~~TOP SECRET~~

Solution of Scientists Internationale

A New Iatrogenic Disease?
a detailed compositional and histopathological analysis of white clots

Authors remain anonymous for safety reasons.

Background

Since the beginning of the COVID crisis, a group of international scientists has been working behind the scenes to unravel the mysteries of the white clots being found by embalmers. After four years of effort, the group has managed to determine the chemical nature of these mysterious white clots which they now call Hirschman clots. They also provide hypotheses regarding their possible mechanism of creation. This press release will provide a brief outline of the principal findings to date.

Methodology

The SOS Internationale scientists obtained a number of samples from embalmers. These were submitted to multiple independent laboratories worldwide for analysis. The labs were kept unaware of the nature of the samples in order to prevent biased analysis.

By using this strategy, a clear and definitive picture was expected to emerge that documented the unique chemistry of the white clots under examination, post 2020. While blood clots are commonly found in deceased bodies, the unique physical and chemical properties of the Hirschman clots indicated a different formation process. The Hirschman clots do not in any way resemble coagulated blood clots commonly formed after death.

The main thrust of the research can be divided into three separate categories: elemental analysis, proteomics, and histology. A brief outline of the principal findings will be detailed below.

Elemental Analysis

Results

Elements of interest were determined as follow: aluminium, boron, calcium, chlorine, copper, iron, magnesium, phosphorus, sodium, sulphur, tin, and zinc.

Results from multiple different laboratories will be presented followed by a brief explanation of the significance.

Mike Adams comparison

The initial stimulation for the SOS research was the comparative analysis conducted by Mike Adams on clot samples versus unvaccinated blood. Mike Adams is a published analytical scientist and the founder and lab director of CWC Labs, an ISO-accredited clean foods laboratory specialising in mass spectrometry analysis of heavy metals, pesticides, herbicides and microbiology.

He was the first person on the planet who put the white clots though a laboratory analysis.

Mike Adams' results showed a significant increase in phosphorus and tin in the white clots. A minor increase in sodium was noted and there were trace amounts of aluminium. The amount of carbon was not significant and to be expected due to the presence of organic material in clot structures and blood.

Table 1: Mike Adams ICP-MS Results

Element	Unvaxxed Blood ppm	Clot - ppm	% Difference
Aluminium	**1.3**	**1.6**	**+ 23**
Carbon	**137.288**	**152.845**	**+11**
Calcium	74	23.8	- 68
Copper	1	0.3	- 70
Chlorine	930	290	- 69
Iron	462	20.6	- 95
Potassium	1,893	12.8	- 99.34
Magnesium	35	1.76	- 95
Sodium	**1,050**	**1,500**	**+ 43**
Phosphorus	**1,130**	**4,900**	**+ 333**
Tin	**0.163**	**0.943**	**+ 479**

