Label free biochemical 2D and 3D imaging using secondary ion mass spectrometry

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Time-of-flight secondary ion mass spectrometry (ToF-SIMS) provides a method for the detection of native and exogenous compounds in biological samples on a cellular scale. Through the development of novel ion beams the amount of molecular signal available from the sample surface has been increased. Through the introduction of polyatomic ion beams, particularly C_{60}, ToF-SIMS can now be used to monitor molecular signals as a function of depth as the sample is eroded thus proving the ability to generate 3D molecular images. Here we describe how this new capability has led to the development of novel instrumentation for 3D molecular imaging while also highlighting the importance of sample preparation and discuss the challenges that still need to be overcome to maximise the impact of the technique.

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Introduction

No analytical technique is perfect, however amongst the imaging mass spectrometries the potential of time-of-flight secondary ion mass spectrometry (ToF-SIMS) to provide label free imaging of molecular species on a subcellular scale is extremely exciting and provides a myriad of possibilities for studying cellular metabolomics, disease progression and prevention/treatment due to its high lateral resolution, the chemical specificity of mass spectrometry and high sensitivity to label free bio-molecules [1•,2]. Energetic (usually 10 s of keV) primary ions can be focused to submicron spots and used to interrogate the surface of almost any sample ejecting species up to 1 or 2 kDa in ideal cases. Using a ToF mass spectrometer allows all the ejected secondary ions to be detected in parallel and a full mass spectrum is recorded at each pixel potentially allowing the technique to be used in a 'discovery' modality. Generally, labelling is not employed although incorporation of mass spectrometric tags including the use of isotopically enriched compounds can provide added information and has been used to great effect for cellular imaging using dynamic SIMS particularly by Lechene and co-workers [3•]. The data from the ToF-SIMS image are examined retrospectively; mass spectra can be extracted from regions of interest in the image or the distribution of ion signals in the mass spectrum can be visualised. Here we describe how advances in ion beam and mass spectrometer development are helping us to realise the potential for ToF-SIMS analysis of biological cells.

SIMS has been used extensively to examine a wide range of samples and is used routinely in the micro-electronics industry for probing the distribution of dopants in silicon. Benninghoven showed in the early 1970s that the technique could also be used to provide molecular type information of the chemistry of a sample surface [4]. Surface scientists utilised the technique in the study of heterogeneous catalysis on both industrial samples, such as automobile catalytic converters [5], and also environmental in the study of ozone depletion reactions [6]. Obviously the complexity of the ToF-SIMS analyses, and the associated data, are very much greater for biological samples compared to traditional targets for SIMS analysis such as semi-conductors and polymers. To meet the demands for analysing such challenging samples considerable effort has been made to develop novel ion beams with which to probe the sample surface. The goal of such endeavours has been to improve the sensitivity of the technique thus enabling higher resolution chemical imaging while particularly increasing the yield of higher mass, more chemically characteristic secondary ions which aid the interpretation of the complex mass spectrum. The simplest way of increasing the secondary ion yield/primary ion is to increase the mass of the incoming projectile; bigger atom–bigger bang!

An excellent example is provided by Ostrowski *et al.* who have demonstrated the use of ToF-SIMS to image the changes in lipid composition during *Tetrahymena* mating using an In^+ primary ion beam [7•]. During mating the *Tetrahymena* (common fresh water protozoa) form a series of highly curved fusion pores at the conjugation site that allow the passage of micronuclei between the cells. Such radical changes in the shape/structure of the membrane

would be expected to involve a change in the lipid composition in that area. SIMS imaging of the *Tetrahymena* was performed following freeze fracture of the cells and inspection of the conjugation site which as hypothesised, showed a change in the lipid composition. A reduction in the signal from phosphocholine (m/z 184) was observed. Principal component analysis was performed on the image and a species was identified at m/z 126 that was associated with the conjugation junction. The peak at m/z 126 was assigned to the headgroup of a group of cone-shaped non-lamellar 2-aminoethylphosphonolipids (2-AEP). The localisation of such lipids at the conjugation site is consistent with the formation of the high curvature structures (Figure 1).

