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Candida auris admission screening pilot in select units of New York City health care facilities, 2017-2019

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Abstract

Background: This pilot project implemented admission screening for *Candida auris* (*C. auris*) using real-time polymerase chain reaction (rt-PCR) in select high-risk units within health care facilities in New York City.

Methods: An admission screening encounter consisted of collecting 2 swabs, to be tested by rt-PCR, and a data collection form for individuals admitted to ventilator units at 2 nursing homes (NHA and NHB), and the ventilator/pulmonary unit, intensive care unit, and cardiac care unit at a hospital (Hospital C) located in New York City from November 2017 to November 2019.

Results: *C. auris* colonization was identified in 6.9% (n = 188/2,726) of admissions to participating units. Rates were higher among admissions to NHA and NHB (20.7% and 22.0%, respectively) than Hospital C (3.6%). Within Hospital C, the ventilator/pulmonary unit had a higher rate (5.7%) than the intensive care unit (3.8%) or cardiac care unit (2.5%).

Discussion: Consistent with prior research, we found that individuals admitted to ventilator units were at higher risk of *C. auris* colonization.

Conclusions: This project demonstrates the utility of admission screening using rt-PCR testing to rapidly identify *C. auris* colonization among admissions to health care facilities so that

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SUPPLEMENTARY MATERIALS

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appropriate transmission-based precautions and control measures can be implemented rapidly to help decrease transmission.

Keywords

Candida auris admission screening; health care facility; Fungal; Colonization; Multidrug Resistance

Candida auris (C. auris), first described in 2009 in Japan, is a multidrug-resistant yeast and a source of health care-associated outbreaks globally, including the United States.[1–6] *C. auris* causes a spectrum of conditions, from colonization to invasive infections with high mortality rates, and in 2017 when this pilot was designed, was difficult to identify with standard laboratory methods.[2,5,7–11] Prompt testing and identification of infected or colonized individuals is essential for timely implementation of infection control (IC) measures to limit transmission within health care facilities (HCFs) and reduce incidence of HCF-acquired infections.[5,8,10]

In response to the emergence of *C. auris* in New York State (NYS), the NYS Department of Health (NYSDOH) Wadsworth Center Mycology Laboratory developed a real-time polymerase chain reaction (rt-PCR) test with a substantially shorter turnaround time for results compared to conventional culture-based methods.[10] NYSDOH utilized rt-PCR testing for timely detection of *C. auris* cases in HCFs, particularly those in the New York City (NYC) metropolitan area, which experienced a high burden of *C. auris*. As of November 2017, when this pilot was implemented, NYSDOH identified 114 clinical and 220 screening/colonization cases of *C. auris* in the NYC metropolitan area.[7,11,12] To improve the timeliness of case identification and subsequent IC response, NYSDOH initiated a voluntary admission screening pilot project using rt-PCR in high-risk units of selected NYC HCFs where multiple *C. auris* cases had been identified, and control of transmission had been difficult.

This pilot aimed to 1) implement *C. auris* admission screening using rt-PCR in selected HCFs, and 2) identify risk factors for *C. auris* colonization among new admissions. Results of this pilot will influence public health IC decision making and inform the implementation of admission screening in additional HCFs.

METHODS

This project was reviewed by the NYSDOH Institutional Review Board (IRB) in September 2017 and was determined to not require IRB oversight, as the screening activity was considered to represent performance of essential public health activities, authorized through statutes or regulations.

Setting

Admission screening was conducted from November 2017 through November 2019 in 5 high-risk units within 3 NYC HCFs, each of which had identified multiple clinical *C. auris* cases.[12] These 3 HCFs participated in the pilot project voluntarily, and included:

***Nursing Home A* (NHA):** A ≥200 bed long-term care facility (LTCF). Admission screening was restricted to the ventilator unit which had a capacity of approximately 30-40 beds.

***Nursing Home B* (NHB):** A ≥200 bed LTCF. Admission screening was restricted to the ventilator unit which had a capacity of approximately 30-40 beds. NHB is closely associated with Hospital C, through referrals and individual transfers.