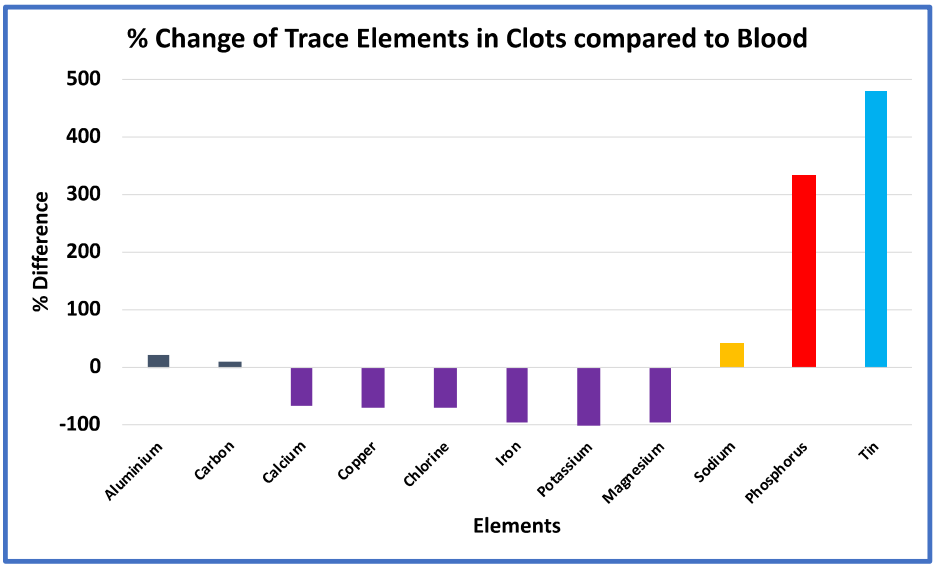


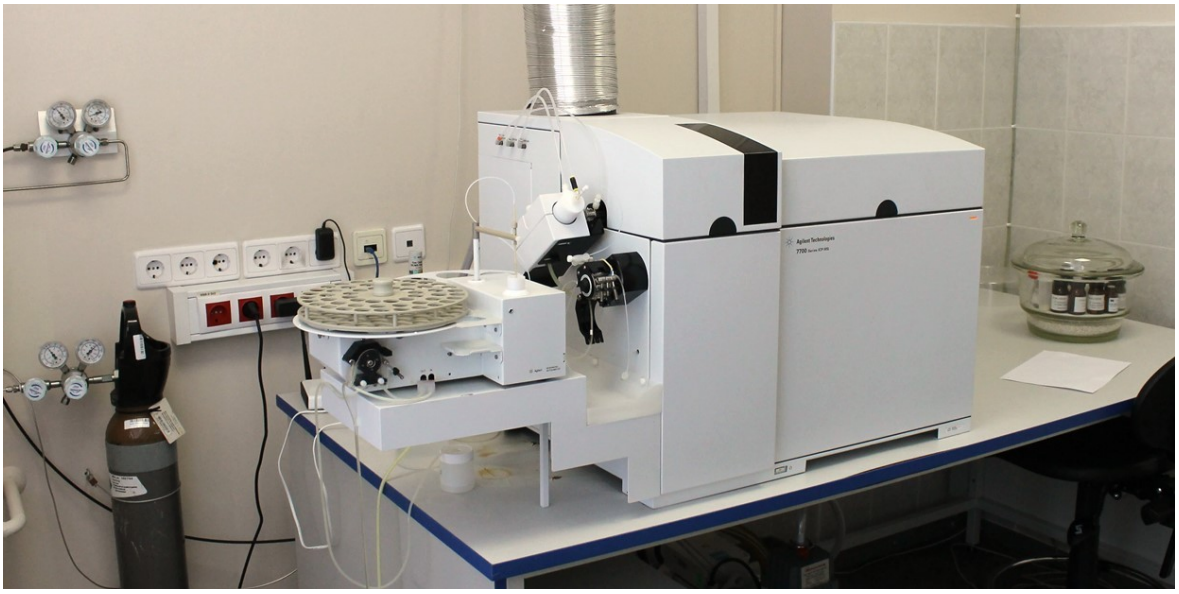
Figure 1: Mike Adams' ICP-MS Results

What sparked the interest of the SOS scientists was the unusually high concentration of tin, an element that serves no purpose in mammalian biochemistry other than acting as an environmental toxin. Its significance lies in its common industrial use as a stabiliser in the manufacture of plastic polymers, such as PVC pipe, which is used in potable water supply lines.

Tin is a highly reactive element with significant electro-negativity. For example, it will replace iron as the central ligand in hemoglobin, thus destroying the molecule's ability to transport oxygen and carbon dioxide. Tin is regarded as a toxin in mammalian biochemistry. Tin is ingested by humans via drinking water and food. However, in polymer chemistry, its role is to stabilise the physical properties of materials and increase elasticity. It is noteworthy that the embalmers' clots, hereinafter referred to as Hirschman clots, are significantly elastomeric (elastic in physical quality). The presence of tin in such alarmingly high quantities in the clots suggests that it is actively sequestered by some chemical process.

