort, and half of these were requested to deliver a saliva sample and the other half were requested to deliver buccal cell samples, either via mouth swabs or FTA cards. The remaining 100 nurses selected from the Copenhagen area were referred to the Department of Clinical Biochemistry, Rigshospitalet, Copenhagen, to deliver a blood sample.

Sample Collection and Processing. The samples were collected between May 1, 2006, and July 31, 2006. Nonresponders received a first reminder on May 23 and a second reminder on June 23. All nurses received information about the study, an informed consent form for signature, a questionnaire on general health and lifestyle issues, and either an Oragene DNA self-collection kit (DNA Genotek), a Catch-all sample collection swabs (Epicentre Biotechnologies), a sterile foam-tipped applicator and a FTA card (Whatman, Inc.) or a blood sample requisition, instruction on how to process the samples, and a prepaid return envelope. The samples were collected as follows.

Blood Samples. The subjects were referred to the Department of Clinical Biochemistry, Copenhagen, Denmark. Three-milliliter whole blood samples were venously collected and treated with sodium citrate anticoagulant. The blood samples were stored at 4°C until DNA extraction.

Saliva Samples. The subjects were asked to wash their mouth once with water and to wait at least 30 s. Then, the subjects were asked to spit in the blue container (DNA Genotek), to cap the blue container with the white lid, and finally to gently shake the sample. The Oragene saliva samples were stored at room temperature until DNA extraction.

Buccal Cells. Half of the subjects were asked to wash their mouth twice with water and to collect the cells by rolling the Catch-All sample collection swabs (Epicentre Biotechnologies) firmly inside the cheek, ~15 s on each side. The swab was air-dried for 15 min at room temperature and placed in the plastic tube. The other half of the subjects were asked to use sterile foam-tipped applicator to rub both cheeks and thereafter to transfer the cheek cells to the indicating FTA card (Whatman). The swabs and FTA cards were stored at −20°C and at room temperature, respectively, until DNA extraction.

DNA Extraction. DNA was extracted from blood samples using the E.Z.N.A. Blood DNA miniprep kit (Omega Bio-tek) as described by the manufacturer. Briefly, 2 mL whole blood sample were transferred to a 15 mL tube, 150 μL proteinase K (20 mg/mL) was added, and the sample was mixed by vortexing. Buffer BL (2.1 mL) was added and the sample was vortexed at 5 min. Then, 20 μL RNase A solution were added and the sample was incubated at 70°C for 10 min. Then, 2.2 mL isopropanol were added and the sample was mixed. The solution was added to a column, centrifuged, washed, and eluted as described by the manufacturer. The DNA was quantified and stored at −20°C until PCR analysis.

P02

DNA was extracted from saliva samples using the Oragene kit (DNA Genotek) as described by the manufacturer. Briefly, the Oragene saliva sample was incubated at 50°C overnight. Five-hundred-microliter sample was transferred to a 1.5 mL Eppendorf tube, 20 μL of Oragene purifier were added, and the sample was mixed by inversion and incubated on ice for 10 min. The sample was then centrifuged for 3 min at 13,000 rpm at room temperature and the supernatant was transferred to a new tube. Five hundred microliters of 95% ethanol were added; the sample was mixed by inversion at least five times and incubated at 10 min at room temperature. The sample was then centrifuged for 1 min at 13,000 rpm at room temperature, the supernatant was discarded, and the DNA was dissolved in 100 μL TE buffer [10 mmol/L Tris-HCl, 0.1 mmol/L EDTA (pH 8.0)] and quantified. The DNA samples were stored at −20°C until PCR analysis.

DNA was extracted from buccal cells using the BuccalAmp DNA extraction kit (Epicentre Biotechnologies) as recommended by the manufacturer. Briefly, 500 μL QuickExtract DNA extraction solution 1.0 were added to a 2 mL Eppendorf tube; the swab was placed in the tube and rotated at least five times before the swab was pressed against the side of the tube to ensure that most of the liquid remains in the tube. The procedure was repeated with a second swab. The sample was vortexed for 10 s, incubated at 65°C for 1 min, and vortexed again for 15 s. Thereafter, the sample was incubated at 98°C for 2 min, vortexed for 15 s, and quantified. The DNA samples were stored at −20°C until PCR analysis.

For DNA extraction from FTA cards, a slice was cut using a Uni-Core puncher (3 mm). The slice was transferred to an Eppendorf tube and 200 μL FTA purification reagent (Whatman) were added and the sample was incubated for 5 min at room temperature. The reagent was removed and the wash procedure was repeated twice. Then, 200 μL TE buffer were added; the sample was incubated for 5 min at room temperature after the buffer was removed. This step was repeated once. Then, 35 μL 0.1 N NaOH, 0.3 mmol/L EDTA (pH 13.0) were added and the sample was incubated for 5 min at room temperature followed by addition of 65 μL of 0.1 mol/L Tris-HCl (pH 7.0). The sample was vortexed five times and incubated for another 10 min. Finally, the sample was vortexed 10 times, the FTA card slice was removed, and the DNA was quantified. The DNA samples were stored at −20°C until PCR analysis.

Quantification of DNA. The concentration of 1 μL DNA sample was determined using the NanoDrop ND-1000 spectrophotometer (NanoDrop Technologies). The 260/280 and 260/230 nm ratios was calculated by the NanoDrop spectrophotometer and used to evaluate the DNA purity. Moreover DNA (5 μL) was loaded on a 1% agarose gel and visualized by ethidium bromide staining.

