Application Note

2021-01

Related product

This application note is related to **SwiftX™ Swabs** (SXS-50 and SXS-200 for Research Use Only).

Topic

The handbook of SwiftX Swabs (Research Use Only) describes standard buffer volumes for processing of swab samples as well as liquid samples. This application note is to inform users that also **smaller reagent and sample volumes** can be processed without impacting the efficiency of the extraction process.

In addition, this application note shall provide more guidance on the **selection of an appropriate heat source** for conducting the extraction step.

Use of lower volumes of reagents

The ***Swab Protocol*** for processing of sample swabs describes the use of 500µL of activated Component E per swab. This volume works for basically all kind of swabs, even those, which absorb a fairly large amount of buffer.

Now, depending on the type of swab, also a smaller volume of activated Component E can be used to perform the nucleic acid extraction. Applicable types are ***swabs having a small sampling head, e.g. nasopharnygeal swabs, or flocked swabs***, e.g. from Copan Technologies. Both types of swabs absorb significantly less liquid buffer than standard swabs. Thus, they ***can be processed with as low as 300µL activated Component E***.

The ***Media Protocol*** for processing liquid samples, such as viral transport media (VTM), describes the application of 100µL liquid sample to a volume of 400µL activated Component E for extraction of nucleic acids.

It has now been validated that it is actually possible to process even smaller sample volumes of VTM without compromising on extraction efficiency. The recommended minimum volume is ***40µl VTM can be processed by mixing with 160µL activated Component E***. This enables the use of 96-microplates for high throughput testing

Fig. 1 – 96-microplate with 200µL working volume

Selection of an appropriate heat source

A key feature of SwiftX Swabs is the sample inhibitor removal based on special enzyme blends. Among the enzymes are also proteases, which securely deactivate RNases. This is required to prevent degradation of RNA after its extraction from the protecting environment, e.g. viral particle or host cell.

In order to avoid an inhibiting effect of the proteases on downstream applications, such as RT-PCR or real-time PCR, it is of ***paramount importance to conduct the heating step of the SwiftX Swabs protocol properly***.

Preferred heat sources are those with direct contact to the sample, such as ***water baths, thermo shakers and dry heat blocks***. If you do not have one of the mentioned equipments available, you can alternatively utilize an heat oven for conducting the inactivation step. However, it is very important to **validate the actual temperature** of the oven in order **to ensure the sample reaches the required 90°C**. The ***heat source must be preheated before incubation of the extraction samples***. 15 min incubation should then be counted down from the time the sample reaches 90°C.