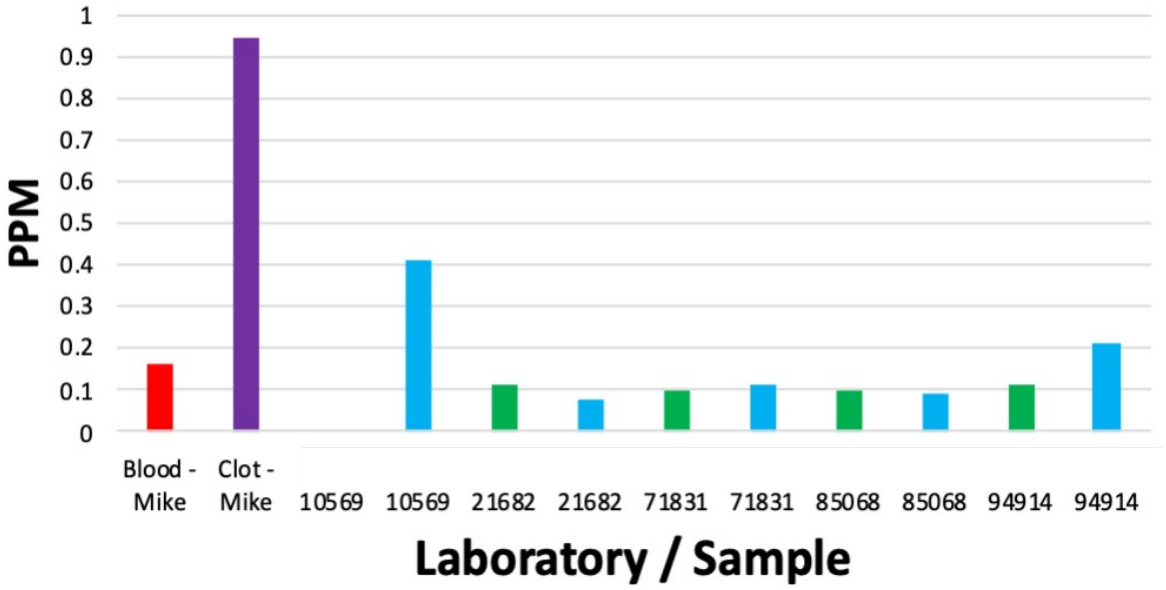
SOS Elemental Analysis Results

The SOS team obtained a number of clots from different sources and submitted these to state-of-the-art chemical analysis using the ICP-MS technique. Inductively coupled plasma mass spectrometry (ICP-MS) uses an inductively-coupled plasma to ionise the sample. This technique is described in more detail in the appendix. The figure below shows a standard ICP-MS instrument.

