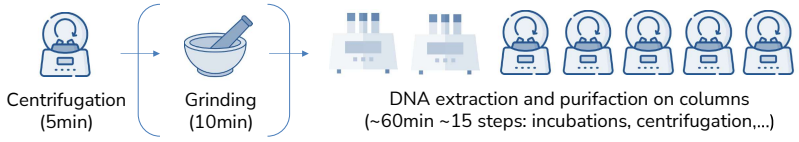
Point-of-care DNA extraction for fungal detection from hair, nail, skin, and liquid samples

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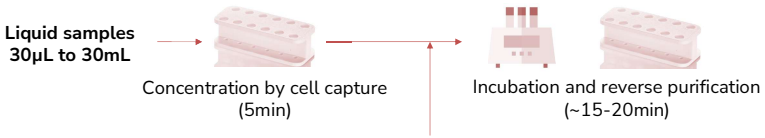
Background and Objective

- Traditional DNA extraction procedures from skin, nail and hair for dermatomycosis are lengthy and cumbersome
- **SwiftX™ extraction** kits work **fundamentally different** than conventional DNA extraction kits
- **Cell capture** and **Reverse purification** enable rapid and user-friendly extraction of DNA
- We aim to provide **robust and sensitive extraction tools** with the following characteristics:
  - Enabling accurate analytical results
  - Simple and easy-to-teach handling
  - Reduced extraction time
  - No hazardous reagents
  - **From liquids – (high) diluted samples**

Reference workflow : QIAGEN QIAamp UCP Pathogen Mini



Xpedite's workflow : SwiftX DNA



Results on solid samples

SwiftX DNA variant **EUROArray SwiftX-traction** is routinely used by EUROIMMUN customers for the characterization of dermatophytes at dermatologists.

EUROArray SwiftX-traction was validated with 134 left-over samples from routine testing (culture, skin, nail, swabs, FFPE): 91 positive samples, 43 negative samples.

Concordance with reference methods (Qiagen DNA Mini, Phenol-Chloroform) was 100%.



Figure 1: Establishment of a rapid method for extraction of DNA from clinical samples for the diagnosis of dermatophytes.

Number of pos. / neg. samples after species identification and after resolution of discordant results. Data from joint publication with Prof. Yvonne Gräser (Nat. Ref. Center Dermatophytes, Charité, Berlin, DE)

		Qiagen DNA Mini		
		positive	*negative*	Σ
SwiftX™ DNA	*positive*	30	2	32
	negative	2	27	29
	Σ	32	29	**61**

Results on liquid samples

SwiftX DNA is a generic toolbox for concentration by cell capturing and purification of nucleic acids by reverse purification.

3 different fungal species were cultured and spiked in saline. The cell capture and lysis + purification by reverse purification was compared to the QIAGEN reference protocol with and without cell disruption by bead beating.

The results show equivalent or better Ct values than with the reference methods except for *Saccharomyces*. It is not yet clear if the difference in performances is due to insufficient lysis or due to lower cell capture efficiency of *Saccharomyces*.

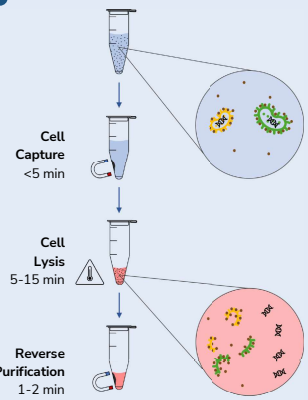
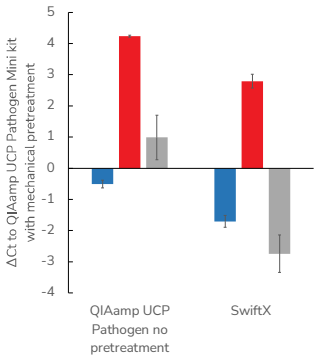


Figure 2: Capture and lysis of 3 different fungal species from saline

Quantification of fungal DNA by qPCR (n=3). Data represented as mean ± standard deviation, benchmarked against Reference method with and without pretreatment.



Conclusion & Outlook

Processing of samples at the site of sampling without compromising the diagnostic performance, without hazardous reagents.

Protocol is simple enough to be performed by semi-professional lab personnel - much faster than reference methods.

Capturing and reverse purification works great for *Candida* and *Aspergillus*. Further investigation needed for *Saccharomyces*.

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