

PART 6 THE BEAST

Remember that I said verification is relatively easy?

1D SQIsign

Verification recomputes a 2^{1000} isogeny

$$\varphi_{\text{resp}} : E_A \rightarrow E_2$$

in a number of blocks

$$\varphi_i : E^{(i)} \rightarrow E^{(i+1)}$$

All of this is done over \mathbb{F}_{p^2} and requires a few essential building blocks that we know for a long time now.

- isogeny-evaluation formulas
- pairing-based techniques
- efficient basis sampling
- point compression
- curve normalisation

2D SQIsign

Verification recomputes a 2^{128} isogeny

$$E_1 \times E_2 \rightarrow F_1 \times F_2$$

in a single block.

All of this is done over \mathbb{F}_{p^2} , and for such “short” 2D-isogenies, we essentially only need formulas to evaluate the isogeny.

These have recently been studied by Dartois, Maino, Pope, Robert using theta-models.

(If you ever heard of Richelot isogenies between hyperelliptic curves, they are essentially the same, but different...)

however

1

Scholten has shown in 2003 that each elliptic curve over \mathbb{F}_{p^2} has a “friend” in dimension 2 over \mathbb{F}_p , using Weil restriction.

2

Costello has shown in 2018 that the same holds for 2-isogenies between curves! They become 2D-isogenies.

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2D 1D-SQIsign

Map the 2^{1000} isogeny from 1D SQIsign over \mathbb{F}_{p^2} to a 2D isogeny over \mathbb{F}_p using Scholten’s construction and Costello’s isogenies.

Requires *tons of work* as we now don’t do a single “short” 2D-isogeny, but a number of blocks.

So, we developed:

- pairing-based techniques
- efficient basis sampling
- point compression
- curve normalisation