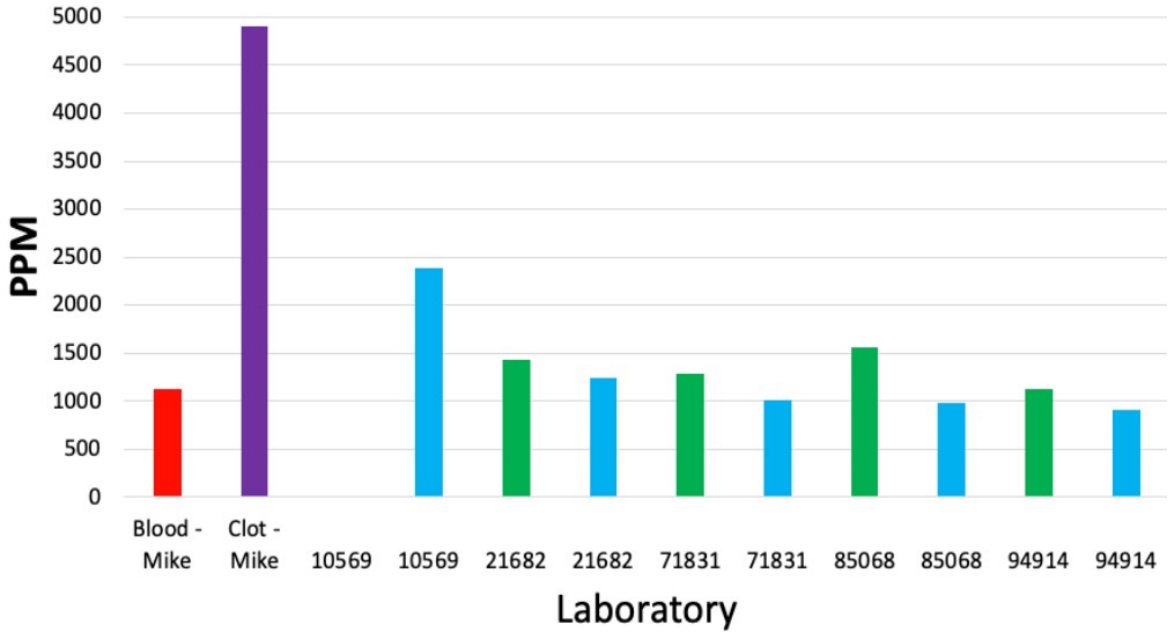


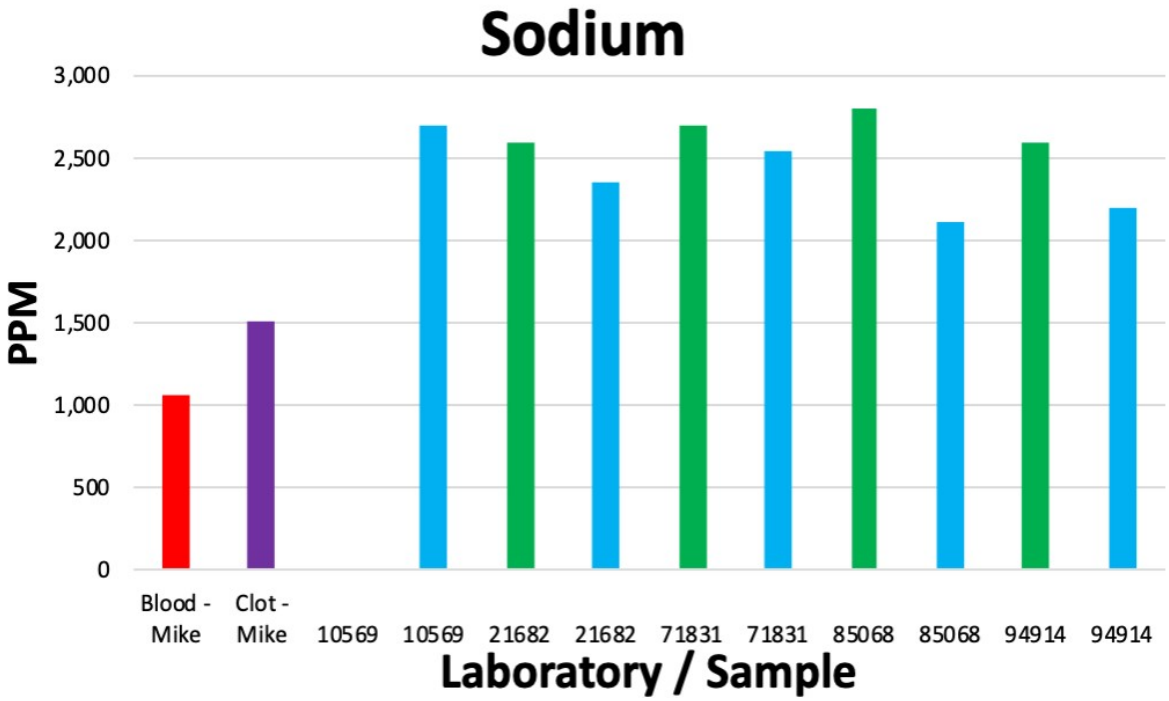
Each laboratory removed the samples from the carrier solution, washed them in distilled water then processed them for analysis by mass spectrometry. The averages of the elemental analysis results were calculated. The results are presented in the graphs that follow.