Cluster and polyatomic ion beams

Even more beneficial than increasing the mass of the primary ion is the so-called cluster effect. Cluster ion guns have been introduced that fire Au_n and Bi_n (n is usually between 1 and 5) [8,9] and take advantage of an effect first observed in the 1970s — there is a non-linear increase in the secondary ion yield as a function of particle nuclearity [10–12]. Of particular benefit for the imaging of biological samples the increase in secondary ion yield is especially pronounced for the molecular type ions $m/z > 200$. Concurrently a number of groups were exploring the use of polyatomic primary ions with the same aims. Initial studies using small carbon clusters [13] and $SF_{5/6}$ [14,15] were superseded by the introduction of C_{60} for routine SIMS analysis [16]. The polyatomic ion beams provided not only the non-linear increase with nuclearity, but also a reduction in the accumulation of ion beam induced chemical damage in the sample.

Conventional mono-atomic and even the metal 'cluster' ion beams deposit energy deep into the sample below the point of impact that leads to loss of molecular information. Hence the extraction of molecular information from a sample is limited to low primary ion beam dose, normally such that only 1% of the sample surface is impacted by a primary ion [17]. This dose commonly referred to as the 'static limit' hence the term static-SIMS is used to distinguish this modality from dynamic-SIMS where high ion beam flux is used to erode a sample while monitoring the secondary ion signals of atomic and/or small fragment species, predominantly in the semi-conductor industry.

The impact polyatomic ion beams have had on organic material analysis by SIMS has been so great that the properties of these ion beams have even been described as 'magical' in the scientific literature [18•]! However any mysticism has been removed, and the low damage accumulation has been explained, through analytical models [19,20] and molecular dynamic simulations of the ion/surface interaction [21]. As the polyatomic ion impacts the surface of the sample it disintegrates into its constituent atoms resulting in the simultaneous impact of

Figure 1
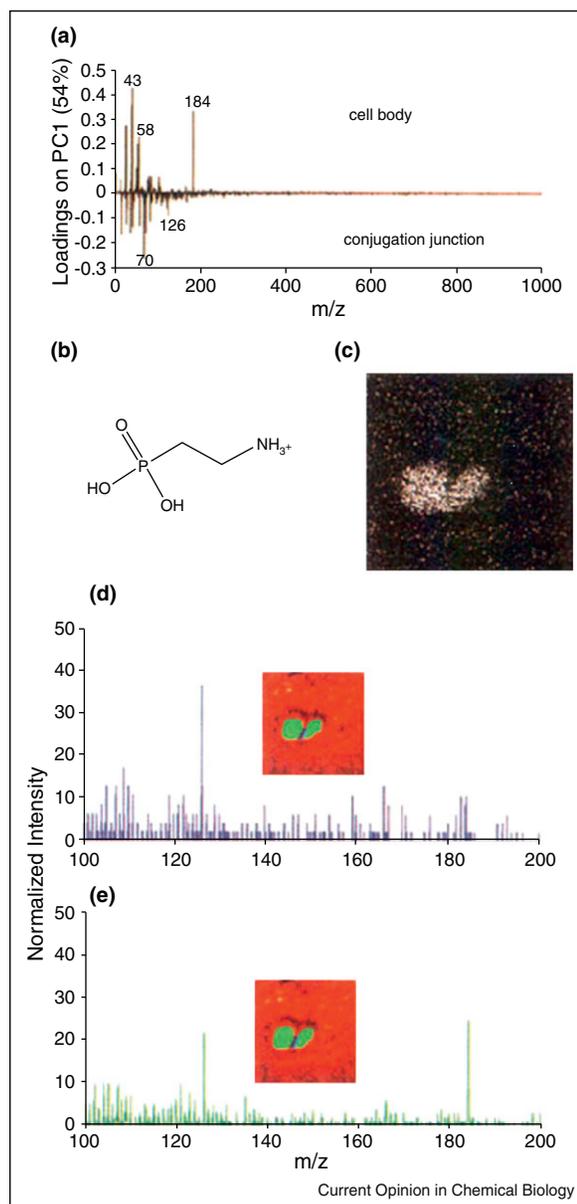
The conjugation junction contains elevated amounts of 2-AEP. Mass spectra from pixels were generated by selecting the pixels of interest using software written in house. **(a)** Loadings plot from principal component analysis comparing the mass spectra of the cell bodies and the conjugation junction. **(b)** 2-AEP headgroup fragment corresponding to m/z 126. **(c)** SIMS image for m/z 126. **(d)** Mass spectrum from the pixels along the conjugation junction, the blue pixels where the cells touch in the inset. **(e)** Mass spectrum from the pixels in the cell bodies, as illustrated by the green pixels from the cells in the inset. Adapted with permission from Ref. [7•].

