noscendo
DISQVER®

Next-Generation Pathogen Detection

Bloodstream infections correlate with high case numbers, high mortality and enormous costs. Up to date, conventional methods show many disadvantages and limitations. **DISQVER®** pathogen test by **noscendo** offers an improved solution to close the gab left by other methods. Innovative bioinformatics allow **DISQVER®** to detect pathogens from patients' blood without prior cultivation or knowledge about the aetiology of infection in an efficient, fast and reliable manner. **DISQVER®** achieves next generation pathogen detection and allows new insights into bloodstream infections, with the help of cell-free DNA as a biomarker, newest sequencing technologies and innovative bioinformatics.

Noscendo

Noscendo is a stand-alone software IVD manufacturer from Germany focusing on solutions in the infectious disease field to detect pathogens from patients' blood in an efficient, fast and reliable manner.

DISQVER® pathogen test

DISQVER® is the NGS (next-generation sequencing) based pathogen detection test by noscendo with CE-marking for IVD.
Innovative bioinformatics allow **DISQVER®** to detect bacteria, fungi, DNA viruses and parasites from a single standard blood draw without prior cultivation or knowledge about the etiology of infection. **DISQVER®** uses proprietary databases and relevance assessment methods to assign a significance value to each detected microbe allowing a precise differentiation of commensals, contamination and infection, thereby enabling you to make informed decisions.

DISQVER® procedure

1. Blood sample
Cell-free DNA isolated from a standard blood draw is prepared for next-generation sequencing analysis.

2. Sequencing
The sample is processed by high through-put (next-generation) sequencing.

3. Bioinformatic analysis
Microbial reads are compared to a large database of more than 15,000 genomes. The relevance assessment enables a statistical evaluation and differentiation of commensals, contamination and 1,500 pathogens.

