

Anatomy of an extensively drug-resistant *Klebsiella pneumoniae* outbreak in Tuscany, Italy

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Emergence of NDM-1-producing CRE Outbreak in Tuscany region

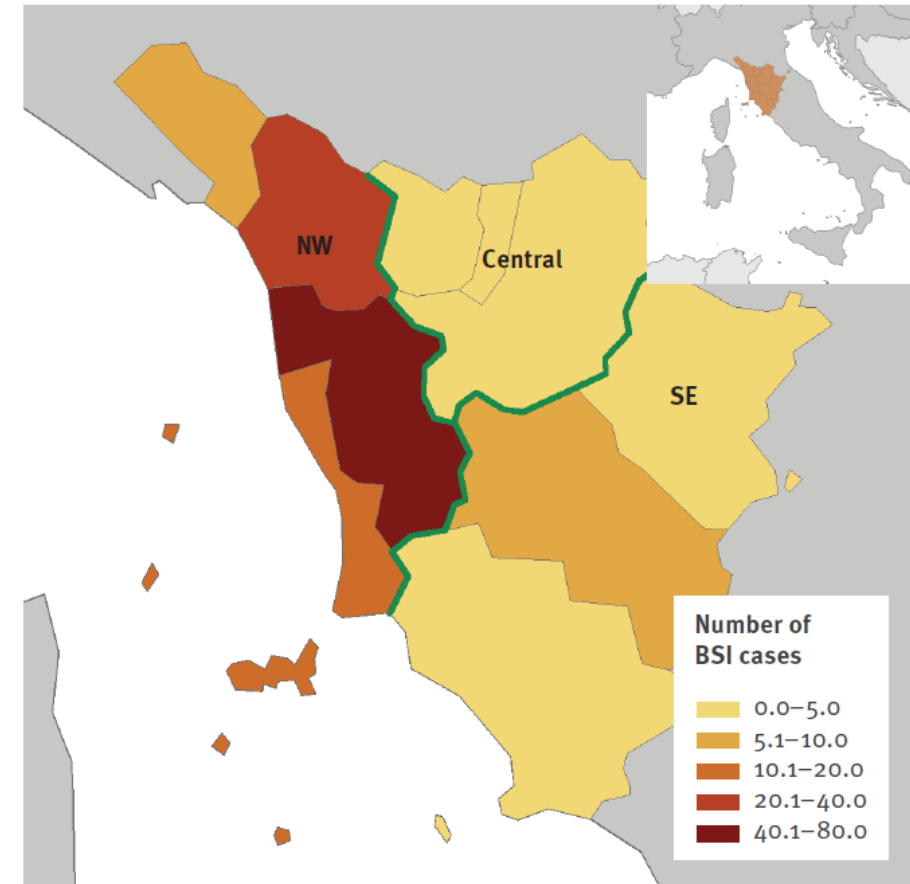


RAPID RISK ASSESSMENT

Regional outbreak of New Delhi metallo-beta-lactamase-producing carbapenem-resistant Enterobacteriaceae, Italy, 2018–2019

