



Next-Generation Pathogen Detection Hematology

 **noscendo**

DISQVER[®] 

Infections and especially bloodstream infections are a major cause of complications for oncological and haematological patients during or after therapy. They are associated with increased morbidity and mortality. Previous methods for detecting bloodstream infections in these indications have significant disadvantages. The DISQVER[®] pathogen test offers a solution to fill the gap left by existing tests. With its open-ended approach without hypotheses, the innovative bioinformatics of DISQVER[®] enables reliable, efficient and rapid identification of pathogens from patient blood. DISQVER[®] represents a new generation in pathogen diagnostics and enables a completely new perspective in the treatment of bloodstream infections.

Pathogen test **DISQVER[®]**

Conventional methods cannot guarantee the rapid detection of bloodstream infections in the field of oncology and hematological oncology, nor can they guarantee the definite exclusion of an infection. In the case of fever states, it has been difficult to distinguish whether they were caused by an infection as a common complication of chemotherapy or by therapy. Therefore, new quantitative methods are needed to identify or exclude bloodstream infections. DISQVER[®] detects bacteria, fungi, DNA viruses and parasites from a standard blood sample in parallel, without prior cultivation or prior knowledge of the possible cause of infection. Beyond the current possibilities of conventional diagnostics, DISQVER[®] can also reliably detect germs that are difficult or impossible to cultivate, regardless of any anti-infective therapy that has already been initiated.

Over 1,500 pathogens are detected by DISQVER[®] using

proprietary bioinformatics and the latest high-throughput sequencing technologies of cell-free DNA in patient blood. The relevance assessment of DISQVER[®] enables precise differentiation between commensals, contaminations and pathogens.

DISQVER[®] areas of application:

- a) pathogen identification, e.g. because previous diagnostics are negative
- b) Exclusion of an infection, e.g. follow-up controls

Over 1,500
pathogens
detected

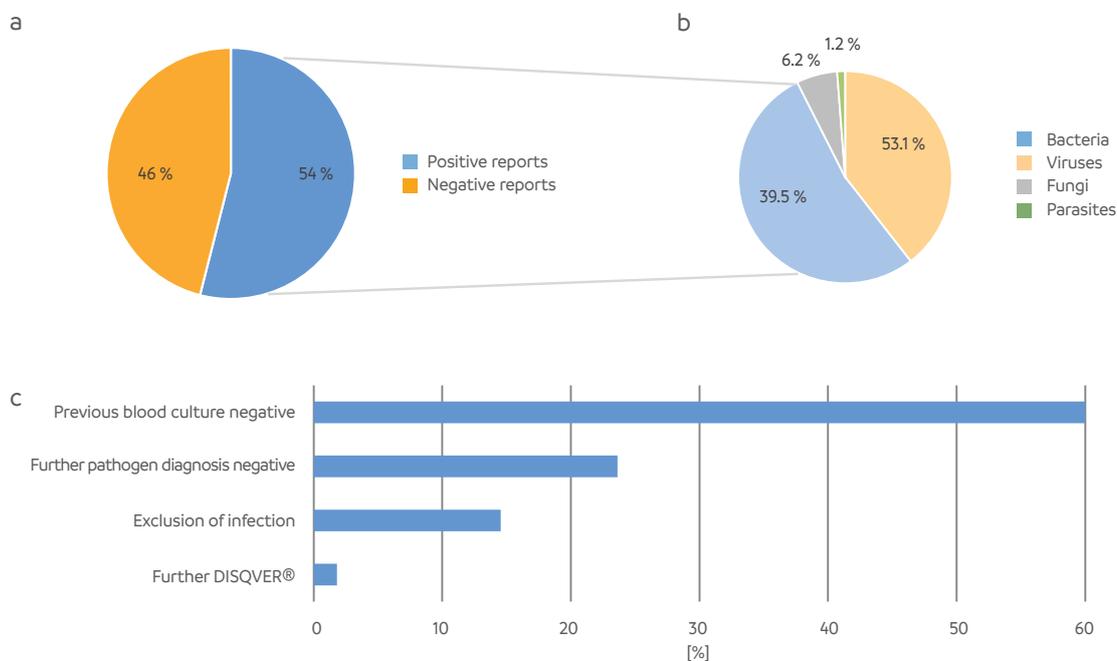


Figure 1: DISQVER® results for the indication group oncology (solid tumours as well as haematooncology)
a) Distribution of positive, negative and subclinical reports
b) Distribution of bacteria, viruses and fungi in positive tested samples
c) Reason for testing

DISQVER® was successfully launched in 2019. Since its launch, more than 28 % of samples analysed by DISQVER® originated from the fields of onco- and haematooncology, including paediatric samples. The average analysis time from sample collection to result notification was 44 hours. The dispatch time of approx. 18 hours included in this could be saved in the case of a laboratory enabling, thus reducing the analysis time to approx. 24 hours. Overall, 54 % positive results with clinically relevant pathogens and a total of 46 % negative results to exclude a bloodstream infection could be provided to the clinician (Fig. 1a).

Analysis time
approx.
24 hours

Most bloodstream infections detected by DISQVER® are bacterial in origin. However, the results of DISQVER® suggest a greater involvement of fungi and viruses in critical conditions than previously suspected (Fig. 1b).

The reason for the investigation was a previously negative blood culture in approx. 60 % of the cases. Furthermore, in almost 15 % of the cases, the exclusion of an infection was indicated, in which DISQVER® can help due to its high sensitivity (Fig. 1c).

Conclusion

Immunosuppressed patients, e.g. due to the start of chemotherapy or after stem cell transplantation, represent a risk group for infections, but are also prone to therapy-related infection symptoms. DISQVER® offers a fast, precise and reliable way of

pathogen detection and also for excluding infections. This means that specific anti-infective therapies can be initiated or possibly avoided altogether in order to keep the additional burden for the patient as low as possible.