many relatively low energy atoms. The result is that the energy is deposited in the upper layers of the sample with very little disruption of the subsurface. If a second ion hits the same spot intact molecular species are still detected.

A reduction in chemical damage accumulation during the SIMS analysis has extremely significant benefits for biological analysis. Imaging can now be performed using much higher ion beam dose, thus increasing the signal in each pixel by sampling a small volume of material (a voxel) leading to improved image contrast. A further more exciting option is the generation of three dimensional molecular images by acquiring and reconstructing a stack of 2D images as the specimen is eroded by the primary ion beam as illustrated in Figure 2a.

3D molecular imaging, following the introduction of polyatomic ion beams began with a number of exploratory studies on drug/polymer blends [22] and simple cellular systems. Fletcher *et al.* demonstrated the initial application of ToF-SIMS using 40 keV C_{60}^+ ions to sputter etch and image *Xenopus laevis* oocyte, thus characterising chemical changes in three dimensions of a biological cell with minimal sample preparation/intervention [23•]. *X. laevis* oocyte is a well-established cell model that has been extensively used in many branches of experimental biology and pharmacological research. It is a large single cell about 0.8–1.3 mm in diameter, the cellular compartments of which are so large that they are accessible to cell biologists for manipulation and visualisation. In addition, *X. laevis* oocyte is remarkably resistant to osmotic