***Hospital* C:** A ≥500 bed acute care facility. Admission screening was restricted to the intensive care unit (ICU), cardiac care unit (CCU), and ventilator/pulmonary unit (VPU). These 3 types of intensive care unit were included to determine whether there were differences in risk between individuals on ventilators compared with those receiving a similar level of high acuity care without ventilation.

Individual admission screening

An admission screening encounter consisted of collecting 2 swabs from individuals and completing a data collection form (Appendix 1). Swabs were collected voluntarily from 3 different high-yield body sites: 1 composite swab of the bilateral axillae and bilateral groin, and a second swab of the bilateral nares.[5,8] HCF clinical staff swabbed individuals within 24 hours of admission to any of the 5 participating units regardless of clinical signs or symptoms. Swabs were shipped from HCFs to the Wadsworth Center Mycology Laboratory for testing. In NHA, admission screening from November 2017 through December 2018 was limited to new admissions and readmissions who had been outside of the facility for ≥30 days. After review, NHA revised the screening methodology to include readmissions who had been outside of the facility for ≥7 days. NHB and Hospital C aimed to screen all new admissions to participating units, as well as readmissions who had been out of the unit for ≥24 hours.

Swabs were tested for *C. auris* using rt-PCR at Wadsworth Center.[10,13] Culture was only performed for swabs with positive or inconclusive rt-PCR results. If either swab was rt-PCR positive, an individual was classified as a confirmed colonization/screening case.[12] NYSDOH staff immediately notified HCF staff of rt-PCR positive laboratory results by telephone to facilitate rapid implementation of IC measures.

When the condition of both swabs of an admission screening encounter were deemed unsatisfactory for testing (eg, damaged, incorrectly packaged), those screening encounters were excluded from analysis. Admission screening encounters for individuals who had previously tested positive for *C. auris* in NYS were also excluded from analyses, such that an individual's first positive screening encounter was included, and all subsequent screening encounters were excluded regardless of result.

Data collection

A standardized screening form, developed by NYSDOH, CDC, and HCF staff (Appendix 1), collected data on all screened individuals including demographics, date and unit of admission, prior location, reason for admission, and whether, in the 7 days before this

admission, an individual had: (1) a tracheostomy or been intubated, (2) a central venous line, (3) any drains in place, (4) received oral or intravenous (IV) antifungal medication, or (5) received oral or IV antibiotics. *C. auris* colonization/screening cases subsequently had a more detailed case report form (CRF) completed by HCF or NYSDOH staff (Appendix 2). When screening data collection forms were incomplete or missing for cases, NYSDOH staff used CRF data to complete them. Additionally, NYSDOH staff were given remote access to NHA's electronic medical record system to collect missing information.

Statistical analysis

Data from NHA and NHB were combined to analyze risk factors, given the lower number of admissions compared to Hospital C. A general linear model was used to analyze continuous variables, while χ^2 and Fisher's exact tests (where noted) were used to compare individuals who test positive and negative for all other variables, with an alpha level of 0.05 used to assess statistical significance. Data were analyzed using SAS (version 9.4) software.

RESULTS

From November 2017 through November 2019, there were a total of 2,836 admission screening encounters at the 3 participating HCFs, of which 36 had swabs in unsatisfactory condition and 74 were from known *C. auris* cases and were excluded from analysis. Of the remaining 2,726 admission screening encounters, 188 (6.9%) tested positive by rt-PCR.

These 2,726 admission screening encounters represent 2,062 individuals, 400 (19.4%) of whom had more than 1 admission screening encounter during the pilot project (range: 2-11 admission screening encounters). Of the 188 individuals who tested positive, 122 (64.9%) tested positive at their first admission screening encounter, while 66 (35.1%) tested negative at least once before testing positive (range: 1-7 negative screening encounters before their first positive). The number of days between individuals' last negative and first positive test ranged from 5 to 725 days (mean = 100 days).

The median number of days from specimen collection to release of rt-PCR results from Wadsworth Center was 5 days, with 2,410 (88.4%) results reported to HCF within 7 days of specimen collection. Across all admission screening encounters, colonization/screening cases were more likely to be identified through the axilla/groin swab than the nares swab, with 93 (49.5%) individuals who tested positive by axilla/groin swab only, 61 (32.4%) individuals who tested positive on both axilla/groin and nares swabs, 32 (17.0%) individuals who tested positive by nares swab only, and 2 (1.1%) individuals who tested positive by a swab of unknown source (due to improper labeling) only.

