SEADM TANDEM DMA-MS SYSTEM – REVIEW

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0.1	J. Rus	9th March 07	-
0.2	J. Rus	15th June 07	Review for web site

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A. DMA-MS coupling. Introduction

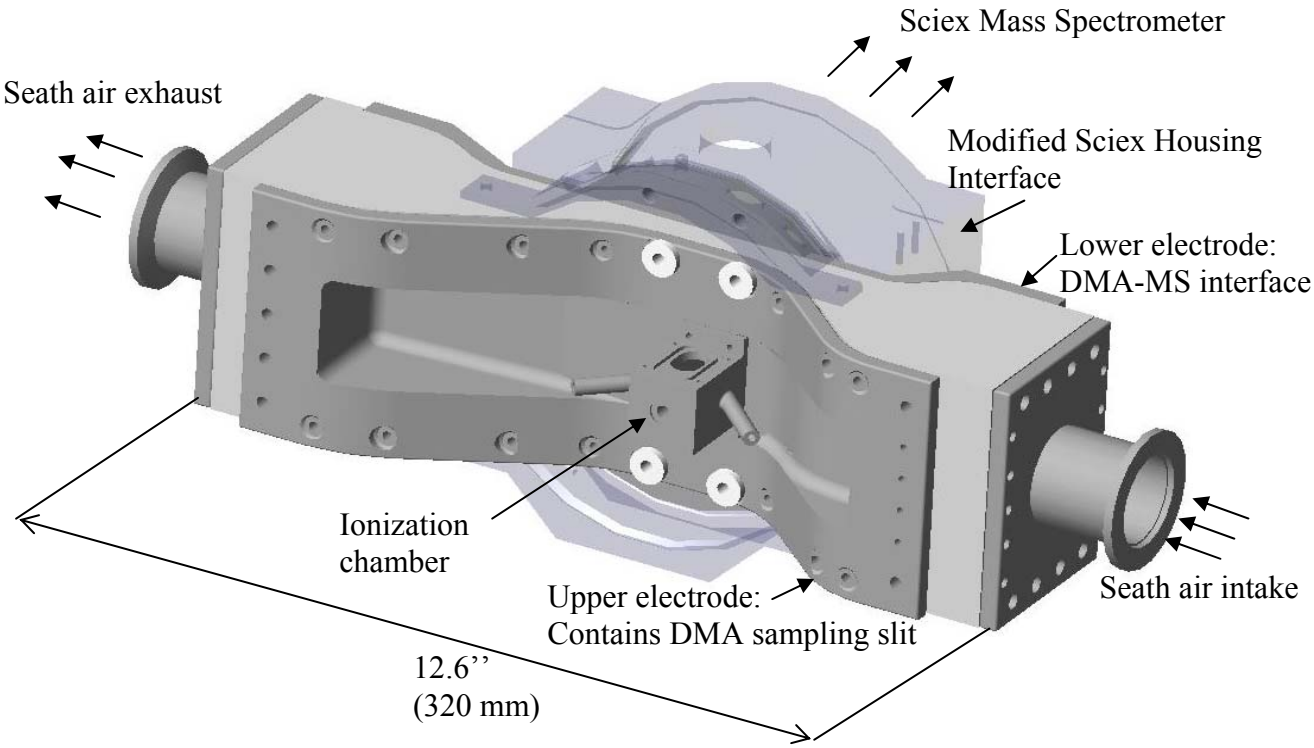

Figure A-1: DMA Sketch

Our DMA prototypes have been designed to be readily coupled to several Applied Biosystems/MDS Sciex Mass Spectrometers: those which share a similar Housing Interface. So far the prototypes have been coupled and tested on three different MS models: QStar (qQTof), API 360 and API 3000 (quadrupoles).

Since a new, modified Housing Interface is provided for the coupling of the DMA, this operation can be completed within ~ 30 minutes, limited only by the Turbomolecular pumps slow-down process. Vacuum recovery following the coupling should take no longer than 1-2 hours, which is the same time as would be required after the standard cleaning procedure of the mass spectrometer (which also requires removal of the Housing Interface).