Table 1. Number and proportion of returned questionnaires obtained at start, first, and second reminder according to DNA collection method

Method of DNA collection	Date of start: May 1, *n* (%)	First reminder: May 23, *n* (%)	Second reminder: June 23, *n* (%)	Respondents, total, *n* (%)
Blood samples (*n* = 100)	21 (21)	21 (21)	11 (11)	53 (53)
Saliva (*n* = 100)	43 (43)	21 (21)	8 (8)	72 (72)
Buccal cells (swabs; *n* = 50)	26 (52)	12 (24)	2 (4)	40 (80)
Buccal cells (FTA cards; *n* = 50)	16 (32)	16 (32)	6 (12)	38 (76)
Participants total, *N* = 300	106 (35.3)	70 (23.3)	27 (9.0)	203 (67.7)

Genotyping. Genotyping was done using TaqMan assay (Applied Biosystems). The PCR reaction was done as described by the manufacturer (Applied Biosystems). The *HFE*-282 primer and probe sequences were 5′-GGCTGGATAACCTTGGCTGTAC-3′ (forward primer), 5′-GTCACATACCCCAGATCACAATGAG-3′ (reverse primer), 5′-VIC-AGAGATATACGTgCCAGGTG-MGB-3′ (probe 1), and 5′-6-FAM-CAGAGATATACGTaCCAGGTG-MGB-3′ (probe 2), whereas the *HFE*-63 primer and probes were 5′-GAAGCTTTGGGCTACGTGGAT-3′ (forward primer), 5′-CATCTGGCTTGAAATTCTACTGGAA-3′ (reverse primer), 5′-VIC-CGTGTTCTATGATcATG-MGB-3′ (probe 1), and 5′-6-FAM-CGTGTTCTATGATgATG-MGB-3′ (probe 2). The allele-specific fluorescence was measured using an ABI PRISM 7900HT Sequence Detector System (Applied Biosystems). Water control and previously genotyped samples were included in each plate to ensure accuracy of genotyping.

PCR Amplification and Sequencing. The quality of purified genomic DNA was examined by amplification of DNA fragments routinely used in our laboratory. *APC* exon 2 and flanking intron sequences (242-bp fragment) was amplified using the following primers *APC*-ex2-F, 5′-TGTAAAACGACGGCCAGTAAATACAGAATCATGTCTTGAAGT-3′; *APC*-ex2-R, 5′-CAGGAAACAGCTATGACCACACCTAAAGATGACAATTTGAG-3′ containing M13 primer extensions. PCR amplification was done in 50 μL containing 0.5 μmol/L primers, ~50 ng genomic DNA, 2.0 mmol/L MgCl, 0.2 mmol/L deoxynucleotide triphosphate, 5 μL *Taq* polymerase buffer (Promega), and 0.4 μL *Taq* polymerase (Promega). Thermocycling was done on an Eppendorf Mastercycler with initial denaturation at 95°C for 4 min. This was followed by six cycles each consisting of 45 s denaturation at 94°C, 45 s annealing at 62°C, and 60 s extension at 72°C. Then, 19 cycles each consisting of 30 s at 94°C, 30 s at 53°C, and 90 s at 72°C were done. The process was concluded with a final extension of 10 min at 72°C. The PCR fragments was resolved on a 1% agarose gel and visualized by ethidium bromide staining. The PCR products were finally purified using Nucleofast 96 PCR plates (Macherey-Nagel), sequenced using the BigDye Terminator v1.1 Cycle Sequencing kit (Applied Biosystems), and analyzed on an ABI3730 DNA analyzer (Applied Biosystems).

Results

Altogether, 203 (67.7%) of the nurses returned the questionnaire. The two reminders almost doubled the response rate, but the rate varied according to DNA collection method. Table 1 shows that the highest rate (80%) was obtained among nurses who were requested to deliver buccal cells via mouth swabs, followed by buccal cells on FTA cards (76%) and saliva (72%), whereas the lowest response rate (53%) were obtained among nurses who were requested to deliver a blood test. However, the actual rate of samples obtained further reduced the response rate, because only 31 of 53 nurses delivered a blood sample, whereas all the nurses who returned a questionnaire also returned a saliva sample, a mouth swab, or a FTA card (Tables 1 and 2). In total, the highest rate of samples (40 of 50) was obtained among nurses who were requested to deliver buccal cells using Epicentre swabs, and the lowest rate (31 of 100) was obtained among the nurses requested to deliver blood samples. Of the returned samples, one Oragene container was empty upon arrival, whereas one mouth swab and two FTA cards did not contain any DNA.

The amount and purity of DNA was examined by Nanodrop analysis. The estimated amount of total DNA extracted from 2 mL blood samples varied between 11.3 and 59.6 μg with a mean of 28.4 μg, from 0.5 mL Oragene saliva samples between 0.9 and 64.2 μg with a mean of 10.8 μg, from mouth swabs between 9.1 and 194.9 μg with a mean of 64.4 μg, and from FTA cards

Table 2. Comparison of DNA yield and quality according to DNA collection method

Method of DNA collection	Blood	Saliva	Buccal cells (swabs)	Buccal cells (FTA cards)
Total amount of samples	31	72	40	38
Failed sample	0	1	1	2
Amount of sample used	2 mL	0.5 mL	2 swabs	One 3-mm punch
Mean DNA concentration (ng/μL)	56.8	108.0	128.8	3.6
Mean total DNA concentration (μg; range)	28.4 (11.3-59.5)	10.8 (0.9-64.2)	64.4 (9.1-194.9)	0.36 (0.09-1.33)
Mean 260/280 nm ratio (range)	1.79 (1.57-1.92)	1.63 (1.13-1.88)	1.15 (1.01-1.39)	0.91 (0.50-1.54)
Mean 260/230 nm ratio (range)	1.44 (1.08-2.14)	0.80 (0.36-1.33)	0.17 (0.03-0.51)	0.21 (0.08-0.46)
Genotyping	100%	72%	None	94%
PCR amplification	100%	84%	23%	None