Tin



Phosphorus

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2,000
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500
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PPM
Blood - Mike
Clot - Mike
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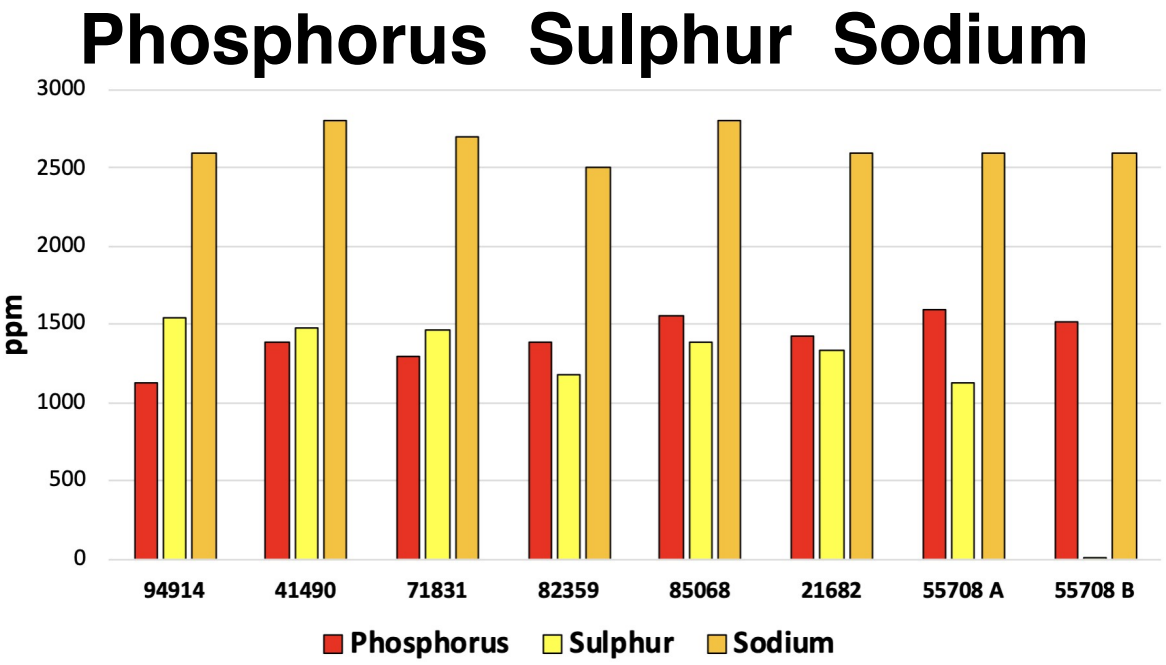
Laboratory / Sample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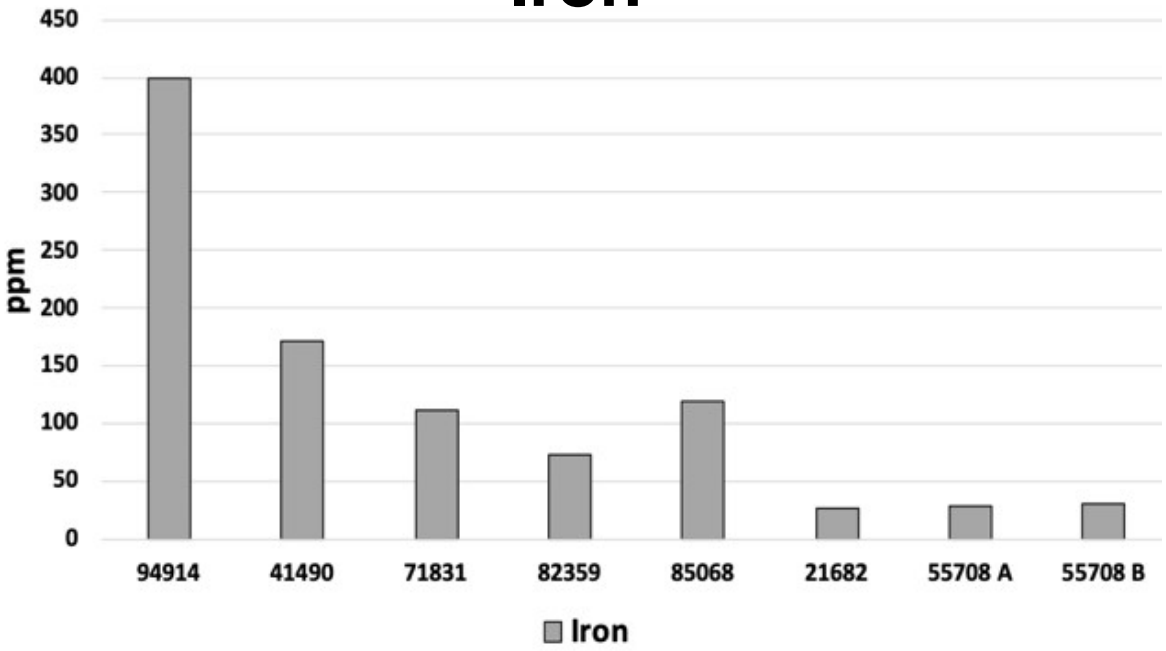
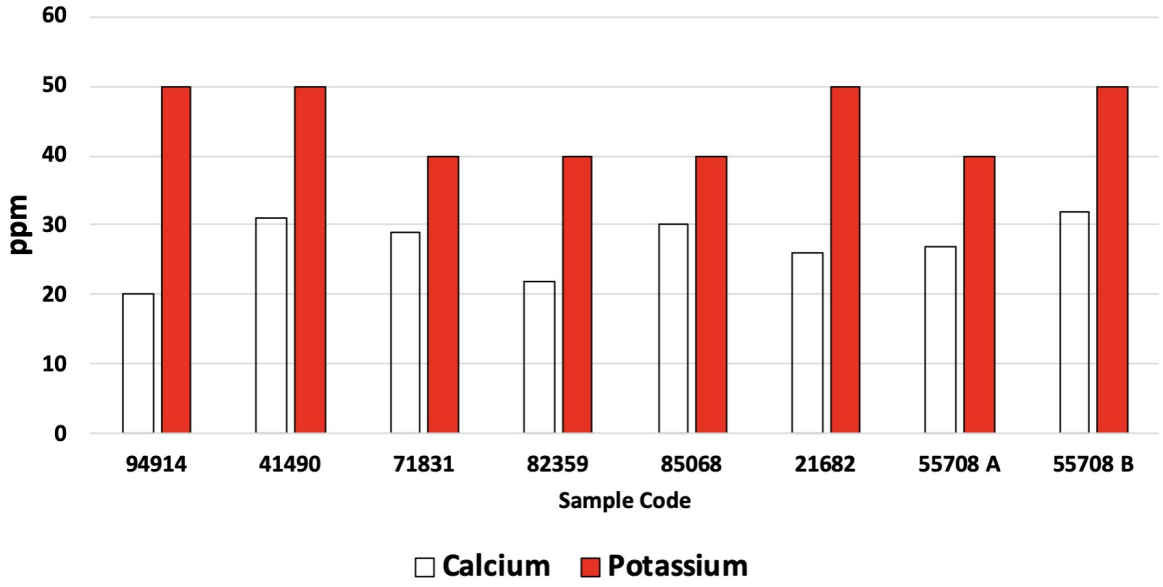
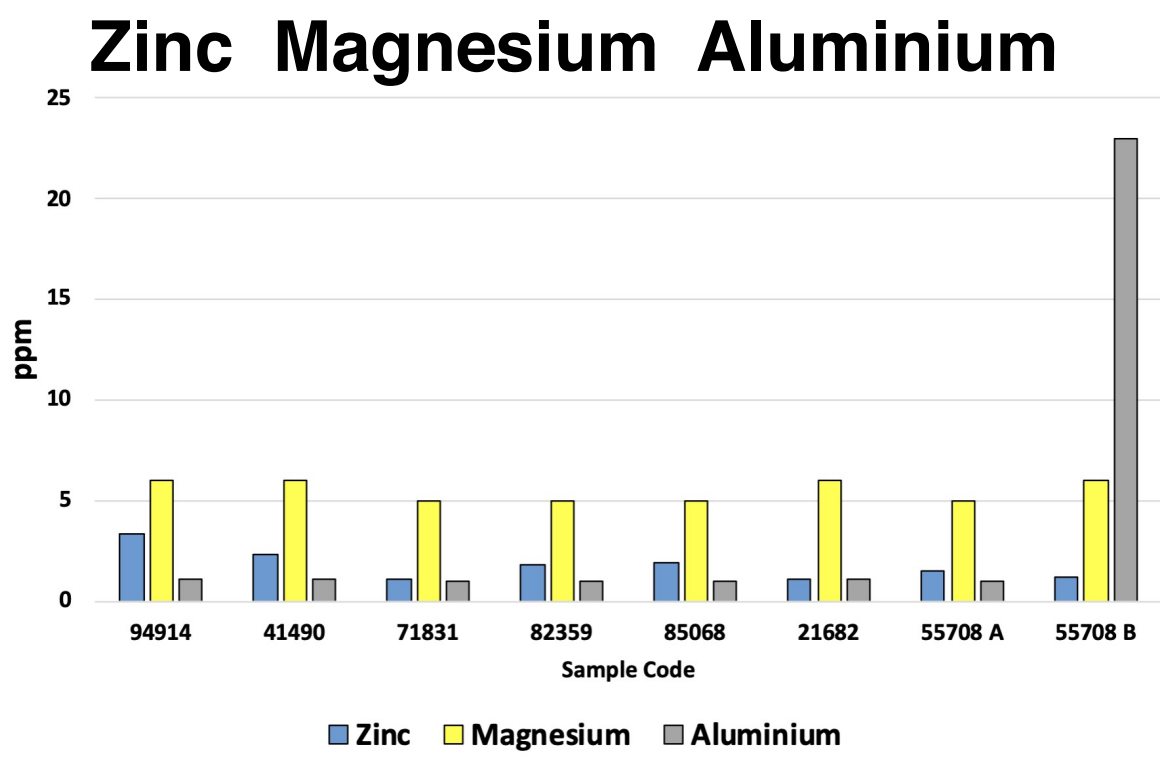
Phosphorus
Sulphur
Sodium