B. Pumping requirements

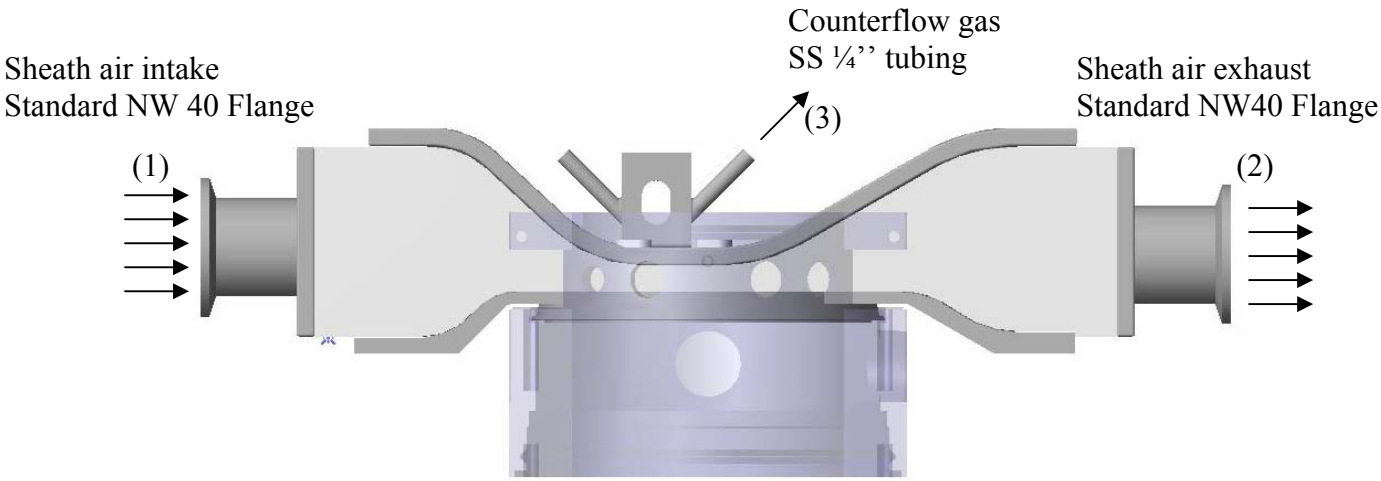

Figure B-1: Top view

- Sheath air: (1) & (2), driven by the same pump
    - Requirements:
        - Up to 70 CFM (2000 l/min)
        - Δp of up to 2 psi at 70 CFM (15 kPa at 2000 l/min)
    - Operation modes:
        - Blow from (1): exhaust (2) blows air into the lab
        - Suction from (2): air lab is suctioned from intake (1)
        - Recirculation
- Counterflow gas: (3)
    - Requirements:
        - Suctioning 0 – 0.2 CFM (5 l/min)
        - Δp of up to 6 psi at 0.2 CFM (40 kPa at 5 l/min)

C. **Ionization source**

Standard ionization source, provided with the DMA, is a microelectrospray ion source, emitting ions from the top of a needle located inside the ionization chamber (see Figure A-1), and directing them towards an entrance slit carved in the upper electrode. A small flow of CO_2 is used as a coating gas around the electrospray cone.

Alternative ionization sources are possible, directing the ions to this entrance slit inside the Ionization chamber, or completely removing this Ionization chamber, which leaves a fair access to the entrance slit. However, SEADM does not assume any responsibility for any other ionization source, and we have been reported on problems when using other standard mass spectrometer ion sources such as nebulizers, producing rather big droplets, which can lead to higher solvation inside the DMA.

D. **High voltage requirements**

- DMA voltage ranges from 0 – 8 kV, with a desirable regulation of +/- 1 V at least. This voltage is applied, referenced to ground, to the Upper electrode and Ionization chamber pieces, built in stainless steel. The mass spectrometer Ionization Source power supply might be adequate for this purpose.
- If our electrospray ionization source is used, a floating high voltage power supply will be used to raise the electrospray voltage 1-4 kV over the Ionization chamber voltage. Any other ionization source used will most likely require a similar floating high voltage power supply.

E. **Analytical performance –DMA characterization**

Most of the graphs and results have been obtained for mobility standards: tetra-alkyl ammonium ions. The following graphs show results for two of them: tetra-heptyl ammonium monomer (THA+, Z ~ 1 cm^2/Vs, 411 amu) and tetra-methyl ammonium monomer (TMA+, ~ 2.2 cm^2/Vs, 74 amu). Unfortunately no experimental results are available yet on higher molecular mass species, of biological interest.

Our DMA prototypes are currently showing a resolving power of up to 80, working between 50 and 80 for the samples under study (mobility standards), over most of the operation range. This range is currently limited by the voltage attainable without sparks (~ 7 kV although we are planning to increase it to 10 kV within a few weeks) and the sheath air speed delivered by our pumps (up to M ~ 0.7).

The following graphs show peaks and resolution data for different prototypes, coupled to a mass spectrometer or working on a stand-alone configuration.