C. auris colonization varied by facility, with a higher proportion of colonization/screening cases reported in NHA and NHB (20.7% and 22.0% respectively) compared to Hospital C (3.6%) (Table 1).

Of the 79 cases identified upon admission to Hospital C, 49 (62%) were admitted from HCFs including: 32 (65.3%) from LTCFs, 14 (28.6%) from another unit within Hospital C, and 3 (6.1%) from another hospital (Fig 1). Examination of CRF data found that of the

remaining cases who had either private residence (n = 27) or unknown location (n = 3) before admission to Hospital C, each had a record of admission to a HCF in the 90 days before their positive *C. auris* admission screening encounter.

Within Hospital C, the proportion of colonization/screening cases identified varied by unit of admission, with the highest rates seen in the VPU (n = 16/282, 5.7%), compared to the ICU (n = 45/1,191, 3.8%), and CCU (n = 18/722, 2.5%). There was no significant difference in age between rt-PCR positive and negative individuals admitted to Hospital C (median age = 70.4 and 68.2 years, respectively; $P = .3485$). Individuals screened upon admission to Hospital C with clinical risk factors of intubation, a central venous line, a drain, or receipt of oral or IV antifungal medication in the 7 days before admission were significantly more likely to test positive for *C. auris* than individuals without those risk factors (Table 2).

Among admissions to both NHA and NHB, most cases were admitted from hospitals (98.5%, n = 66/67 and 88.1%, n = 37/42, respectively); few were admitted from another LTCF (1.5%, n = 1/67 and 7.1%, n = 3/42, respectively). There was no significant difference in age between rt-PCR positive and negative individuals admitted to the nursing homes (median age = 77.6 and 76.6 years, respectively; $P = .1830$). Individuals admitted to NHA and NHB who had a drain placed were significantly more likely to test positive for *C. auris* on admission; however, there was no significant difference in test result by other risk factors (Table 3).

DISCUSSION

This pilot project implemented *C. auris* admission screening using rt-PCR in select units of 3 HCFs in NYC. Admission screening proved to be a useful tool to identify colonized cases and helped inform implementation of IC measures and public health decision making. This pilot used targeted admission screening in ventilator and intensive care units to maximize the likelihood of identifying cases while minimizing the screening of individuals likely to be negative. The proportion of colonization/screening cases identified varied by facility and unit type, with the highest rates found in nursing home ventilator units compared to any of the units within Hospital C. However, within Hospital C, the VPU had a higher rate than either the CCU or ICU. Consistent with prior research, individuals who tested positive for *C. auris* upon admission to Hospital C were more likely to have been admitted to a HCF or nursing home in the 90 days prior, and to be intubated, to have an indwelling medical device (central venous line or drain), and to have received antifungal medication in the 7 days before a positive screening test than those who screened negative.[2,3,9,11,14] Higher rates of colonization/screening cases upon admission were found in NHA and NHB than each of the participating units in Hospital C, and the individuals in NHA and NHB ventilator units were more homogenous than those in Hospital C in terms of risk factor data collected. The data collected in this pilot, including risk factors and prior location, can be used by facilities to help inform targeted admission screening strategies. Additionally, given the high rate of prior health care exposures seen among cases, future admission screening projects should consider collecting more detailed data on health care exposures in the 90 days prior to admission screening. Following this project, screening admissions to the ventilator units in NHA and NHB continued. However, at Hospital C, admission screening was discontinued

in the CCU, where the proportion of positive admission screening encounters was lowest and was modified in the medical ICU and VPU to target individuals with HCF exposure in the previous 90 days.

HCFs considering implementing a *C. auris* admission screening program should be mindful that we found that after NHA reduced the criteria for the amount of time a readmitted individual had been out of the facility from ≥30 to ≥7 days, additional screening cases were identified that may not have been otherwise. If feasible, it is recommended that readmissions who had been outside the HCF for even shorter periods of time should be included in admission screening. This is particularly relevant given the densely populated area, with many HCFs and individuals circulating between facilities, in which NHA, NHB, and Hospital C were located.