Iron



Calcium & Potassium

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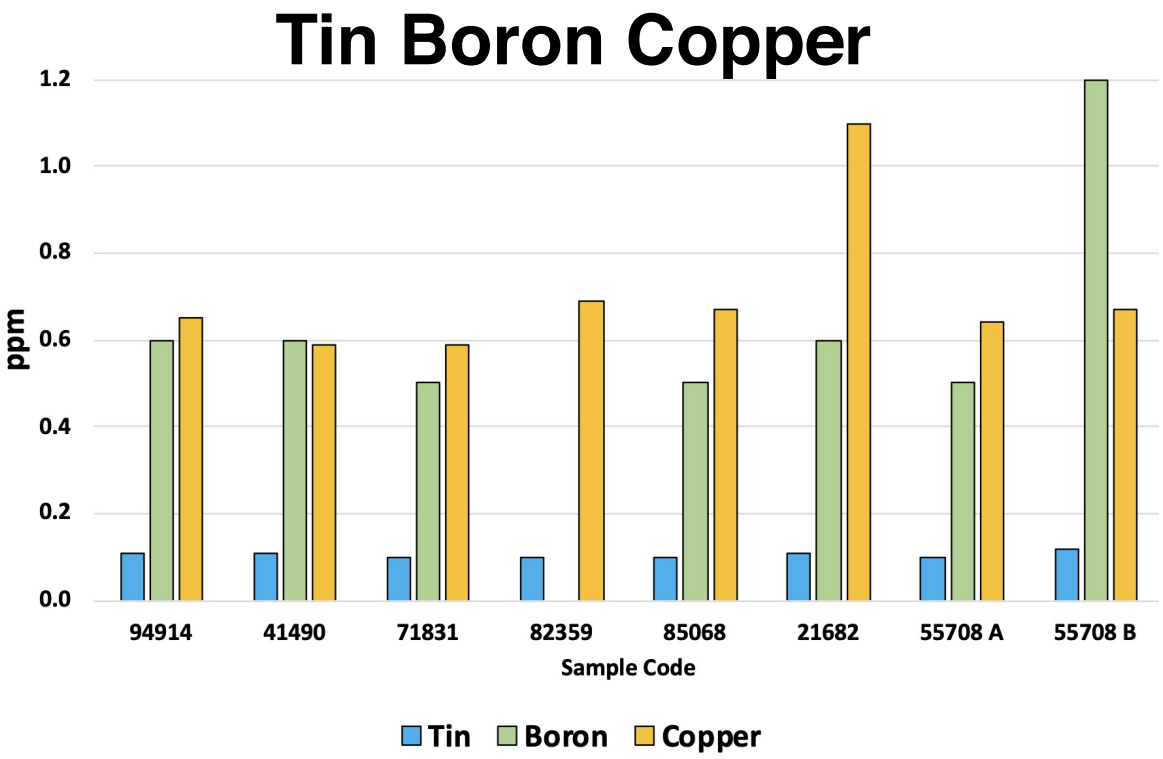
Tin Boron Copper
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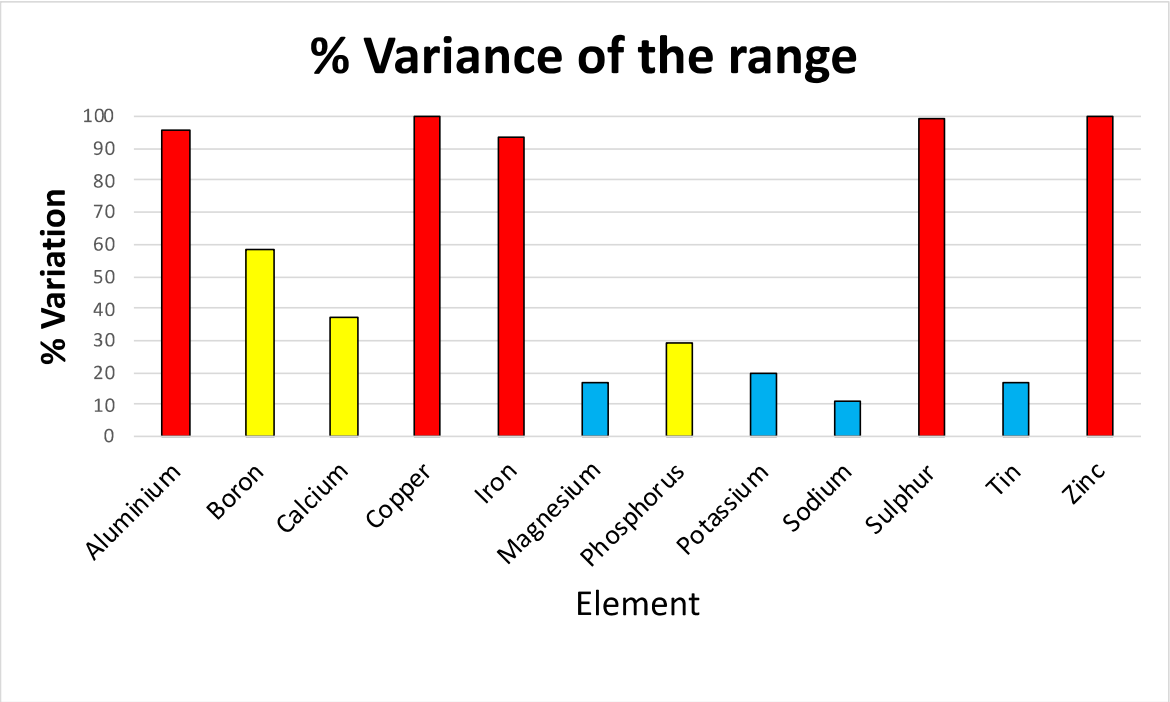


Initial observations

The high tin values of the Hirschman clots are significant. The researchers expected much lower values. The presence of such quantities sequestered in the clots indicated chemical reactivity specific to the clot components. The tin values showed low variance across the samples, although generally in lower quantities than those found by Mike Adams.

One possible explanation for the different levels may be that the clot Adams analysed came from a very elderly individual. It is possible that the slow accumulation of tin from various environmental sources reflects a build-up concomitant with age.

Given that tin is highly electronegative and promiscuous in the variety of substrates it can bond to, there is strong reason to believe it is involved in cross-linking of amino acid chains in proteins.

The high phosphorus levels are chemically significant and likely the result of cross-linking between proteins. As with tin, the phosphorus levels show low variance across the samples.