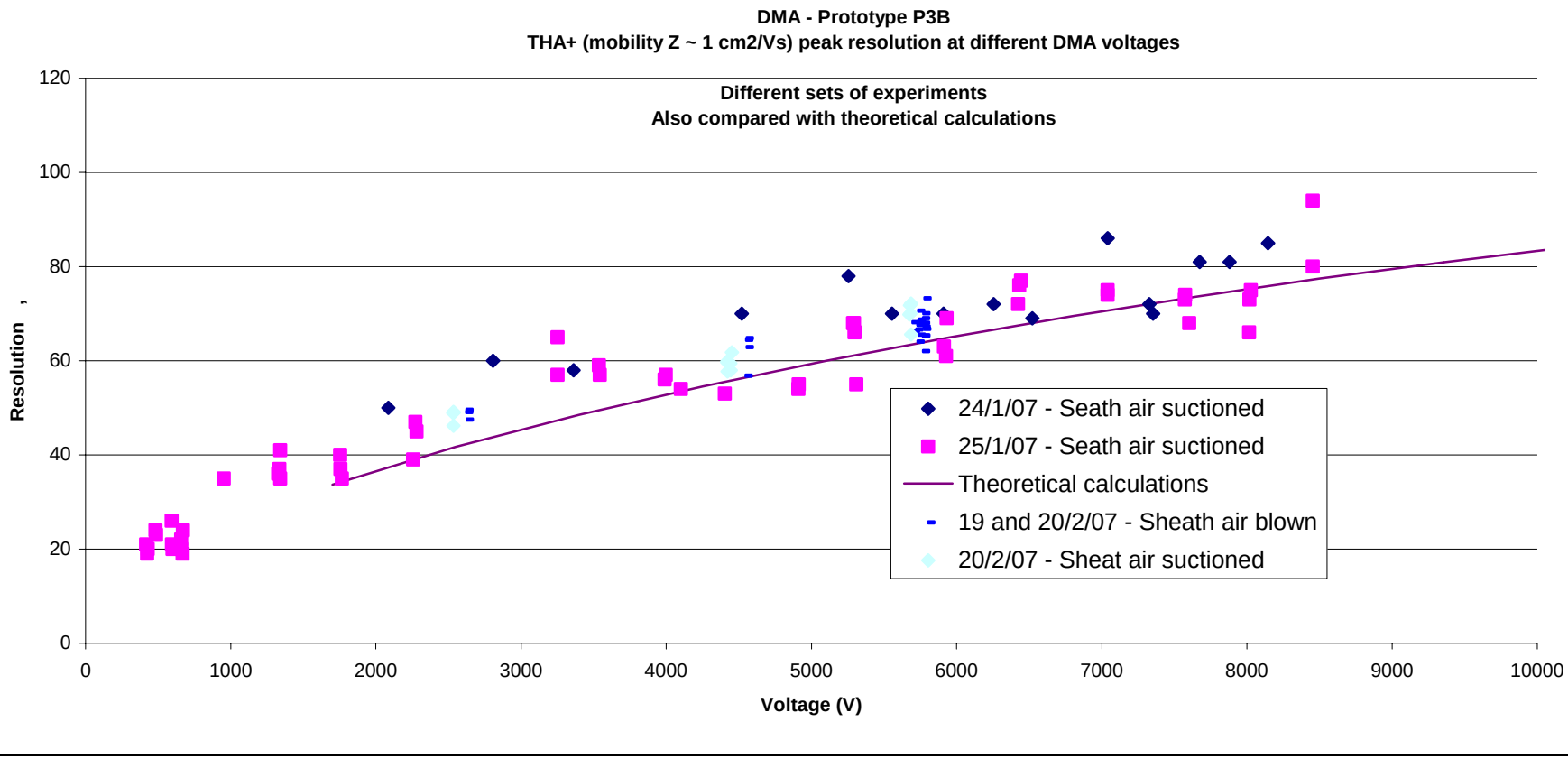

Figure E-1

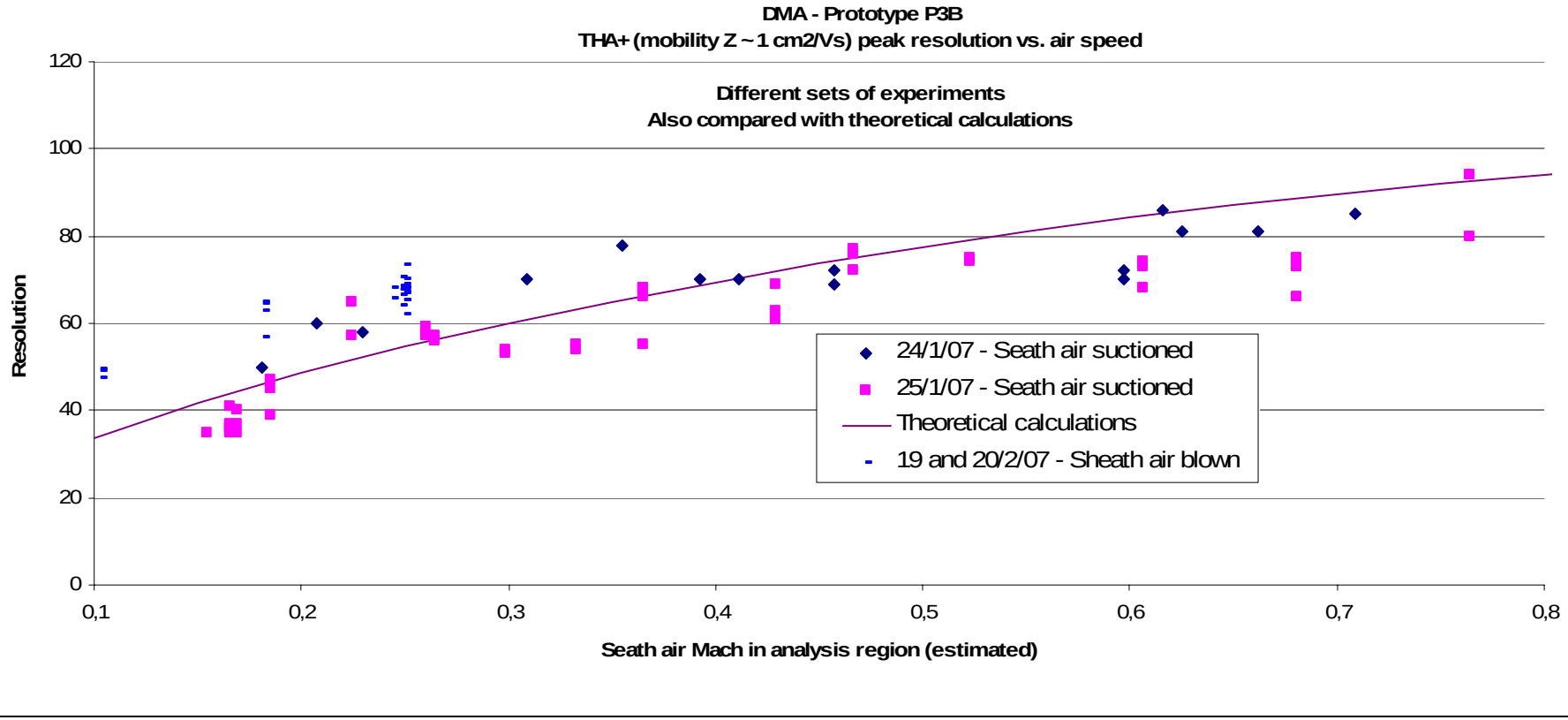

Figure E-2

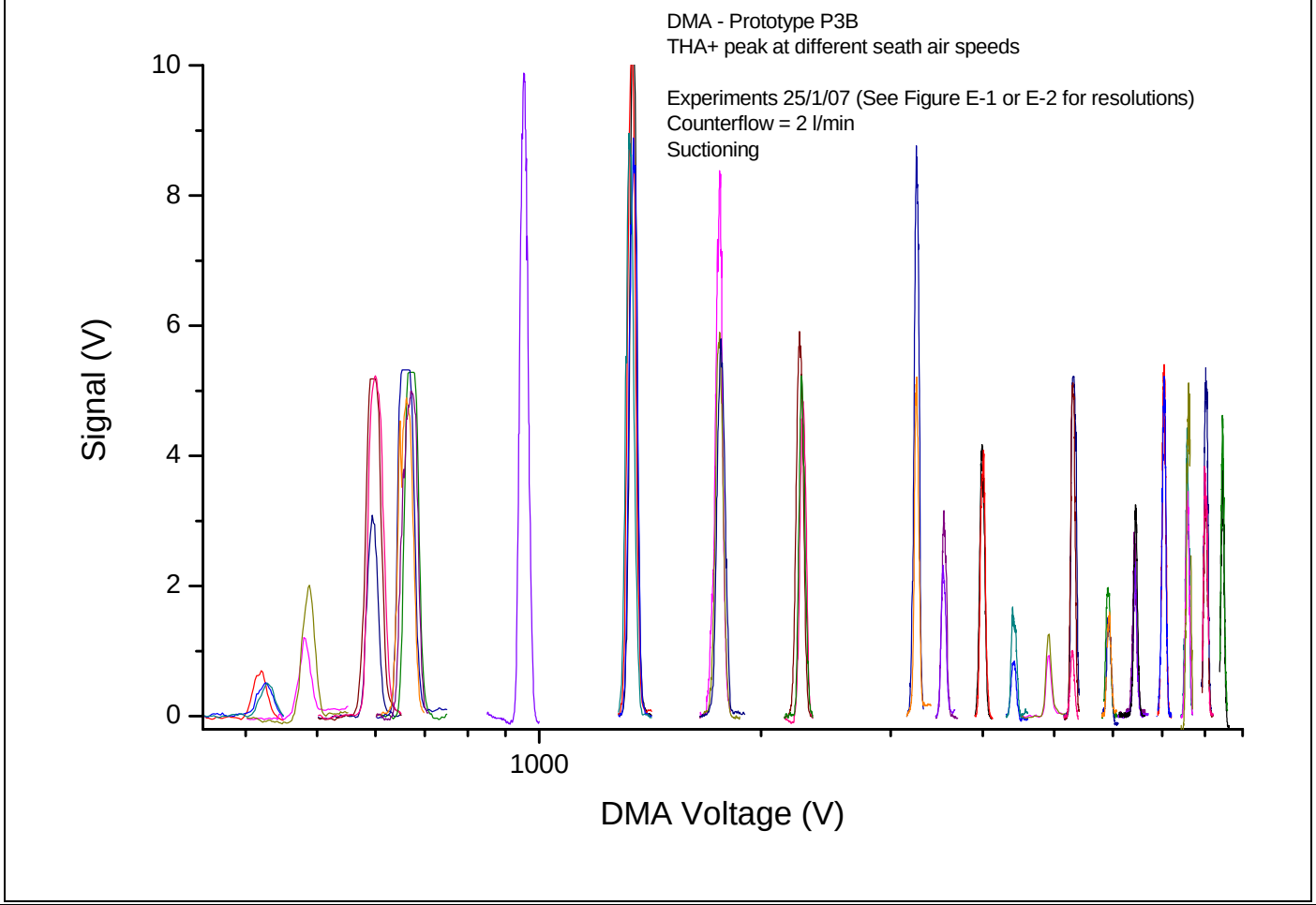

Figure E-3

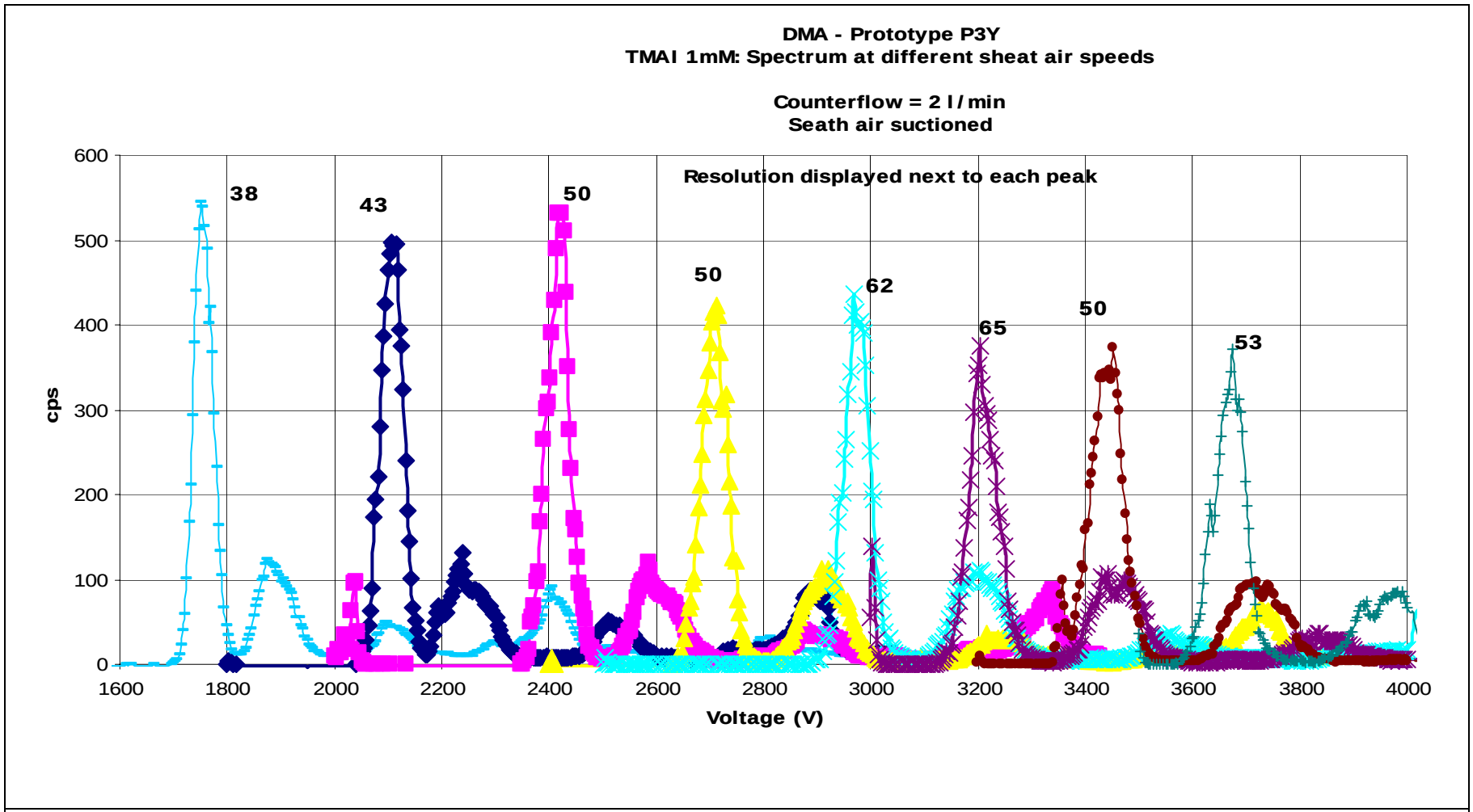

Figure E-4

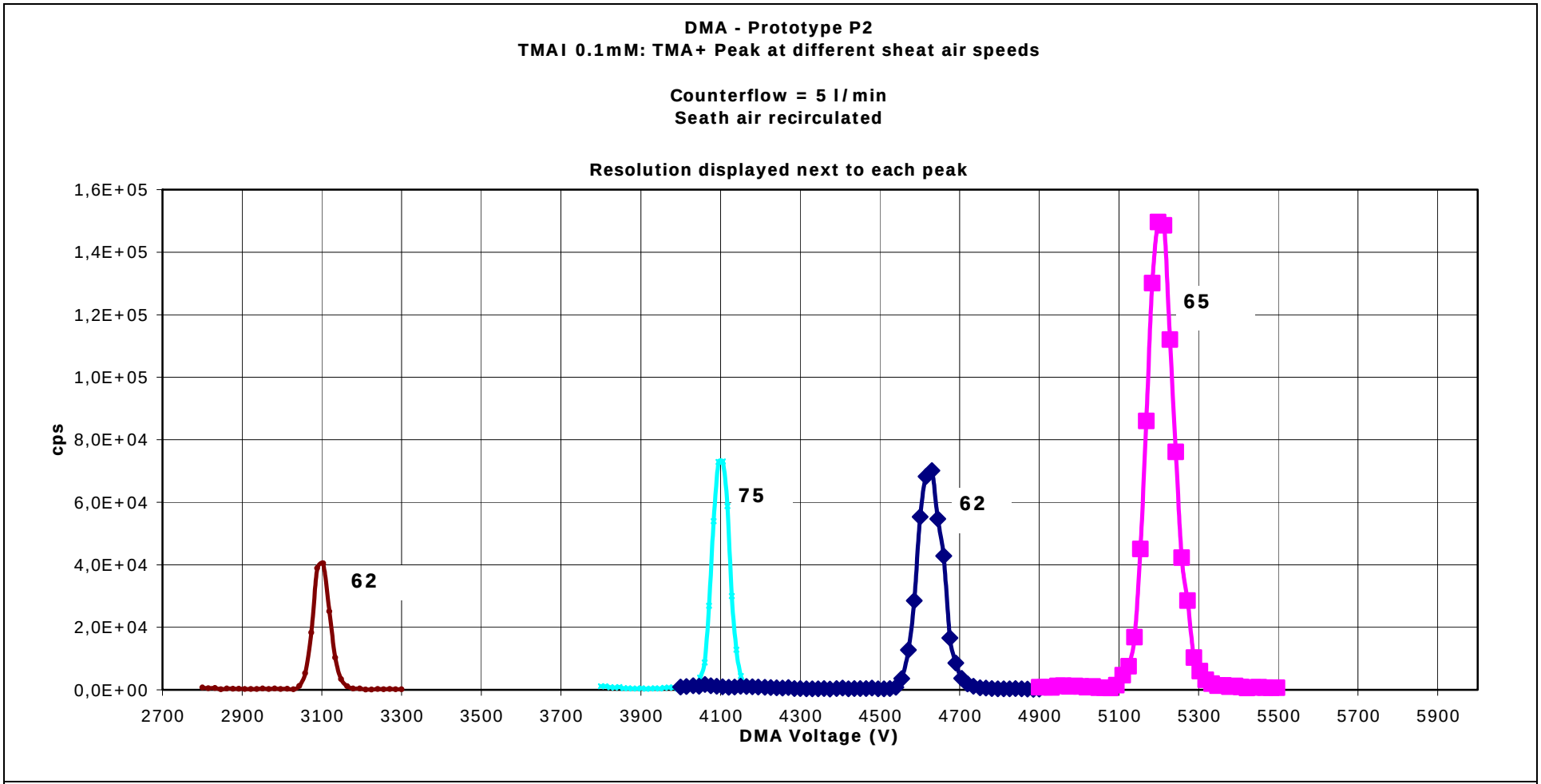

Figure E-5

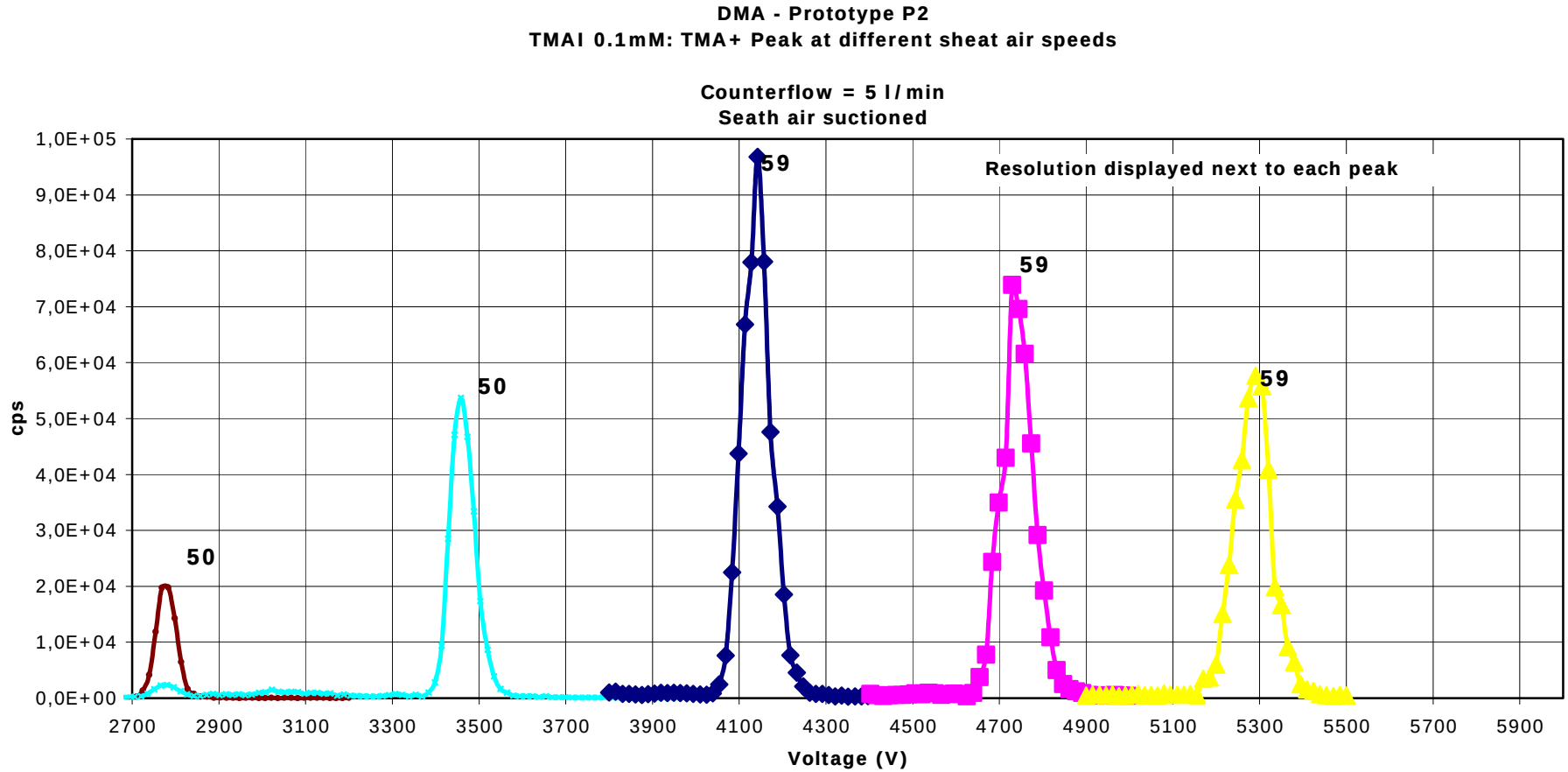

Figure E-6

F. Analytical performance – DMA-MS tandem spectrometry

This section shows present results on DMA/MS coupling. We have studied the detection of traces amounts of a substance in the air with an analysis time as short