We found that the admission screening performed in this pilot required substantial effort by HCF staff. While identifying *C. auris* colonization among new admissions may help to reduce the likelihood of within-facility transmission, the staff and space requirements to implement appropriate IC measures may be a challenge for some HCFs. In addition to training before starting this project, staff at all 3 participating HCFs estimated that admission screening (collecting specimens and completing forms) required approximately 30 minutes per individual screened. For individuals who test positive for *C. auris*, an additional 1-2 hours were required to isolate and disinfect their room. HCFs also highlighted the logistical challenges of managing newly admitted individuals with pending *C. auris* test results and managing discharge planning and transfer of cases to other HCFs. These logistical challenges present a barrier to HCF administrators accepting similar admission screening projects in additional HCFs. Given the high intra and interfacility transfer rate of many of these cases, it is imperative that HCFs ensure that they notify facilities receiving transferred individuals who have tested positive for *C. auris*, so that appropriate IC measures can be implemented immediately upon arrival at a new unit or HCF.

The turnaround time achieved in this pilot project was a median of 5 days from specimen collection to release of rt-PCR results; however, the median number of days from specimen receipt at Wadsworth Center to release of results was 1 day, with most of the turnaround time due to specimen batching and transportation from NYC to the Wadsworth Center in Albany. Given the rapid turnaround time of rt-PCR testing through the advancement of semiautomated high throughput *C. auris* detection systems developed and validated at the Wadsworth Center Mycology Laboratory, timely identification of colonization/screening cases could be further improved if additional local laboratories were able to adopt this testing methodology, thus reducing the time from specimen collection to receipt at the laboratory.[10,13]

Challenges and limitations

This pilot project has several limitations, some of which were due to practical implementation realities and the iterative nature of this project, as the project was implemented during the active response to *C. auris*, and therefore protocol adjustment was necessary.

HCFs did not enumerate new admissions who were not screened, and consequently the proportion of new admissions tested compared to the total number of new admissions was not documented. Therefore, it is unknown how many individuals were not screened upon admission according to the protocol due to refusal versus personnel constraints at HCFs. However, according to communication with participating HCFs, the number of new admissions that may have been missed for screening was minimal. Additionally, despite collecting information regarding prior location, our data could not be used to determine where an individual acquired *C. auris* unless they had only been in 1 HCF since a previous negative screening result.

Data quality was another challenge. Despite the brevity of the admission screening form, some training or orientation was required for staff completing the forms, and in spite of this training being provided some questions on the form were missed or skipped, and instances of illegible handwriting made data entry difficult. In Hospital C, due to rotation of staff who may not have been familiar with the form, the overall completeness was lower than NHA and NHB. In particular, questions that required examination of individuals' charts or medical records (eg, risk factors enumerated in Tables 2 and 3) had varying rates of missing data. However, while there were some differences by facility type, these were presented separately in Tables 2 and 3, and the rate of missing data appeared to be randomly distributed between individuals testing positive and negative. Future admission screening programs should add greater clarity to the risk factor definitions on screening forms (eg, a more specific definition of a "drain") to ensure that HCF staff responses are consistent.

While this pilot project was useful to identify *C. auris* colonization/screening cases and implement timely IC measures to reduce transmission within HCFs, it does not provide sufficient data to determine where case patients acquired *C. auris*, particularly as many cases had multiple potential health care exposures. Admission screening is a valuable tool in identifying and controlling new introductions of *C. auris* into a facility or unit, however it does not assess internal spread between individuals already within a facility. Therefore, it is recommended that admission screening be used alongside other testing strategies, such as regular point prevalence surveys, to help HCFs determine where to best direct their resources to control the spread of this fungal pathogen.

The challenges of controlling *C. auris*, along with the additional interventions that took place throughout affected HCFs, make it difficult to quantify the impact of the admission screening pilot on *C. auris* rates overall. This project was implemented in an area heavily impacted by *C. auris*, and therefore findings may not be generalizable to areas with lower *C. auris* prevalence, or other differences in local transmission that could impact generalizability. Additionally, given the differences in positivity rates between units within Hospital C, and the exclusion of nonventilator units within the nursing homes, the findings of this pilot may not be generalizable to nonventilator units within hospitals or nursing homes.

