eradication, and reduce the risk of long-term complications. Due to the complexity of *S. aureus* bacteremia, early involvement of infectious diseases (ID) specialists is strongly recommended.

Methods. This retrospective, single-center study was designed to evaluate the current management of *S. aureus* bacteremias, including compliance to the elements of the *S. aureus* order set and bundle. Patients 18 years and older who had a positive blood culture for *S. aureus* were included in this study. Recurrence of *S. aureus* infection was assessed at 6 months. Data was analyzed to compare patients with and without ID consults.

Results. Eighty-four patients met inclusion criteria. ID consultation resulted in a higher percentage of patients achieving 100% compliance with the bundle elements compared to patients without ID consults (73% vs 25%, respectively; p=0.009). For further breakdown of compliance see Table 1. No statistical difference was detected in recurrence rates (11% vs 33%, respectively; p=0.18) or mortality (8% vs 25%, respectively; p= 0.17) possibly due to the small sample size.

Table 1. Outcomes

	Endpoint	No ID Consult (n=8)	ID Consult (n=76)
Bundle	Negative Culture Achieved	75% (6)	100% (76)
	TEE/TTE	67% (5)	86% (65)
	CT, MRI, Xray	50% (4)	97% (59)
	Source Identified	50% (4)	92% (70)
	Source Removed	50% (1)	95% (34)
	Appropriate Placement of New Line	50% (2)	92% (52)
Patients with 100% Compliance❖		25% (2)	74%(56)
Recurrence Rate*		33% (2)	11% (8)
Mortality^		25% (2)	8% (6)

* p=0.18, ^ p=0.17, ❖ p=0.009

Conclusion. ID specialist involvement for the treatment of *S. aureus* bacteremia resulted in greater compliance with the *S. aureus* bacteremia bundle. No statistical difference in recurrence or mortality rates was detected.

Disclosures. **All Authors**: No reported disclosures

214. Prospective Evaluation of the GenMark Dx ePlex® Blood Culture Identification Gram Negative Panel

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Background. The ePlex BCID Gram-Negative (GN) panel utilizes electrowetting technology to detect the most common causes of GN bacteremia (21 targets) and 6 antimicrobial resistance genes from positive blood culture bottles. Rapid detection of extended spectrum β-lactamases (ESBL; CTX-M), carbapenemases (KPC, NDM, IMP, VIM, OXA 23/48), and highly resistant bacteria such as *Stenotrophomonas maltophilia* enables early optimization of antimicrobial therapy.

Methods. In this prospective study, we evaluated the performance of the BCID-GN panel compared to traditional standard of care culture and susceptibility testing with organism identification using the BioMerieux Vitek MS Matrix Assisted Laser Desorption Ionization (MALDI) Time of Flight mass spectrometry. Samples submitted for standard of care testing in Biomerieux BacT/Alert resin FA/FN blood culture bottles on the BacT/Alert VIRTUO automated blood culture system with GN bacteria on direct exam (n=108) were included.

Results. All but two GN bacteria identified by MALDI were represented on the BCID-GN Panel (106/108, 98.1%) and most tests (107/108, 99.1%) yielded valid results. Discordant analyses revealed a positive percent agreement (PPA) of 102/105 (97.2%) with 3 false negatives (2 pan-susceptible *Enterobacterales*, 1 ESBL *E.coli*) and a negative percent agreement (NPA) of 105/105 (100%). Consistent with alternative resistance mechanisms, only 8/12 (66.7%) of Enterobacterales with resistance to 3rd generation cephalosporins harbored the CTX-M gene. In contrast, 8/8 (100%) of isolates from samples harboring the CTX-M gene were resistant to 3rd generation cephalosporins.

Conclusion. Detection of 1 *S. maltophilia*, 1 *Acinetobacter baumannii* expressing OXA 23/48, and 8 Enterobacterales expressing CTX-M represent opportunities for early optimization of antimicrobial therapy in 10/108 (9.3%) of samples. The BCID-GN Panel provides rapid accurate detection of resistant gram negative bacteria enabling high quality data driven optimization of antimicrobial therapy.

