

The Same Question: Are Migrants from the Middle East to Greece Carriers of Resistant Bacteria? In 2015, the Answer was No, but in 2019 it is Yes (Letter to editor)

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Original Article

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Abstract:

In 2015, the surveillance cultures from respiratory tract and wounds in migrants and refugees to Greece showed only few strains of multi-resistant bacteria. In 2019, about 33-40% of all isolates were multi-resistant to several antimicrobial agents, however the majority of refugees in 2015 (90%) were from Syria and Iraq, but in 2019 the majority are from Afghanistan (40%) and Sub-Saharan Africa (60%). Longer travel, bad travel and housing conditions following by frequent respiratory and intestinal infections cause overuse of oral and OTC (over the counter) antibiotics resulting in resistance (MRSA ESBL but also KPC).

To the Editors,

In 2016, two papers in Clinical Social Work and Health Intervention (1,2) showed that cultures obtained from migrants from Turkey to Greece and transiting in UNHCR Camps in Greece (Alexandria, Veria) showed an absence of resistant bacteria like MRSA or ESBL. Only less than 5% available ATB were resistant to the migrants (1,2).

Therefore in the summer of 2019 we performed random screening of respiratory and wound isolates of those arriving at the new (2016) UNHCR camp on Lesbos Island in Greece. Results showed a very different situation in phenotypes of isolated bacteria.

While in 2015, MRSA (Methicillin resistant *S. aureus*) and ESBL-producing multi-resistant *E. coli* and *Enterobacteriaceae*, and *Pseudomonas aeruginosa* and *Acinetobacter baumannii* (PA and ABBA) were exceptional and represented less than 10% of isolates. *Candida* was the commonest isolate. In 2019, the commonest isolates were *Moraxella catarrhalis* (all ampicillin resistant

(MOCCA); followed by ESBL (extended spectrum betalactamase producing); *Enterobacteriaceae*, including two KPC producing pan-resistant EC and ABBA. In addition there was a dramatic decrease of *Candida* spp and an increase of multi-resistant *S. aureus* and *Enterobacteriaceae*. This phenomenon was observed in isolates from 2019 with an increase representation of so called marine or environmental pathogens such as *Stenotrophomonas maltophilia*, *Aeromonas hydrophila*, *S.gallinarum* - all related to soil and water exposure during long migrations.

Trying to explain this dramatic change which may have great impact in 2020 on screening policy, again need to search for MR bacteria in addition to HIV HBV HCV and TB. We analyzed the origin of refugees and migrants and time (distance) of travel. Data on travel and nationality in 2019 in contrast to 2015 showed that while in 2015 more than 90% were from Syria and Iraq, in 2019, majority (about 75%) are

Tab 1: Comparison of ATB resistant phenotypes in respiratory and wound isolates from refugee camps in Greece in 2015 (Veria, Alexandria) versus 2019 (Lesbos)

Organism type	2015(Veria,Alex)	2019(Lesbos)	significance P
No of isolates tot	101	98	ns
MOCCA AMP-R	12	21	0.045
MRSA multi R	4	8	0.041
MSSA suscept	12	6	
H.influenzae	6	1	
S.gallinarum	0	4	
StrPyogenes ERYR	2	5	
Enteriobact ESBL	1	2	
Enterobac.Sucept	16	8	
Candida spp	21	1	0.0002
Ps aeruginosa	5	4	ns
Acinetobacter spp	2	4	ns
Str pneumoniae	8	1	
Streptococcus NP	8	10	
marine org.	0	4	0.045
other/negatives	4	19	

from Afghanistan and Sub-Saharan Africa, where the spectrum of infections is very different, and the distance and the duration of travel is significantly longer.

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