

Extended-spectrum beta-lactamase *Klebsiella pneumoniae* and carbapenemase-producing *Enterobacter spp.* in algae products marketed as health supplements



L. Ryan (ryanlaurab@gmail.com), M. Molloy, L. Evans, A. Quinn, E. Burke, E. McGrath, M. Cormican
 Department of Clinical Microbiology, Galway University Hospital, Ireland and National University of Ireland Galway, Galway, Ireland



Introduction

Chlorella, Spirulina and Super Greens are three popular nutraceutical food supplements available widely in Ireland

Nutritional supplements are popular worldwide claiming many health benefits, however, these claims are unsubstantiated by clinical studies.¹ These ready to eat foods are most commonly consumed mixed in water or smoothies or sprinkled on foods and consumed without cooking or other heat treatment.

- Chlorella is natural green algae
- Spirulina is filamentous microalgae
- Supergreens contain Chlorella and Spirulina as well as wheat grass and barley grass

Figure 1. Illustration of algae supplements



Production is possible by a number of methods: open systems, raceway ponds and closed systems, the latter preventing contamination from the environment.

Most large-scale commercial production is by open systems.

Spirulina and Chlorella are sold as dietary supplements, without any kind of processing except drying. Most producers of micro-algal products are located in Asia and Australia with China being one of the leading producers of Spirulina and Chlorella.²⁻³

Figure 2 1. Example of an open production system



In April 2015, the Food Safety Authority of Ireland (FSAI) announced recall of a batch of a specific brand of Chlorella powder due to contamination with *Salmonella* Rissen.

Study Aims:

1. Test recalled and related products for other *Enterobacteriaceae spp.*
2. Test isolates for multi-drug resistance

Methods

8 samples were selected for testing:

- five Chlorella
- two Spirulina
- one Super Greens

Twenty-five gram samples of the supplements were diluted in 225g of peptone buffer solution and cultured for 24 hours at 37°C

They were then inoculated onto

- Columbia Blood Agar
- Mueller-Hinton Agar
- selective chromogenic agars for vancomycin-resistant *Enterococci*, extended-spectrum beta-lactamases, carbapenemase-producing enterobacteriaceae, and methicillin-resistant *Staphylococcus aureus*

Incubated at 37°C for a further 24 hours

Colonies were identified using MALDI-TOF MS (Bruker)

Susceptibilities performed using EUC AST disk diffusion methods.

Zone diameters were interpreted according to EUCAST criteria.

Isolates that were ESBL-producers or had increased meropenem MICs were evaluated by molecular methods.

PCR using specific primers was used for detection of

- CPE (KPC, OXA-48, VIM, IMP, NDM, GES, IMI, OXA-23, OXA-51, OXA-24/40, OXA-58)
- CTX-M (Group 1, 2, 9, 8, 25)
- Plasmid encoded ampC (ACC, ACT, CIT, DHA, FOX)

Results

Cultured from all samples

- *Enterococcus faecium*
- Range of *Enterobacteriaceae*
- Anaerobes

Cronobacter sakazakii (4 samples)

Bacillus cereus (2 samples)

Sample	Isolates	Sample	Isolates
A Chlorella	<i>Enterobacter cloacae</i>	E Super Greens	<i>Enterobacter kobei</i>
	<i>Enterococcus faecium</i>		<i>Acinetobacter baumannii</i>
	<i>Cronobacter sakazakii</i>		<i>Klebsiella pneumoniae</i>
	<i>Citrobacter sedlakii</i>		<i>Cronobacter sakazakii</i>
	<i>Clostridium butyricum</i>		<i>Enterobacter cloacae</i>
	<i>Clostridium perfringens</i>		<i>Enterococcus faecium</i>
B Chlorella	<i>Cronobacter sakazakii</i>	F Chlorella	<i>Clostridium tetani</i>
	<i>Escherichia coli</i>		<i>Klebsiella pneumoniae</i>
	<i>Enterococcus faecium</i>		<i>Enterobacter asburiae</i>
	<i>Enterobacter cloacae</i>		<i>Enterococcus faecium</i>
	<i>Clostridium perfringens</i>		<i>Enterobacter cloacae</i>
	<i>Clostridium perfringens</i>		<i>Klebsiella pneumoniae</i>
C Spirulina	<i>Enterococcus faecium</i>	G Chlorella	<i>Clostridium tetani</i>
	<i>Enterobacter cloacae</i>		<i>Clostridium glycolicum</i>
	<i>Clostridium cochlearium</i>		<i>Enterobacter cloacae</i>
	<i>Clostridium perfringens</i>		<i>E. faecium</i>
	<i>Clostridium tertium</i>		<i>Enterobacter cloacae</i>
	<i>Lysinibacillus sphaericus</i>		<i>Klebsiella pneumoniae</i>
D Spirulina	<i>Bacillus cereus</i>	H Chlorella	<i>Anaerobes (unidentified)</i>
	<i>Enterobacter cloacae</i>		<i>E. faecium</i>
	<i>Clostridium cochlearium</i>		<i>Enterobacter cloacae</i>
	<i>Clostridium perfringens</i>		<i>Enterobacter cloacae</i>
	<i>Bacillus cereus</i>		<i>Clostridium butyricum</i>
	<i>Bacillus badius</i>		<i>Clostridium cochlearium</i>

Table 1. Organisms isolated by sample

Klebsiella pneumoniae – Sample E

Resistant

amoxicillin, amoxicillin-clavulanate, gentamicin, cefotaxime, and cefpodoxime.

Intermediate

ciprofloxacin

Susceptible

amikacin, piperacillin-tazobactam, meropenem, cefoxitin and ertapenem.

Meropenem MIC was 0.023 mg/L

Molecular characterisation – **CTX-M Group 9**

Enterobacter kobei – Sample E

Resistant

amoxicillin, amoxicillin-clavulanate, piperacillin-tazobactam, cefotaxime, ciprofloxacin, ertapenem, cefoxitin and cefpodoxime.

Susceptible

gentamicin, amikacin and meropenem.

Meropenem MIC 1.5 mg/L

Molecular characterisation- **OXA-51**

Klebsiella pneumoniae – Sample F

Resistant

amoxicillin, cefotaxime and cefpodoxime.

Susceptible

amoxicillin-clavulanate, piperacillin-tazobactam, gentamicin, amikacin, ciprofloxacin, meropenem, ertapenem and cefoxitin

Phenotypic ESBL (CPD:CPDCV = 26:12)

Molecular characterization- blaCTX-M not detected (presumed blaSHV or blaTEM)

Conclusions

Clinicians caring for vulnerable patients should be aware of the risk with regard to the use of these supplements.

More extensive surveys are required to establish frequency of contamination and patterns of use of these supplements to determine need for a code of practice or regulation in relation to the production and sale.

References

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Figure 3. *Klebsiella pneumoniae* PM:PML Etest showing phantom zone.

