

# Increasing Infections with *Candida* spp. and Marine Species of *Pseudomonas* among Migrants from Syria crossing Mediterranean Sea between Greece and Turkey

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Original Article

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**Abstract:**

The data about the epidemiological situation and public health risk of migrants crossing the sea is still lacking, their colonisation with bacteria with potential resistance is questionable. The aim of this study was to describe the most frequent bacteria species colonising migrants who crossed the sea during their journey to Europe in comparison to those who used Balkan route via Turkey and Greece. Commonest pathogens in samples tested in patients with pneumonia were *S. aureus* (18%), Enterobacteriaceae (17%) and *M. catharralis* (15%). *Candida* species and marine microorganisms replaced the pathogenic flora in patients with respiratory tract infections, who previously stayed long time in the nature or had to cross the sea during their journey.

**Conflict of interest:**

The authors whose names are listed in the title of the article certify that they have NO affiliations with or involvement in any organization or entity with any financial interest (such as honoraria; educational grants; participation in speakers' bureaus; membership, employment, consultancies, or other equity interest), or non-financial interest (such as personal or professional relationships, affiliations, knowledge or beliefs) in the subject matter or materials discussed in this manuscript.

**Introduction**

Over the past 4 years, Europe has experienced an increasing influx of migrants crossing the Mediterranean Sea seeking humanitarian protection and/or improved living conditions. Most are fleeing war, persecution or extreme poverty. The number of sea migrants has escalated substantially since 2011 (62,500 in 2011, 43,000 in 2013, 170,000 in 2014) following the Syrian war, the rise of the *Islamic State*, as well as the political crisis in Libya. In 2015 about a million of them have reached Europe.(1,2) There have been several studies of their health status; most of them suffer respiratory tract infections, acute diarrhoea and other conditions caused by poor hygiene

and infrastructure on the move. (2-5) The health status and spectrum of diseases can vary according to origin and previous social status. (6-7) However we are still lacking data about the epidemiological situation and public health risk of migrants crossing the sea, their colonisation with bacteria with potential resistance is questionable.

The aim of this study was to describe the most frequent bacteria species colonising migrants who crossed the sea during their journey to Germany in comparison to those who used Balkan route via Turkey, Greece, Slovenia, Hungary and Austria.

## Patients and methods

Only symptomatic patients presenting with signs of lower respiratory tract infection – fever, tachycardia, respiratory distress and cough were included. Previous travelling history was obtained, together with informed consent. Patients were divided into three groups: of those, who crossed the Mediterranean Sea, those who used land for whole journey and stationary migrants. Samples of nasopharyngeal swabs and sputum were collected and send to the National reference microbiological laboratory in Nitra, for susceptibility test. Patients were given empiric treatment due to the unavailability of further monitoring. In total, 101 patients were included.

## Results and discussion

Commonest pathogens in samples tested in patients with pneumonia were *S. aureus* (18%), Enterobacteriaceae (17%) and *M. catharralis* (15%). All pathogens were susceptible for tested antimicrobials, in both groups – stationary migrants and migrating migrants. The most probable explanation for this may be the fact, that patients were coming from rural (less exposed) environment.

As far as Enterobacteriaceae were concerned (17%), 95% were ESBL negative and susceptible for tested antimicrobials. *S. pneumoniae* was rare and *H. influenzae* we found only in few cases (2-3%), probably due to the vaccination of the coming population. Two things were statistically significantly different in both groups (see table 1). First was colonisation of the patients with *Candida* spp., mainly with *Candida albicans*, which was significantly more common in group of SM. The other was finding of marine microorganisms in patients who had to cross the sea during their journey (5%), such as *A. hydrophila*, *S. maltophilia* and others.

## Conclusions

*Candida* species and marine microorganisms replaced the pathogenic flora in patients with respiratory tract infections, who previously stayed long time in the nature or had to cross the sea during their journey. Despite the *Candida* was the leading species among both groups of migrants, we assume, it was rather colonising, not causing pathogen, in contrast to marine microorganisms. This fact should be considered when prescribing empirical therapy for migrants.

**Table 1** Comparison of microbial etiology in respiratory tract isolates among migrants with LRTI

Venue of clinic/health post	Total	Austria	Slovenia	Greece	p	p	p
Number of LRTI	101	35	29	37	At vs. SL	AT vs. GR	SL vs. GR
Type of migrants	NA	MM	MM	SM (camp)			
<i>S. aureus</i>	18 (17,9%)	10 (29%)	5 (17%)	3 (9%)		0.01	
MRSA	0	0	0	0			
<i>S. pneumoniae</i>	3 (3%)	1 (3%)	2 (6,5%)	0			
PRP	0	0	0	0			
<i>H. influenzae</i>	2 (2%)	2 (6%)	0	0			
BLPAR	0	0	0	0			
<i>M. catharralis</i>	17 (14,9%)	9 (27%)	4 (17%)	4 (11%)			
Enterobacteriaceae	17 (17%)	7 (20%)	6 (21%)	4 (12%)			
ESBL+	1	1	0	0			
<i>Ps. aeruginosa</i>	3	1 (2,5%)	1 (3,3%)	1 (2,8%)			
Non-aeruginosa ps. species	6	0	1 (3,3%)	5 (14%)		0.01	0.04
<i>Candida</i> spp.	42	10 (29%)	9 (32%)	23 (60%)		0.04	0.04
<i>Candida albicans</i>	30	5 (14,2%)	4 (17%)	21			
Non-albicans <i>Candida</i>	12	5 (14,2%)	5 (17%)	2 (5,4%)			

\* MM- migrating migrants on the move

\*\* SM – stationary migrants in camps

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