4. Report
An analytical report containing all relevant pathogens detected in the patient's sample is generated.

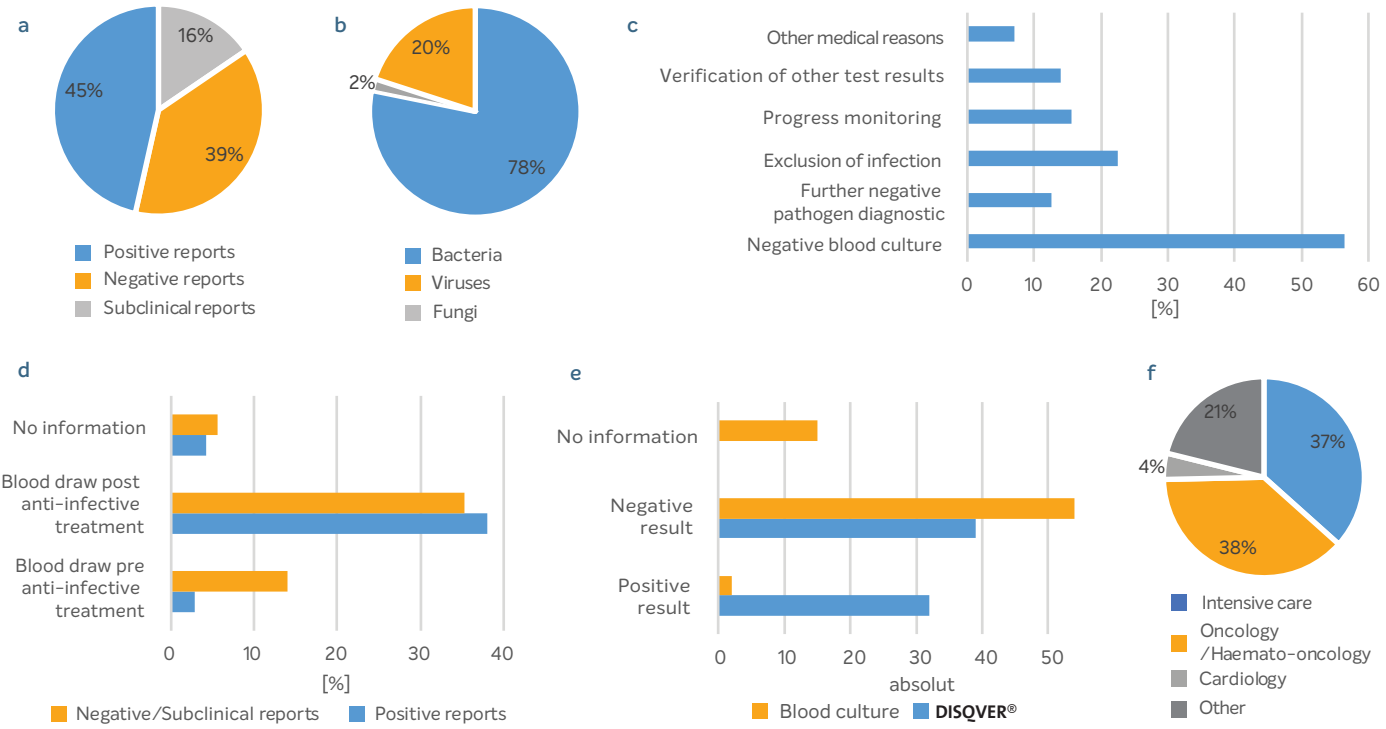

Figure 1: **DISQVER®** Pilot results. a) Result distribution. b) Distribution of bacteria, viruses and fungi in positive reports. c) Reason of investigation. d) Anti-infective pretreatment. e) Positivity rate. f) Indication areas.

DISQVER® Pilot results

DISQVER® was succesfully launched in 2019 during a pilot phase. Eight maximum care hospitals across Germany participated and approx. 100 samples were analysed within a two weeks timeframe to introduce the **DISQVER®** test. The average turnaround time amounted to 44 h (including logistics with an average time of 18 h). In order to reduce the turnaround time to less than 24 h, noscendo is offering an enabling model. This enabling model bring the test into your laboratory.

Overall, 45% positive results with clinically relevant pathogens and 55% negative or subclinical results to exclude bloodstream infections were reported (fig. 1a).

Without prior culture and unknown aethiology of the infection **DISQVER®** was able to detect bacteria (78%), viruses (20%) and fungi (2%). The most common blood stream infection detected by **DISQVER®** was caused by bacteria. However, the **DISQVER®** pilot results suggest a more frequent contribution of viruses in critical clinical conditions than previously presumed (fig. 1b). The majority of positive samples showed a monomicrobial infection, whereby more polymicrobial infections were suggested by **DISQVER®** than conventional methods, such as blood culture, did before.

The reason of investigation in more than 40% was a negative blood culture and in approx. 10% a further negative pathogen diagnostic. Furthermore, 15% of the cases were analysed to exclude an infection (fig. 1c).

The majority of cases (73%) were analysed after the start of anti-infective treatment. In those cases, positive and negative reports were distributed equally. Whereas, more negative results were reported for cases bevore anti-infective treatment started (fig. 1d).

DISQVER® has a higher positivity rate compared to conventional blood culture (fig. 1e). Half of the blood culture negative cases resulted in **DISQVER®** positive reports.

The underlying diseases of the pilot cohort can be assigned to indications associated to intensive care medicine (37%) including sepsis, solid organ transplantation, pneumonia and peritonitis, as well as onco- and haemato-oncology (38%, adult as well as pediatric samples) or cardiology (4%, e.g. endocarditis, fig. 1f).

Conclusion

DISQVER® pathogen test is open-ended and free of hypothesis. It is independent from current anti-infective therapy and offers a higher rate of positivity than conventional methods. Thereby, **DISQVER®** was used either for detection of clinically relevant pathogens, with presumption of a sepsis or serious infections with potential bacteremia when conventional methods stayed negative or for exclusion of an infection. Therefore, **DISQVER®** offers a pathogen analysis if all previous methods failed.

DISQVER® achieves a next generation of pathogen detection with the help of cell-free DNA as biomarker, newest sequencing technologies and innovative bioinformatics. In conclusion **DISQVER®** enables a new possibility for a reliable, efficient and fast analysis of blood stream infections.

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