Figure 2
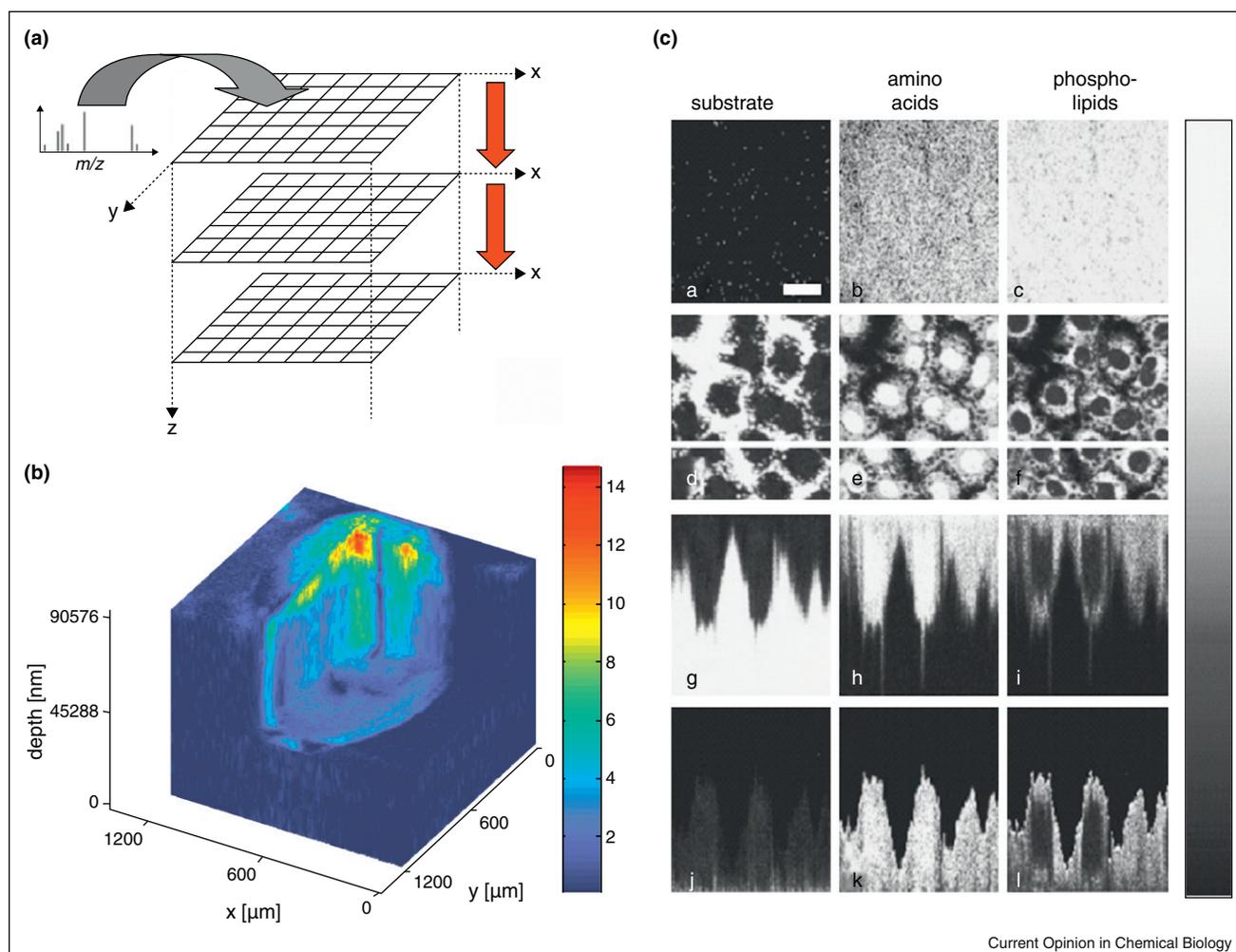
First examples of 3D biological imaging using ToF-SIMS. **(a)** A stack of images is acquired using interleaved analysis/etch cycles. **(b)** The distribution of triacylglyceride species over the mass range *m/z* 815 − 960 imaged during the erosion of approximately 100 μm of material from a *Xenopus laevis* oocyte using C_{60}^+. Using a liquid metal ion beam for analysis combined with C_{60}^+ for etching subcellular 3D structure can be observed in panel **(c)** where mass-resolved secondary ion images of the surface of normal rat kidney cells before any sputter cycle had been applied (a–c) and within the cell after the 45th sputter cycle (d–f) images are based on the following secondary ions: (a), (d), (g) and (j): Na⁺; (b), (e), (h) and (k): amino acid fragment ions (pooled signal for *m/z* 30, 44, 70, 101, 110, 136); (c), (f), (i) and (l): phospholipid fragment ions (pooled signal for *m/z* 58, 166, 184, 760). (g), (h) and (i) are cross-sectional images in the plane of the white horizontal marker line in (d), (e) and (f) while (j), (k) and (l) are the same data but with the interface with the silicon wafer substrate set to be flat and truncated at that interface in order to display the cells with a more realistic shape. The scale bar in (a) corresponds to 20 μm. Adapted with permission from Refs. [23•,24•].

changes. This facilitated the preparation of the cells for mass spectral imaging as they are reasonably resistant to washing of exogenous substances using de-ionised water. Although the handling of the sample was simplified due to the size of the specimen the variation in topography over the analysis area resulted in reduced mass resolution and meant that over the course of the analysis only the outer section of the oocyte could be consumed. Despite this the sample provided clear proof of principle for molecular depth profiling of biological cells using C_{60}^+. Persistent secondary ion signals were observed through the analysis, where over 75 μm of material was eroded, for a range of species including cholesterol and diacylglycer-ides associated with previously identified, by extraction and MS analysis, lipid species known to be abundant in *X. laevis* oocyte membranes (Figure 2b).