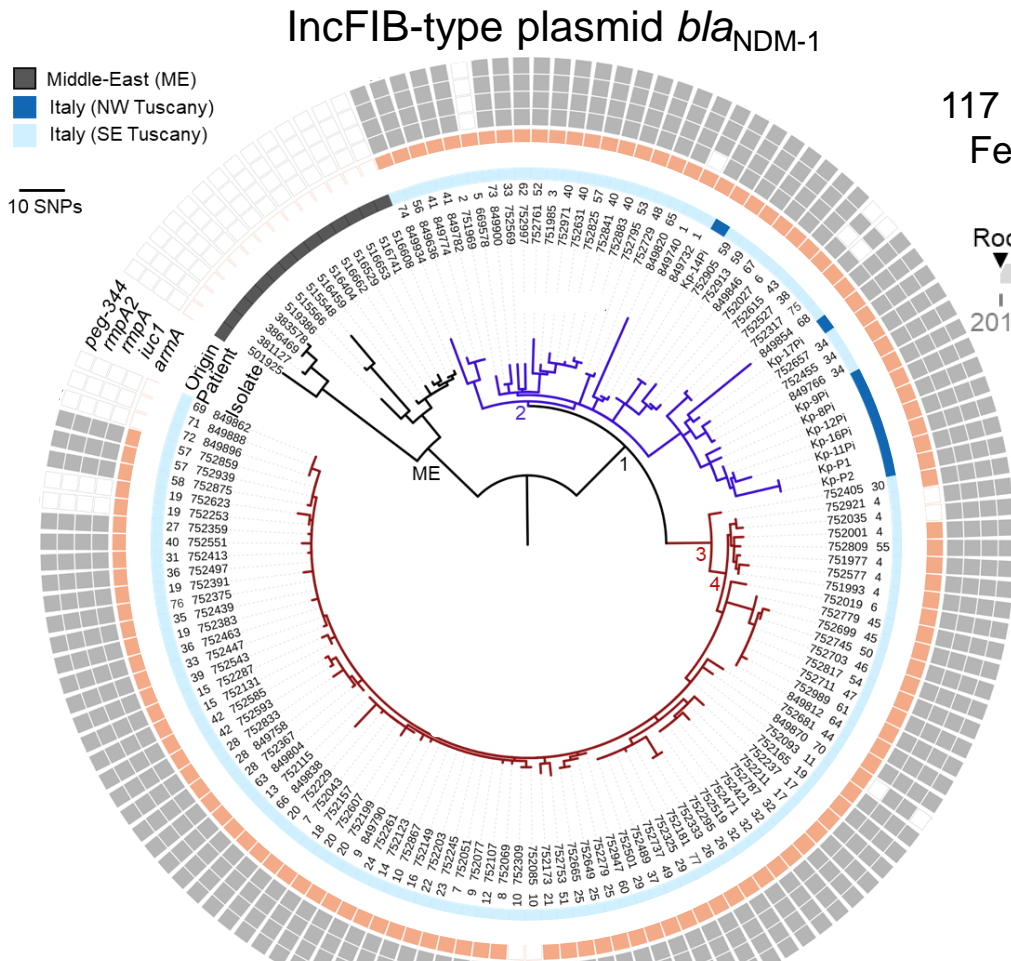
4 June 2019

1. Change in epidemiology: KPC to NDM
2. Reduced treatment options
3. Source of outbreak undetermined

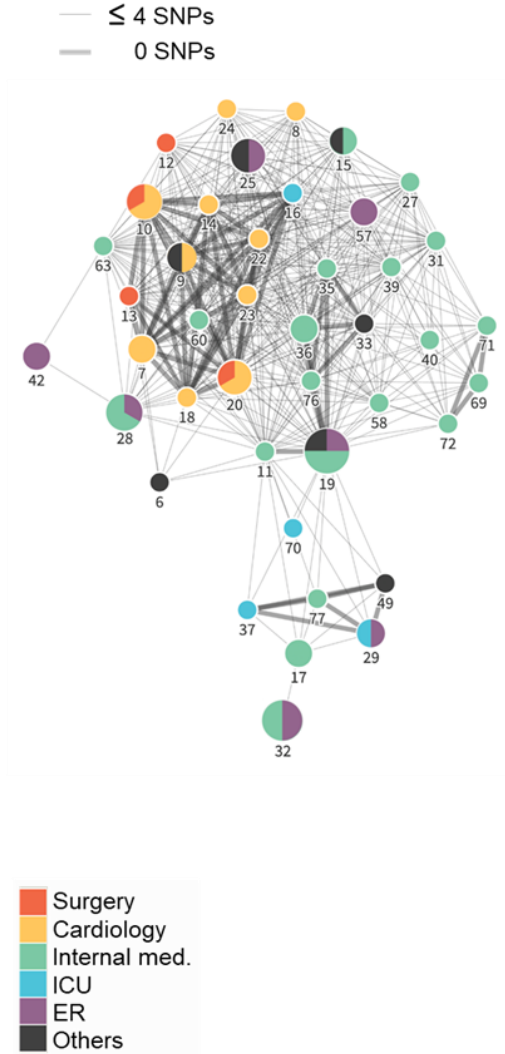
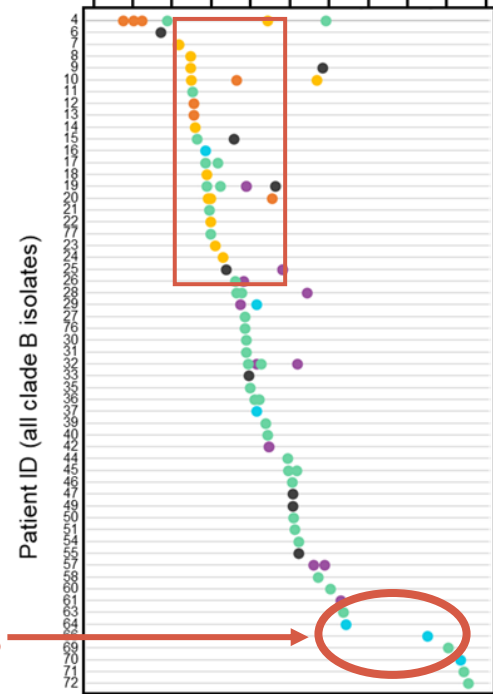
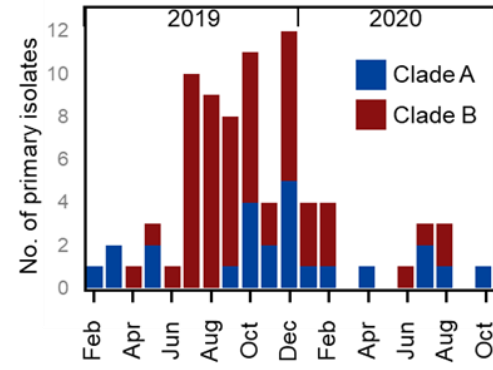


