This TDF scan is mainly used in proteomics applications

- Time Delayed Fragmentation Scan – This scan mode can be used to simplify the low half of an MS/MS spectrum of a peptide. After a TDF scan, mainly y-ions are found in the lower region of the spectrum, this can be a good tool for figuring out the de novo sequence of a peptide.

- In TDF, ions are activated in the lower pressure region between Q2 and Q3. Because of the lower pressure, the relaxation rate of the activated ions is reduced. Higher energy ions will fragment rapidly and have the possibility of producing secondary fragment ions that complicate the low mass portion of the spectrum. The fragment ions lower than the Q3 fill mass are ejected from the trap for a specified period of time (Q3 cool time). Lower energy ions fragment more slowly, with less possibility of producing secondary fragment ions. After the Q3 cool time, these fragments are stored in the trap. These ions will tend to be the low energy primary fragments such as y-ions. The trapped fragment ions are then scanned out of the trap.

- Q0 trapping can be turned on in this scan mode to increase the sensitivity on the ion of interest. Sensitivity increases of 3-10 are typically seen Q0 trapping in this scan mode.
Time Delayed Fragmentation (TDF)-simplified product ion spectra where low energy fragments are predominant

1. Precursor ion selection in Q1.
2. Ions activated in the lower pressure region between Q2 and Q3 ($2-3 \times 10^{-5}$ torr)

Because of the lower pressure, the relaxation rate of the activated ions is reduced.

Predominantly used for Proteomics applications with multiply charged fragments but can be used for small molecule work such as steroid research.
Time Delayed Fragmentation (TDF)-Fragmentation

3. Fragmentation
   a. Higher energy ions fragment faster and are **ejected** from Q3 in the initial stage where only ions **above** the RF fill mass are trapped. These ions will tend to be the high energy secondary fragments.
   b. Lower energy ions fragment slower. These fragments are **trapped** in the second stage when all ions are trapped. These ions will tend to be the low energy primary fragments.
4. The trapped fragment ions are then scanned out with a normal LIT scan.
Extra TDF Slides
Time Delayed Fragmentation (TDF)

After activation, fragmentation efficiency is determined by:

\[ \text{AB}^+ + \text{M} \rightarrow \text{AB}^+ \rightarrow \text{A} + \text{B}^+ \]

\(\rightarrow\) Unimolecular Dissociation Rate
\(\leftarrow\) Relaxation or Cooling Rate

Relaxation rate is **reduced** due to activation at lower pressure vs. Q2. This allows observation of lower rate constant unimolecular processes.
Time Delayed Fragmentation

Ions are fragmented in an area of low CAD gas pressure in Q3, allowing for differentiation between primary and secondary ions.
Time Delayed Fragmentation

Normal fragmentation: During normal fragmentation in Q2, ions are activated in the high pressure region between Q0 and Q2. Product ions with excess energy can relax quickly to a lower energy state by collisional cooling. Lower energy ions cool rapidly while higher energy ions fragment to both primary and secondary fragments. The higher energy fragmentation tends to happen very quickly in this state.

Steps of TDF Fragmentation:

1. In TDF Ions are activated in the lower pressure region between Q2 and Q3.

2. Because of the lower pressure, the relaxation rate of the activated ions is reduced.

3. Higher energy ions will fragment more rapidly and are ejected from Q3 in the initial stage where only ions above the RF fill mass are trapped. These ions will tend to be the high energy secondary fragments.

4. Lower energy ions fragment more slowly, these fragments are trapped in the second stage when all ions are trapped. These ions will tend to be the low energy primary fragments.

5. The trapped fragment ions are then scanned out with a normal LIT scan.
Time Delayed Fragmentation

Activate ions via collisions

Ions with $E > E_0$ can fragment

Ions with $E > E_{\text{critical}}$ will be observed

After activation

\[ AB^+ + M \rightarrow AB^{+*} \rightarrow A + B^{+*} \]

$B^{+*}$ secondary products

Reduce $E_{\text{critical}}$ by changing the time scale of the experiment.
Time Delayed Fragmentation

- fill Q3
- Cooling (~2ms)
- Prescan (~5-10 ms)

Product Ion Mass Spectrum

mass scan