The C_{60}^+ beam, arising from a gas phase electron impact source, is more difficult to finely focus than a liquid metal ion gun (LMIG) while maintaining enough current to enable analysis on a useful time scale. Sometimes a useful compromise is to use and LMIG for the imaging cycles of the experiment and a polyatomic ion beam for the inter-leaved etching periods. Breitenstein *et al.* employed this method of analysis for the 3D ToF-SIMS imaging of normal rat kidney (NRK) cells [24•]. Bi_3^+ ions were used for imaging while C_{60}^+ was used for etching. In this experiment the imaging capability of the Bi_3^+ allows the sample to be imaged with subcellular resolution in 3D. Figure 2c shows the cells clearly outlined against the substrate while the combination of amino acid associated peaks also highlights the cells while the nuclear region can clearly be defined by the absence of pooled phos-pholipid signal.

These initial results were very encouraging but also highlighted inadequacies with the conventional ToF-SIMS instrumentation. The imaging was performed with low mass resolution, using a longer than normal primary ion pulse, with a non-imaging high mass resolution mass spectrum required for accurate peak assignment. This is because in high-resolution ToF-SIMS imaging too rapid pulsing and/or bunching of the primary ion beam can prevent the realisation of the full focus of the ion beam and the low ion currents from the focused and apertured ion guns means that the experiment time becomes much longer. It is therefore desirable to increase the number of primary ions in each shot thus increasing the duty cycle of the experiment in terms of ion dose over time. This mode of operation obviously has a detrimental effect on the quality of the mass spectrum. Also the useful spatial resolution in molecular imaging SIMS is often limited by the amount of signal from a single pixel. The dual beam approach to depth profiling can help speed up the acquisition, as it is usually possible to deliver more ion beam current into a smaller spot, but each image/layer of the depth profile is then restricted to analysis in the static

regime. The etching cycle not only allows 3D molecular imaging but is essential for the removal of subsurface damage caused by the LMIG.

New instrumentation for a new SIMS paradigm

What the analyst wants is a dynamic SIMS instrument with all the advantages of the ToF analyser. Hence, we embarked on projects at Penn State and the University of Manchester to meet these demands. At Penn State a commercially available 'Q-Star' MALDI mass spec-trometer was fitted with an adapted C_{60}^+ ion gun [25•]. The ion beam can be used continuously while sections of the resulting secondary ion stream are pulsed orthog-onally into a ToF mass analyser. Although, not without its challenges, the approach adopted at the University of Manchester was much more ambitious. A new concept of ToF-SIMS instrument, the 'J105 — *3D Chemical Imager*' has been developed in collaboration with Ionoptika Ltd. (Southampton, UK) and uses a linear buncher placed before a quadratic field ToF mass analyser [26•]. The buncher squeezes a 30 cm long section of the secondary ion stream into a tight bunch of ions at the entrance to the ToF, the mass resolution of the instrument is now de-pendent on the quality of the bunching as opposed to the pulsing of the ion gun on a conventional instrument. Both the instruments provide a huge increase in duty cycle ($\times 10^3$) facilitating 3D imaging and also large area analysis of tissue samples. 3D imaging of cells can now be per-formed on the J105 without the need for etching cycles where precious signal is discarded. Instead a stack of high dose images are generated, mass resolution and accuracy are also preserved in all modes of analysis as it is now de-coupled from the ion beam bombardment of the sample even on topographically challenging specimen thus improving identification of chemical species which is vital for biological analysis. The ability to perform routine 3D imaging experiments on a useful timescale has allowed systematic studies to be performed in order to investigate a number of additional challenges associated with biological analysis. Figure 3 contains schematics of the two DC ion beam SIMS instruments, both are also capable of performing tandem MS experiments to eluci-date secondary ion structure. Tandem MS in the J105 uses a ToF–ToF configuration with the collisionally induced dissociation occurring in the collision cell be-tween the buncher and reflectron at high energy (1–6 keV). The Q-Star performs tandem MS by low energy (10's of eV) collisionally induced dissociation in Q2.