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215. *Candida glabrata* (*CG*) Bloodstream Infections (BSIs) Are Characterized by Genetically Diverse Populations of Strain Variants Recovered from Positive Blood Cultures (BCs)

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Session: P-10. Bacteremia

Background. The long-standing paradigm is that almost all BSIs stem from a single, clonal organism ("single-organism" hypothesis). We hypothesized that *CG*-positive BCs were comprised of genetically diverse strain variants.

Methods. Five to ten *CG* colonies were isolated from positive BC bottles from ten distinct patients (pts) for a total of 94 clones, which underwent NextGen short-read sequencing (Illumina). Variants were analyzed using SNPeff, and a phylogeny was constructed with Maximum Likelihood method.

Results. BCs harbored a diverse population of *CG* strains that were unique to each pt [Fig. 1]. All strains were genetically distinct, differing by unique SNPs and insertions-deletions (indels) [Fig. 2-3]. SNPs were ~8-fold more common than indels. Individual genomes from the same time point in the same pt exhibited consistent magnitude of variations relative to reference genome; however, variations were unique, pointing to significant genomic variability that could be both intra- and interclonal. The number of variant sites for within-pt pairwise clone comparisons ranged from 1924-8500. There were 124,145 variant sites when all clones are compared. Roughly half of all SNPs were identical in different samples from a given pt; the remainder were present/absent in at least one sample per pt. Long-read WGS revealed strains with structural variants in each pt, including chromosomal recombinations and gene duplications that were not evident by short-read WGS. A genomic phylogeny construction showed that 94 clones spanned 3 distinct clades that were distinct from the reference strain. Finally, comparison of non-synonymous mutations among intra-pt clones showed overwhelming overrepresentation of adhesin and adhesin-like genes, pointing to possible importance in host adaptation.

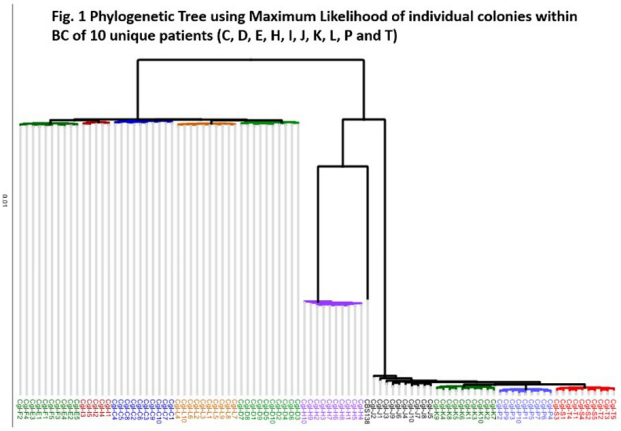

Fig. 1 Phylogenetic Tree using Maximum Likelihood of individual colonies within BC of 10 unique patients (C, D, E, H, I, J, K, L, P and T)

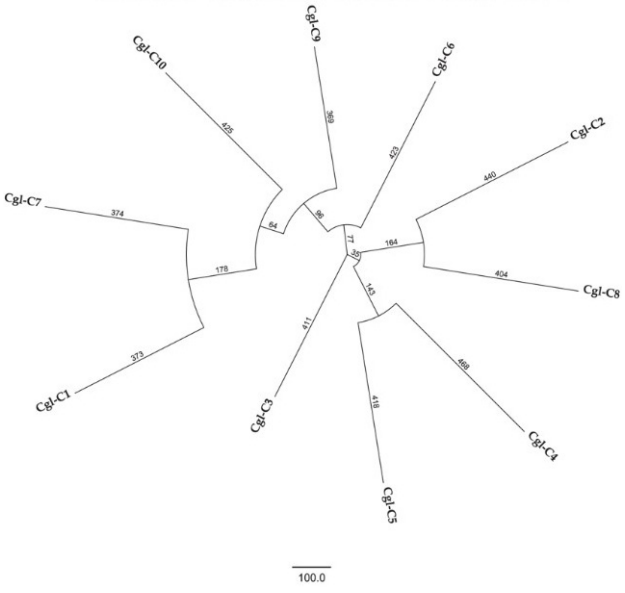

Fig 2. Within Patient Phylogenetic Tree (Patient C)