The new MRTOF mass spectrograph following the ZeroDegree spectrometer at RIKEN's RIBF facility[†]

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The newly assembled multi-reflection time-of-flight mass spectrograph (MRTOF-MS) at RIKEN's RIBF facility has been finalized and became fully operational after its first online operation in the spring of 2020. Further modifications and performance tests using stable ions were completed in early 2021. This system was coupled with a cryogenic helium-filled gas cell[1)] located behind the ZeroDegree (ZD) spectrometer to slow down the high-energy reaction products from initially relativistic energies to thermal equilibrium with the helium gas, and perform high-precision mass measurements of radioactive ions at low kinetic energies.

The setup underwent a successful commissioning[2)] leading to first important mass results recently published.[3)] Follow-up mass measurements were performed in dedicated beam times using the SRC accelerator[4)] (NP2012-RIBF 199/202).

A new optimization procedure for electrostatic mirror voltages has been implemented, which uses the pulsed-drift-tube technique to modify the ions' energy in a wide range and optimize the isochronicity of the system. The TOF could be made insensitive to the kinetic energy of the ions in a wide range. This procedure provided valuable initial settings of the mirror voltages, which have been used for further fine tuning. Figure 1 shows drift corrected TOF spectra obtained after the full optimization, which show a mass resolving power of $R_m \approx 1\,000\,000$. This result was reached for a total time-of-flight of only 12.5 ms for $A \sim 40$, which denotes a world record for such mass spectrometers. The new capabilities may allow for the study of short-lived nuclei possessing low-lying isomers.

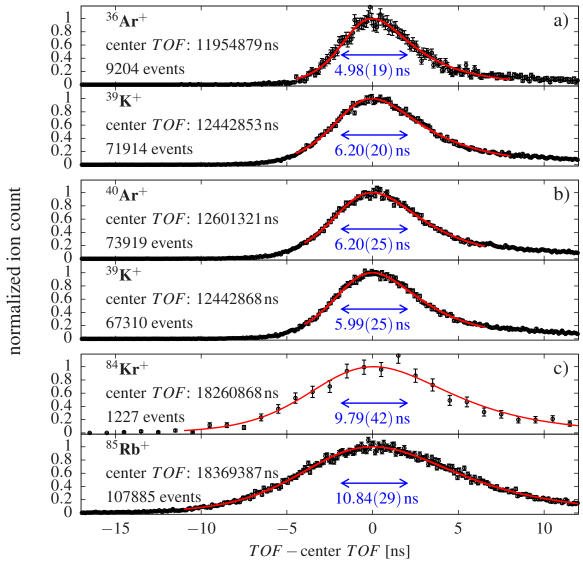

Fig. 1. Pairs of TOF spectra for one hour measurement time (Ar/Kr from gas cell K/Rb and from a thermal ion source). Numbers below double arrows: FWHM of the TOF signals.

Furthermore, a first accuracy benchmark of the setup was performed using isobaric species including stable molecules and well-known radioactive ions from BigRIPS. The mass deviations are shown with uncer-

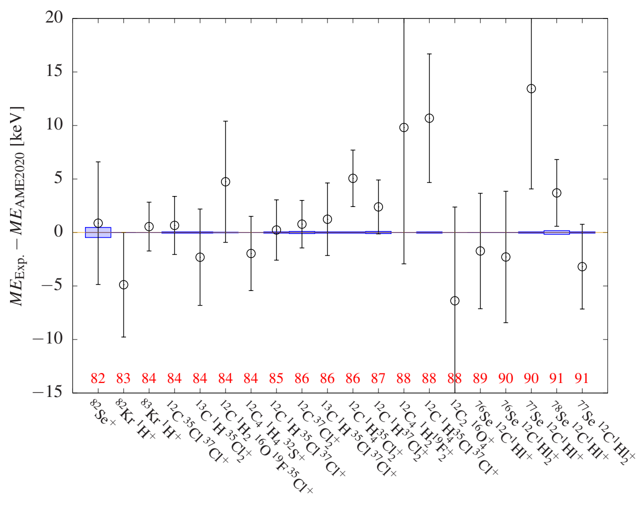

Fig. 2. Benchmark of the mass accuracy using well-known species between $A = 82$ and $A = 91$.

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tainties in Fig. 2. The precisely known masses of the analyte ions could be reproduced with an overall mean deviation of $\delta m/m = 2.8(99) \times 10^{-8}$, which is a value competitive with Penning-trap systems.

References

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