One complication for ToF-SIMS analysis of biological samples is the requirement of a high vacuum in the analysis chamber of the instrument and much work has been performed to investigate the most appropriate methods of introducing samples into the instrument while maintaining biochemical integrity for imaging. It is always desirable, and sometimes a requirement to

Figure 3
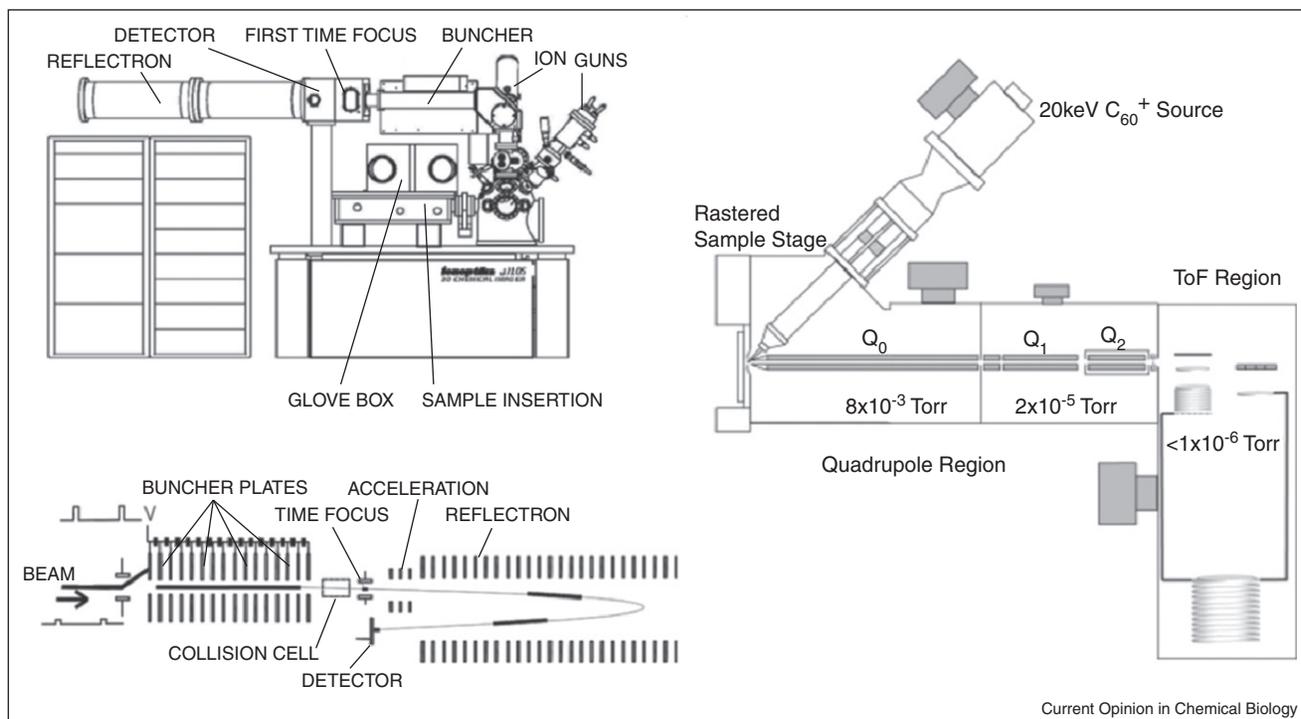
Schematics of the J105 — 3D Chemical Imager (left) and the C_{60} equipped Q-Star (right) instruments. Both instruments can use continuous beams. The J105 bunches the secondary ion stream to a focus at the entrance to the ToF analyser while the Q-Star orthogonally pulses sections of the secondary ion stream in to a ToF analyser.