as possible, as part of a project where monitoring the sample to detect any of a large amount of target substances in a short time is required. Additionally, first studies on separation of complex mixtures (Lysozyme mass-mobility spectrum) have been presented in a conference in ASMS 2007 (link to the presentation slides).

Figure F-1 shows the signal of the target analyte received by the mass spectrometer (API 350 quadrupole), configured to continuously sample in 5 milliseconds windows. Vertical axis presents counts per second, this is, the number of the target ions (selected as a window of +/- 0.7 amu around the target mass) reaching the MS detector, while horizontal axis shows the evolution in time of the signal received. Each blue mark in the graph shows the amount of the target ion (plus any other species of the same mass) detected during 5 milliseconds. Average value of this signal in time is 873 cps, and standard deviation is 841 cps, therefore signal to noise ratio is essentially one: noise equals the signal. Moreover, signal drops to zero occasionally, showing that 5 milliseconds is a time span too short to ascertain detection of the target substance making only one measurement.

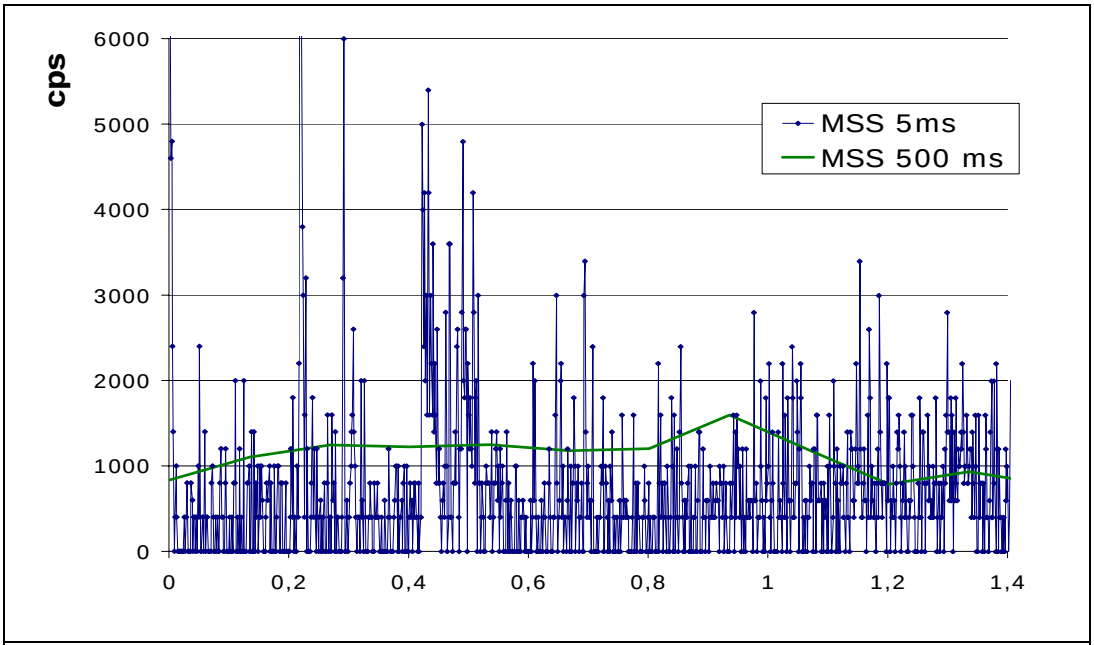

Figure F-1 – Signal/noise MS alone

The green line in the graph shows the same experiment collecting the sample during 500 milliseconds, instead of the previous 5 milliseconds. This measurement already allows for a safe identification of the target analyte, with a stable signal of an average value of 1172 cps.

Next Figure F-2 presents exactly the same MS experiment (collecting time of 5 milliseconds on the same window) where a DMA is coupled to the MS to perform the tandem DMA/MS experiment. The horizontal axis is still time, while the DMA

voltage is scanned in time so it can be associated to a certain mobility scale. It can be seen how noise is almost completely eliminated except for two close mobility peaks, corresponding to the two ionization modes of the target analyte. The average value of the strongest peak is around 1300 cps with a standard deviation of 691 cps (signal to noise ratio of 2:1).