The publication of this admission screening pilot project was delayed due to the COVID-19 pandemic. During the time since this project began, other areas have identified their first *C. auris* cases, and admission screening projects were undertaken around the United States and the world.[14–20] However, rates of colonized cases identified through screening have varied,

and identification methods have depended on local incidence rates.[11,14,16–20] This pilot project remains relevant given the sparse literature, uniquely high burden of the pathogen before the COVID-19 pandemic, and the subsequent rise in reports of *C. auris* during and after COVID-19 waves. Future admission screening projects should investigate how the epidemiology of *C. auris* colonization and IC practices has been impacted by the COVID-19 pandemic.

CONCLUSIONS

Findings from this admission screening pilot might inform future screening practices through the use of rt-PCR testing; utilization of composite swabs including single axilla, groin, and nares samples; and by targeting admission screening in ventilator units within facilities, and individuals with risk factors and previous health care exposures who are more likely to test positive.

While admission screening may be a valuable tool for HCFs to create “safe zone” units that house individuals at high-risk, it does not guarantee the absence of internal *C. auris* transmission and robust IC is still necessary. Auditing of IC practices and point prevalence surveys can help monitor to prevent and control internal transmission. Enhanced communication and cooperation using a coordinated approach between HCFs are a critical part of controlling transmission and limiting spread between HCFs.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Availability of data statement:

Due to the sensitive nature of the data collected in this pilot, facilities participated on the condition that facility names would not be released and were assured raw data would remain confidential and would not be shared.

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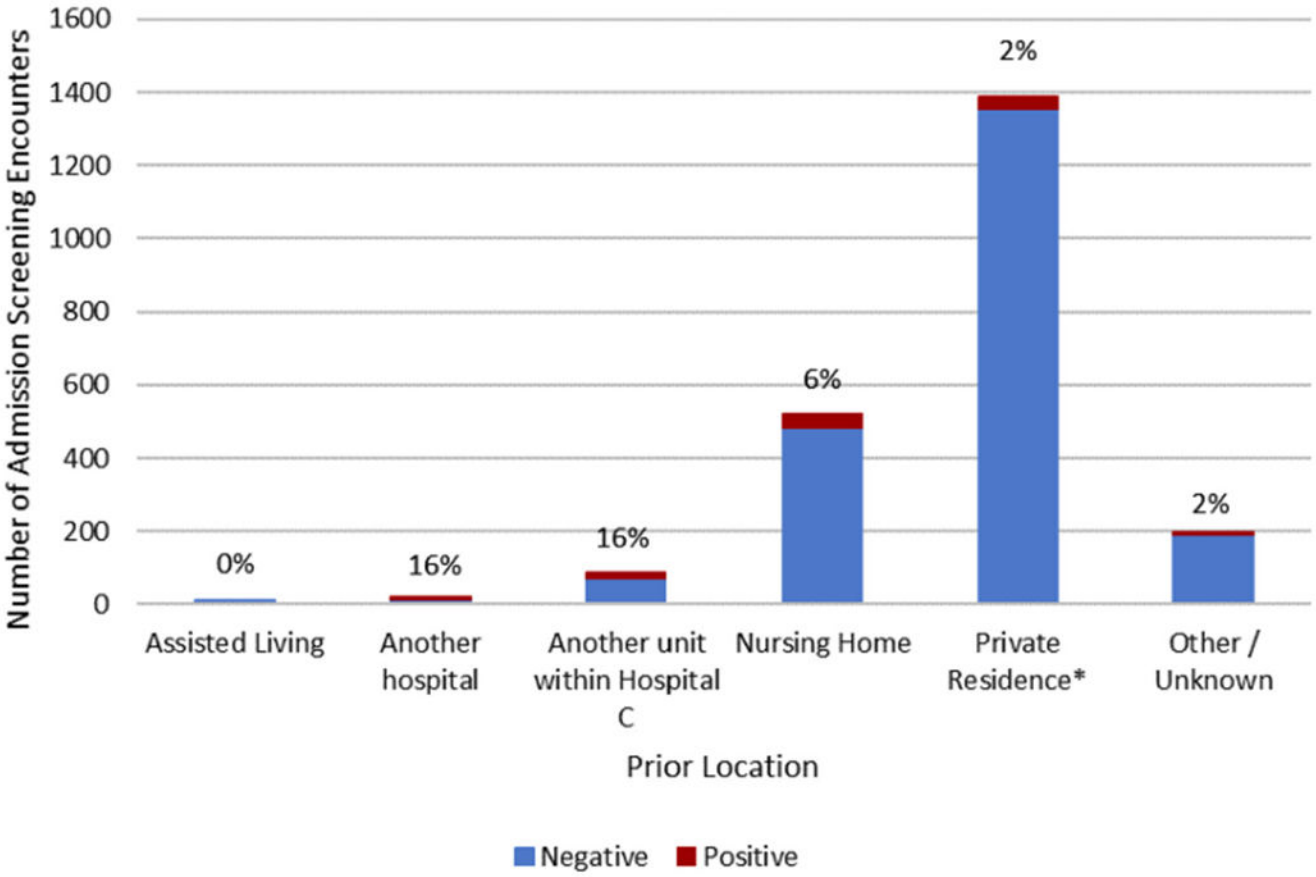