remove excess salt from the surface of cells before analysis. Sjövall introduced a protocol that involved washing the samples with a volatile salt, usually ammonium formate, as this maintains osmotic pressure during the washing but evaporates away during freeze drying of the sample [27]. Careful freeze drying has been shown to maintain much of the physical structure of cells analysed by ToF-SIMS, however as the majority of the compounds detected by SIMS are relatively small, and therefore highly mobile, the distribution of at least some of them would be expected to change upon drying. Flash freezing the sample in a suitable cryogenic such as liquid propane and analysing the sample in this frozen hydrated state may represent the gold standard for sample preparation for ToF-SIMS. Not only does limiting the potential for diffusion of small molecules improve image contrast, there are other potential benefits from analysing samples at low temperature that have come to light in a number of recent studies. Conlan *et al.* [28] reported an increase in $[M+H]^+$ signal when amino acids when analysed in a water matrix. Suppression or enhancement of a particular species in the mass spectrum based on its chemical environment (the matrix effect) is a particular challenge in all imaging mass spectrometries because it can lead to misinterpretation of the image results [1] and *inter alia* the

matrix effect has been shown to be related to the gas phase basicity of the sample components [29]. Again the excess protons may help to ameliorate this effect. Preliminary work has shown some relaxation of the matrix effect when condensing water onto a mixture of cytosine and 2,4,6-trihydroxyacetophenone (THAP) during SIMS analysis [30]. Zheng *et al.* have also shown that when depth profiling model molecular systems, including two alternating Langmuir–Blodgett film layers and an Irganox delta-layer sample, depth resolution is improved when performing the analysis at cryogenic temperatures [31,32]. An improvement in depth resolution has also been observed during the 3D imaging of frozen hydrated cells — less chemical mixing was observed at the interface between the nucleus and the cell membrane [33•]. To explore this effect a number of studies have examined different frozen sample preparation techniques. The low damage properties of the polyatomic beams have allowed ice condensate layers to be etched away revealing the organic sample beneath [34], while freeze fracturing a sample within the instrument can be used to remove surface ice layers and also under the right conditions, remove the upper membrane leaflet to expose internal cellular chemistry (particularly useful before the advent of molecular depth profiling) [35,36]. Unfortunately

Figure 4
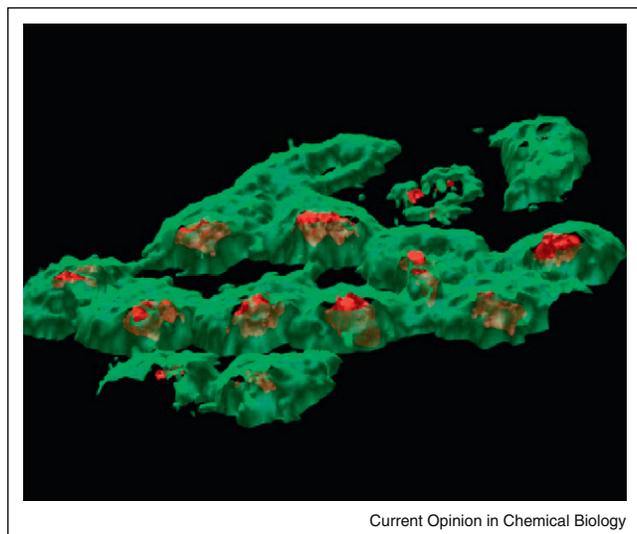
3D visualisation of the membrane (green, *m/z* 184.1, phosphocholine) and nucleus (red, *m/z* 136.1, adenine) chemistry in the frozen hydrated HeLa-M cells following the use of PCA to identify the interface between the cells and the substrate to allow more representative data reconstruction. The visualised area is 250 μm × 250 μm, but inclined in order to aid 3D visualisation. Reproduced with permission from Ref. [33•].