L. Tavoschi *et al*, *Euro Surveill*, Feb 2020
M. Falcone *et al*, *Euro Surveill*, Oct 2020

NDM-1-producing *K. pneumoniae* ST-147 in SE Tuscany



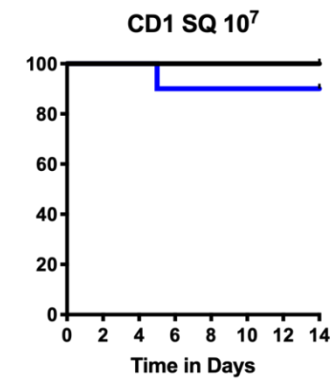
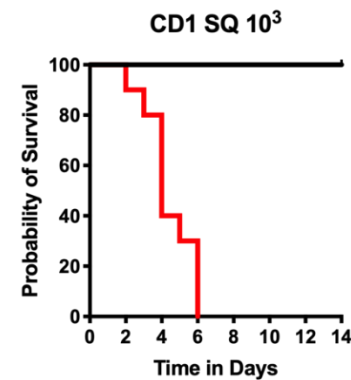
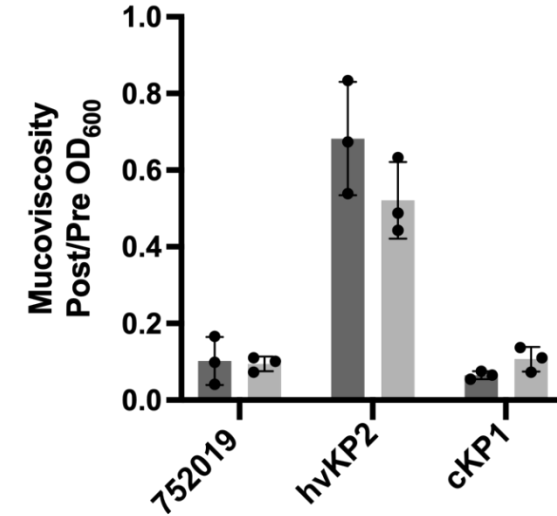
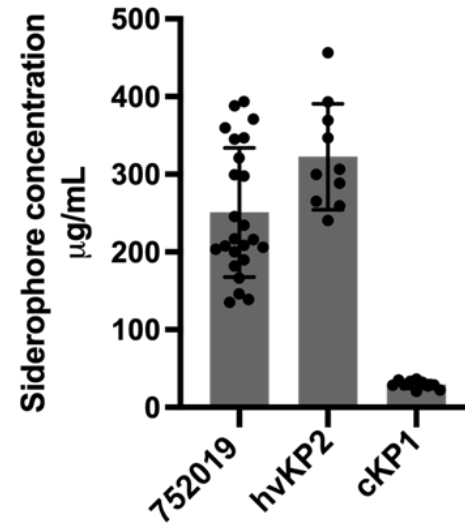
117 isolates, 76 patients
Feb 2019 - Oct 2020



IncFIB/IncHIB-type hybrid virulence/resistance plasmid (335 kb)= **Genotypic convergence of MDR and virulence**