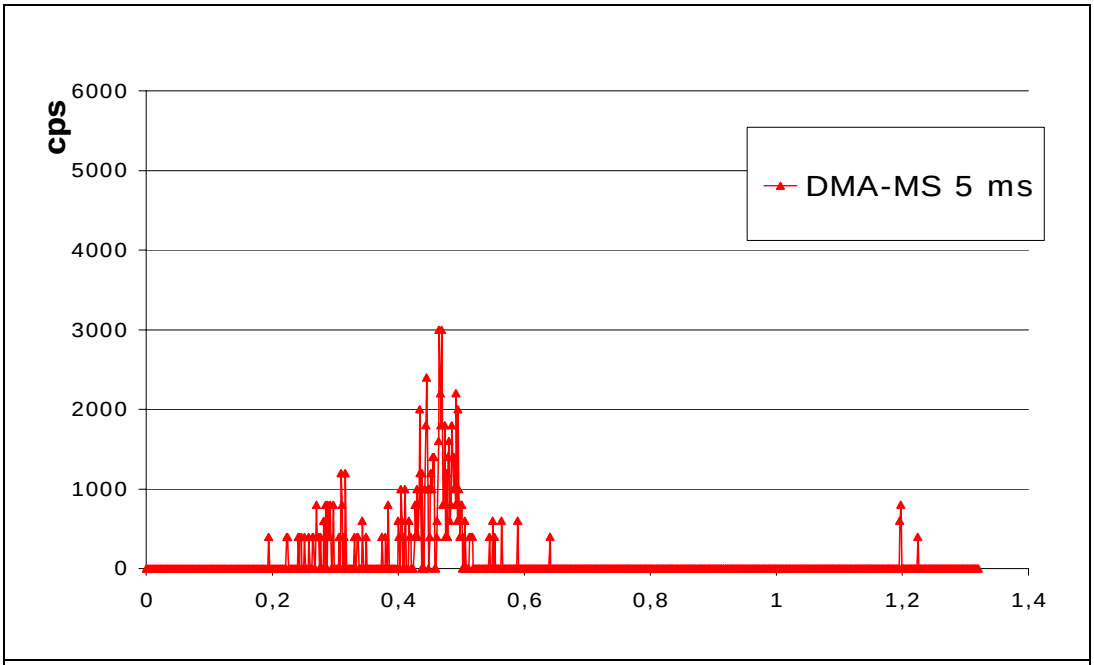

Figure F-2 – Signal/noise DMA-MS

Therefore, the signal to noise ratio when detecting the target substance (being noise the variation in time of the signal when DMA and MS are configured to detect that substance), has been doubled from the MS experiments. Moreover, we can see how the DMA signal to noise ratio is excellent (being noise the target ions detected by the MS when the DMA is set to a different mobility than the target one). In fact, it is difficult to give a number for it given the almost inexistent noise outside of the two peaks.

An additional experiment is shown in order to evaluate noise level for non-selected mobilities: Figure F-3 includes additional spectra, varying the sheath air speed so that the mobility peaks appear at different DMA voltages. Noise out of the mobility peaks is not completely zero, since some noisy counts appear at random voltages. Average noise is obtained adding them and dividing over the total sampling time, which gives an average noise of 3.5 cps and a noise to signal ratio of between 700 and 950, which is an excellent result for the differential mobility separation.

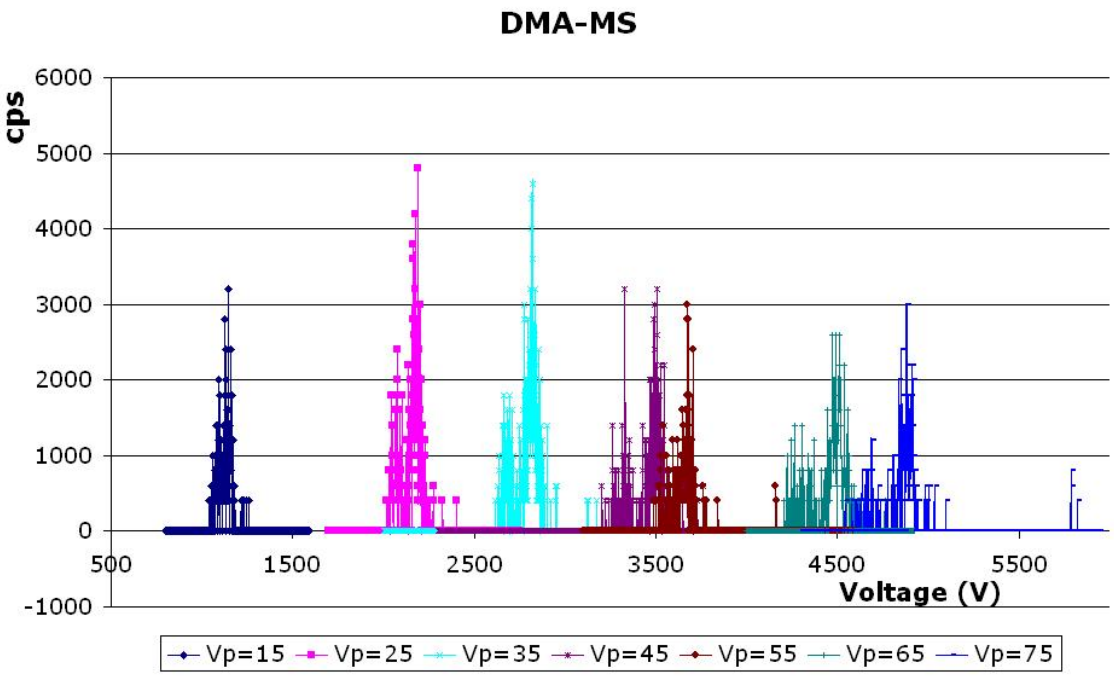

Figure F-3 – Noise spectra for different DMA configurations