freeze fracture as well as frozen hydrated analysis is often laborious with the result that most analysts still choose the easier method of freeze drying samples instead. To overcome the barrier to such analyses we have developed for the J105 — *3D Chemical Imager* a simple, automated freeze fracture system that resembles as mousetrap [1], a variation of this device (the 'bug trap') has also been demonstrated for conventional ToF-SIMS instruments [37]. Figure 4 shows the result of the reconstruction of a ToF-SIMS analysis of freeze fractured HeLa-M cells using the mousetrap on the J105. Membrane phospholipid signal is imaged using the phosphocholine headgroup ion (*m/z* 184.1) in green and the nucleus is visualised by the intense adenine [M+H]$^+$ signal (*m/z* 136.1) in red. The phospholipid signal has been adjusted to be slightly transparent allowing the nucleus to be seen within the cell. Several of the cells have clearly had their upper membrane layer removed during the fracture process.

Conclusions and future direction

The imaging mass spectrometries are potentially of enormous benefit to biological research particularly cellular imaging. We have demonstrated here, and argued in a number of recent critical reviews that ToF-SIMS offers particularly powerful capabilities in this area, but there still remain a number of important challenges [38•,1•,2,39•]. Through recent forward leaps in the instrumental capabilities of ToF-SIMS 3D subcellular label free molecular imaging is becoming routine in a number

of laboratories worldwide. Proof-of-concept experiments have clearly demonstrated the unique capabilities of the technique for biological analysis. The technique must now prove itself in the answering of biological questions. Cross validation with conventional, accepted approaches will no doubt be important in providing confidence in the SIMS interpretation and such experiments are under way in a number of laboratories where the imaging of fluorescent tags by ToF-SIMS has been reported [40,41]. There is also a natural complementarity between SIMS and MALDI analysis, particularly for larger samples such as tissue sections and as the resolution of MALDI improves, also for (large) single cell analysis. Potentially SIMS can really provide subcellular 2D and 3D molecular images for which other imaging MS technique has the capability. However the accessible mass range is limited and it seems unlikely that SIMS will ever move into protein analysis. It is therefore potentially excellent for metabolites and lipids. However, the yields of ions above *m/z* 500 are still quite low and species of this mass are seldom detected in sufficient quantity for imaging at high resolution (as is required for cells) and this is part of the sensitivity challenge. Topography and the matrix effect are issues for all of imaging mass spectrometry and the reported results should always acknowledge the possibility that their influence may render the conclusions less certain. The matrix effect means that although MS imaging seductively seems to offer discovery mode analysis, it can never truly provide this, because we can never be sure that the absence of a signal means that the related chemistry is absent.

The push for improved signal from the SIMS experiment has not ended, the developments described in this article have improved many aspects of the technique and opened doors to new avenues of analysis but none have so far overcome the relatively low ionisation efficiencies with SIMS. Methods exist for promoting ionisation of specific chemical species by treating the sample with metals or a MALDI type matrix but these are not compatible with the new 3D imaging experiments [42,43]. A method of globally increasing ionisation of secondary species is the current 'holy grail' in ToF-SIMS development. The presence of water (and/or ice) on [28] and in the sample has shown varying enhancement for species where ion formation is through proton transfer with experiments reported where water has been squirted onto the sample during analysis [44]. Alternatively developments in laser post ionisation of the neutral portion of the secondary species (>99% of ejected material) have the potential to deliver huge increases in signal if the problem of photon-induced fragmentation can be overcome.

Acknowledgements

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