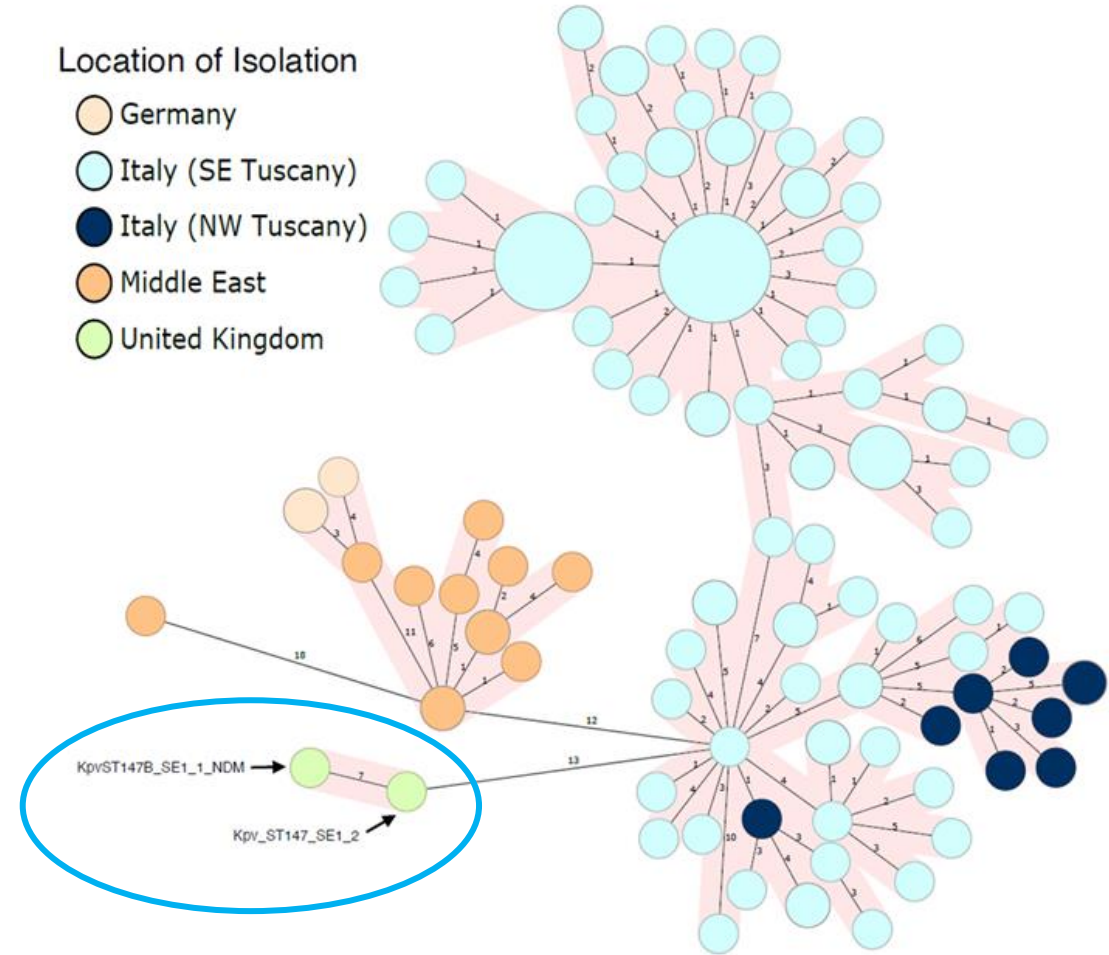
Pathogenicity of the convergent ST-147 clone

Reference strain	Gene		
	<i>iuc</i>	<i>rmpA</i>	<i>rmpA2</i>
752019	+	+	+
hvKP2	+	+	+
cKP1	-	-	-



— hvKP2 — cKP1 — 752019

Global spread of near-identical plasmids and highly genetically related ST-147 isolates



Minimum spanning tree constructed from cgMLST data

Conclusions

- XDR ST-147 outbreak caused by nosocomial transmission in Tuscan hospitals
- Possibly emerged from ST-147 MDR-cKp lineage previously shown to be endemic in ME
- Acquired hybrid resistant/virulence plasmid (found globally in distinct lineages)
- Convergent clone did not result in hypervirulent phenotype

Thank you

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