Fig 1.

Proportion of Hospital C admissions who screened rt-PCR positive for *C. auris* by prior location.

*All individuals who tested positive admitted from a private residence had an admission to a HCF in the 90 days prior. rt-PCR, real-time polymerase chain reaction; *C. auris, Candida auris*.

Table 1

C. auris rt-PCR results of individuals screened upon admission by admitting facility, November 2017—November 2019

Facility	Positive n (%)	Negative n (%)	Total
Nursing Home A	67 (20.7%)	256 (79.3%)	323
Nursing Home B	42 (22.0%)	149 (78.0%)	191
Hospital C total *	79 (3.6%)	2,133 (96.4%)	2,212
(Hospital C subtotals by unit) *			
Hospital C: CCU	18 (2.5%)	704 (97.5%)	722
Hospital C: VPU	16 (5.7%)	266 (94.3%)	282
Hospital C: ICU	45 (3.7%)	1,163 (96.3%)	1,208
Total	188 (6.9%)	2,538 (93.1%)	2,726

* Hospital C Total includes all 3 units where the admission screening pilot project was performed (CCU, VPU, ICU).

Table 2

Characteristics of Hospital C admissions by *C. auris* rt-PCR screening result (n = 2,212)

	Positive		Negative		*P*-value[δ]
	n[*]/t[†]	%	n[*]/t[†]	%	
Total	79	3.6%	2,133	96.4%	
Sex					
Female	36/79	45.6%	1,095/2,133	51.3%	.3140
Male	43/79	54.4%	1,038/2,133	48.7%	
Intubated/tracheostomy	12/61	19.7%	159/1,822	8.7%	.0034
Central venous line[‡]	8/49	16.3%	74/1,176	6.3%	.0096
Drain[‡]	7/62	11.3%	36/1,651	2.2%	.0006
Antifungal[‡] (oral or IV)	4/46	8.7%	29/1,440	2.0%	.0142
Antibiotic (oral or IV)	8/44	18.2%	210/1,491	14.1%	.4429

[*] n represents the number of screening encounters where an individual had each risk factor.

[†] t represents the total number of screening encounters where this question was completed (excludes missing/unknown) where appropriate.

[‡] Fisher's exact test used.

[δ] Excluding forms where question is missing/unknown.

Table 3

Characteristics of Nursing Home A and B admissions by *C. auris* rt-PCR screening result (n = 514)

	Positive		Negative		*P*-value‡
	N*/t†	%	n*/t†	%	
Total	109	21.2%	405	78.8%	
Sex					
Female	58/109	53.2%	208/405	51.4%	.7311
Male	51/109	46.8%	197/405	48.6%	
Intubated/tracheostomy	95/101	94.1%	325/356	91.3%	.3682
Central venous line	30/65	46.2%	69/208	33.2%	.0574
Drain	49/75	65.3%	132/252	52.4%	.0476
Antifungal (oral or IV)	3/61	4.9%	21/210	10.0%	.2188
Antibiotic (oral or IV)	21/62	33.9%	115/259	44.4%	.1317

*n represents the number of screening encounters where an individual had each risk factor.

†t represents the total number of screening encounters where this question was completed (excludes missing/unknown) where appropriate.

‡Excluding forms where question is missing/unknown.