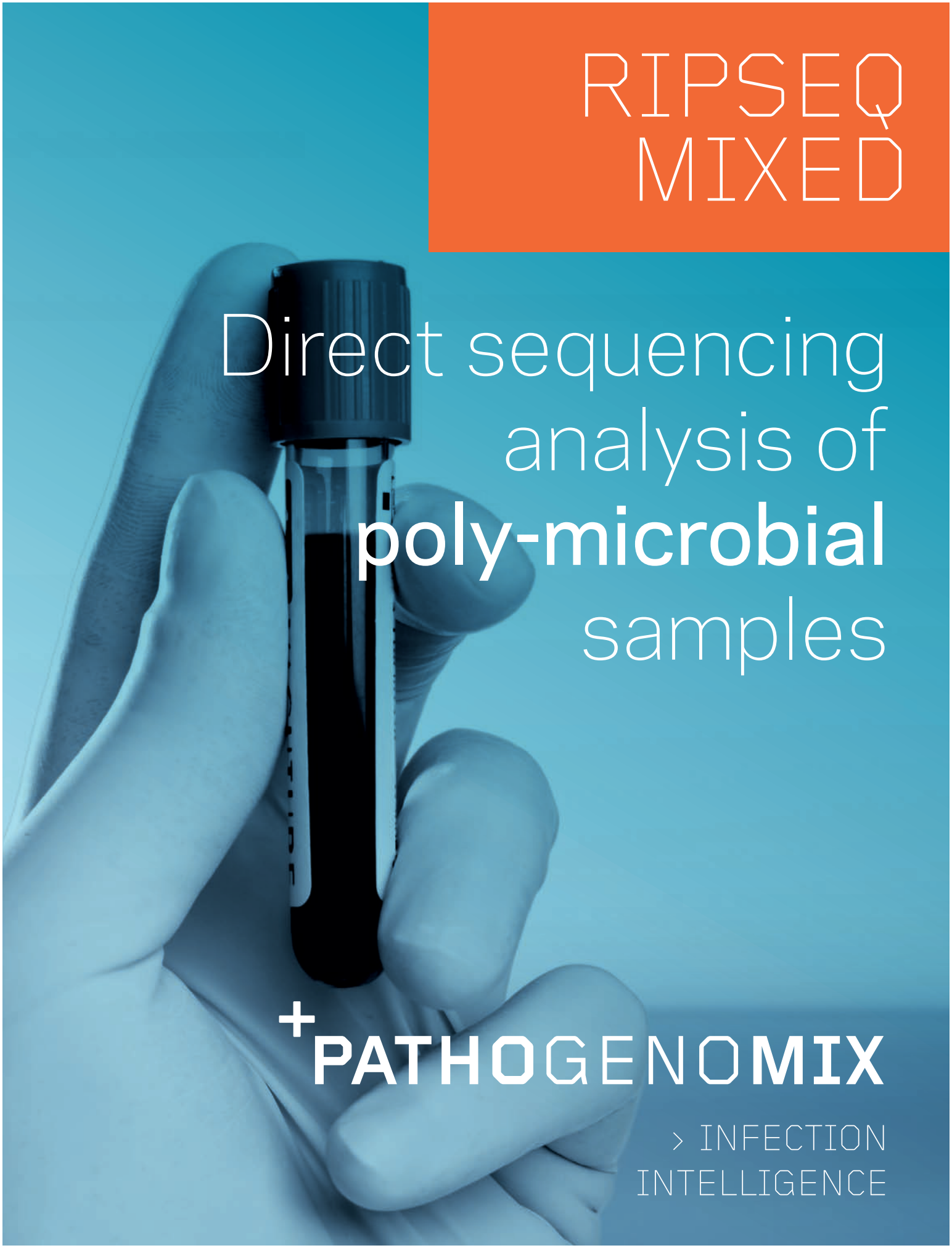
RIPSEQ MIXED

Direct sequencing analysis of **poly-microbial** samples



+PATHOGENOMIX

> INFECTION INTELLIGENCE

RipSeq® Mixed is an online software tool for rapid bacterial identification, with focus on analyzing mixed clinical samples. Through the use of advanced algorithms, we remove the need for manual isolation and re-cultivation of colonies from poly-microbial samples prior to 16S rDNA sequencing. This makes direct sequencing relevant for a broader range of clinical samples, including abscesses and pleural fluids.

Compared to culture, the possibility to analyze mixed bacterial populations with direct sequencing offers a significant reduction in time to identification, in particular for samples containing slow growing bacteria, or bacteria for which phenotypical identification is not readily available.

More importantly, it provides a powerful diagnostic tool for patients who have received antibiotics prior to sample collection. For this patient group, culture is unreliable and should never be trusted as the sole diagnostic approach. Even if growth is obtained for some species, others can already be dead or too affected by antimicrobials to be cultured.

Identification time using traditional methods: **2-7 days or more**

Day 1
PATIENT SAMPLE

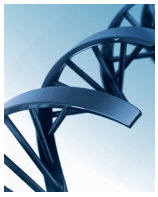
Growth and separation of the bacteria followed by new growth of the separated bacteria

Day 2-4
CULTIVATION

Antibiotics make culture unreliable – sequencing should **always** be a supplement

Chemical testing is usually run before attempting to sequence

Day 3-7
CHEMICAL TESTING



If chemical tests fail to identify the bacteria, the sample is sent to Sequencing for identification

RipSeq Mixed identifies multiple bacteria in one sample in just: **5-8 hours**

Day 1
PATIENT SAMPLE

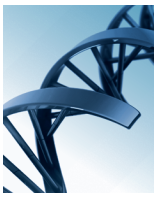
Sequence directly from sample

Day 1

Universal primers

Group specific primers

Day 1
SEQUENCING



Day 1
IDENTIFICATION AT WWW.RIPSEQ.COM

Up to 3 species in <30 sec.

Up to 9 species in <30 sec.

Don't wait for culture

REFERENCES

Kommedal O, Lekang K, Langeland N and Wiker H G. 2011. Characterization of polybacterial clinical samples using a set of group-specific broad-range primers targeting the 16S rRNA gene followed by DNA sequencing and RipSeq analysis. J. Med. Microbiology. March 2011. **Epub** ahead of print.

Kommedal Ø, Kvello K, Skjåstad R, Langeland N and Wiker H G. 2009. Direct 16S rRNA Gene Sequencing from Clinical Specimens, with Special Focus on Polybacterial Samples and Interpretation of Mixed DNA Chromatograms. J. Clin. Microbiology. **47**(11):3562-3568.

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