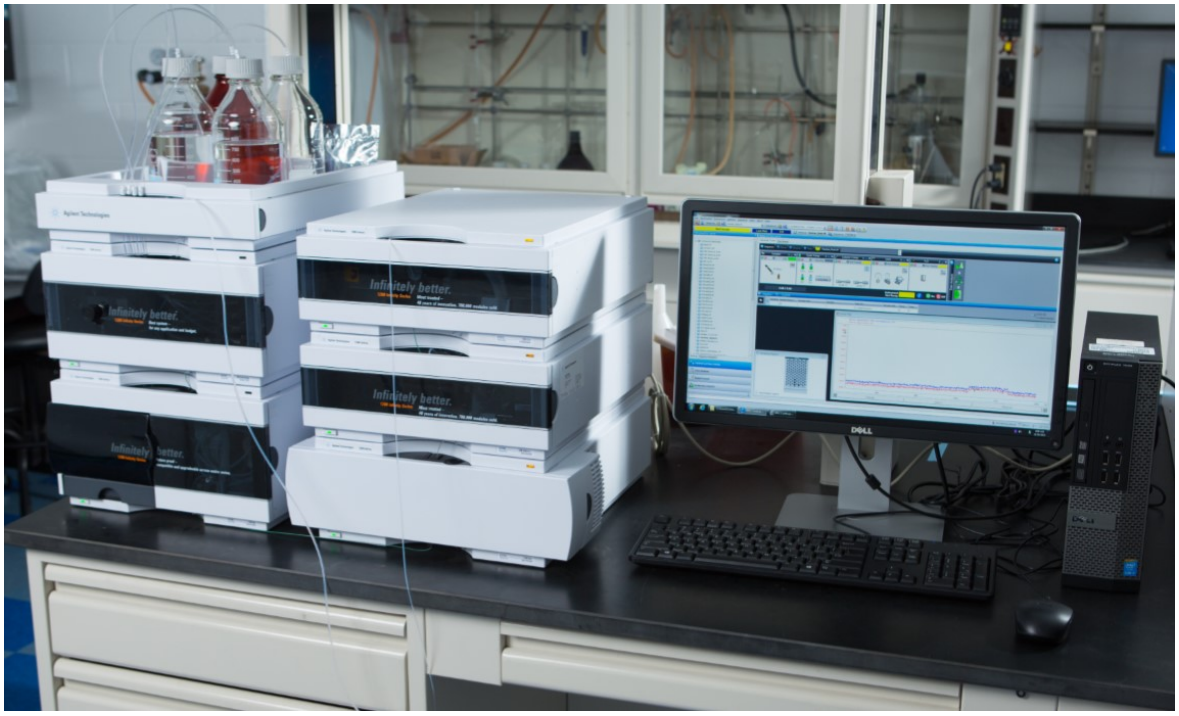
The sulphur levels were higher than expected (Adams did not test for sulphur). This is likely indicative of increased disulphide bonds which may be a consequence of a higher concentration of sulphur-containing amino acids.

In conclusion, these results are indicative of a chemical process, or a cascade, responsible for actively building the Hirschman clots before death. These clots strongly resemble what are generally known as white thrombi, which can occur in response to disease. White thrombi usually develop in high-pressure, high-blood-flow areas, such as arteries. However, the Hirschman white clots under analysis are being found in both arteries *and veins* (*where white thrombi would not normally appear*). Veins typically support the formation of red thrombi in response to disease, such as the classic Deep Vein Thrombosis (DVT) or Pulmonary Embolism (PE/Lung clots).

Hirschman clots were only discovered by embalmers after the rollout of the COVID vaccines. Prior to that, they were notably absent. While temporal relationships do not provide strong evidence for causation, they are often significant as markers for disease pathologies and, as such, are worthy of serious investigation. These clots are clearly a danger signal that has been ignored and then denied by health authorities worldwide. This raises the question: Why?

SOS Proteomic Analysis

The likely chemical architecture of the Hirschman clots, given their physical and elastomeric properties, is that they are proteinaceous in origin. To determine if this is the case and to identify any proteins present, the SOS scientists repeated their protocol of dividing clots among different labs in various countries to carry out proteomic analysis. The technique of choice was HPLC-MS, a full description of which can be found in the index. A typical ICP-MS instrument is shown in the figure overleaf:



In brief, High-Performance Liquid Chromatography-Mass Spectrometry (HPLC-MS) is a powerful analytical technique widely used in proteomics, the large-scale study of proteins, their structures, functions, and interactions. HPLC-MS combines the separation capabilities of liquid chromatography with the identification and quantification power of mass spectrometry, making it an essential tool in proteomics research.

In total, 541 proteins, all of human origin, were discovered in the clot samples processed using HPLC-MS. This contrasts with the findings of a prominent German pathologist, Professor Arne Burkhardt, who reported only 139 proteins, of which only 3 were of human origin. It should be noted that Burkhardt used a different analysis technique—MALDI-TOF (a description of this technique also appears in the index). Given this information, it is likely that he missed many proteins due to the molecular weight cutoff often associated with this method.

Proteomic Analysis Results — Top 12 Proteins

The top 12 proteins are tabulated below in their approximate proportions by % weight.

Table 2: Top 12 Proteins

Protein	F31286 -Young teenager	M63731 ≈33y/o female	U17894 ≈41y/0 gender?	M80324 ≈70y/o male	Sum
Hemoglobin subunit beta	17	10	30	14	71
Fibrinogen beta chain	5	11	3	35	54
Fibrinogen gamma chain	2	4	2	16	24
Hemoglobin subunit alpha	3	2	7	3	15
Fibrinogen alpha chain	1	2	0	5	7
Myeloperoxidase	4		1	1	6
Immunoglobulin heavy constant gamma 1	0	1	1	2	5
Actin, cytoplasmic 1	1	1	0	3	4
Peroxiredoxin-2	1		2	0	3
Fibronectin	0	1	1	1	3
Cathepsin G	1	1	0	1	3
Vitronectin	0	0		1	1

The results may be more clearly visualised in a graph, which also details the approximate age of the deceased. See overleaf.

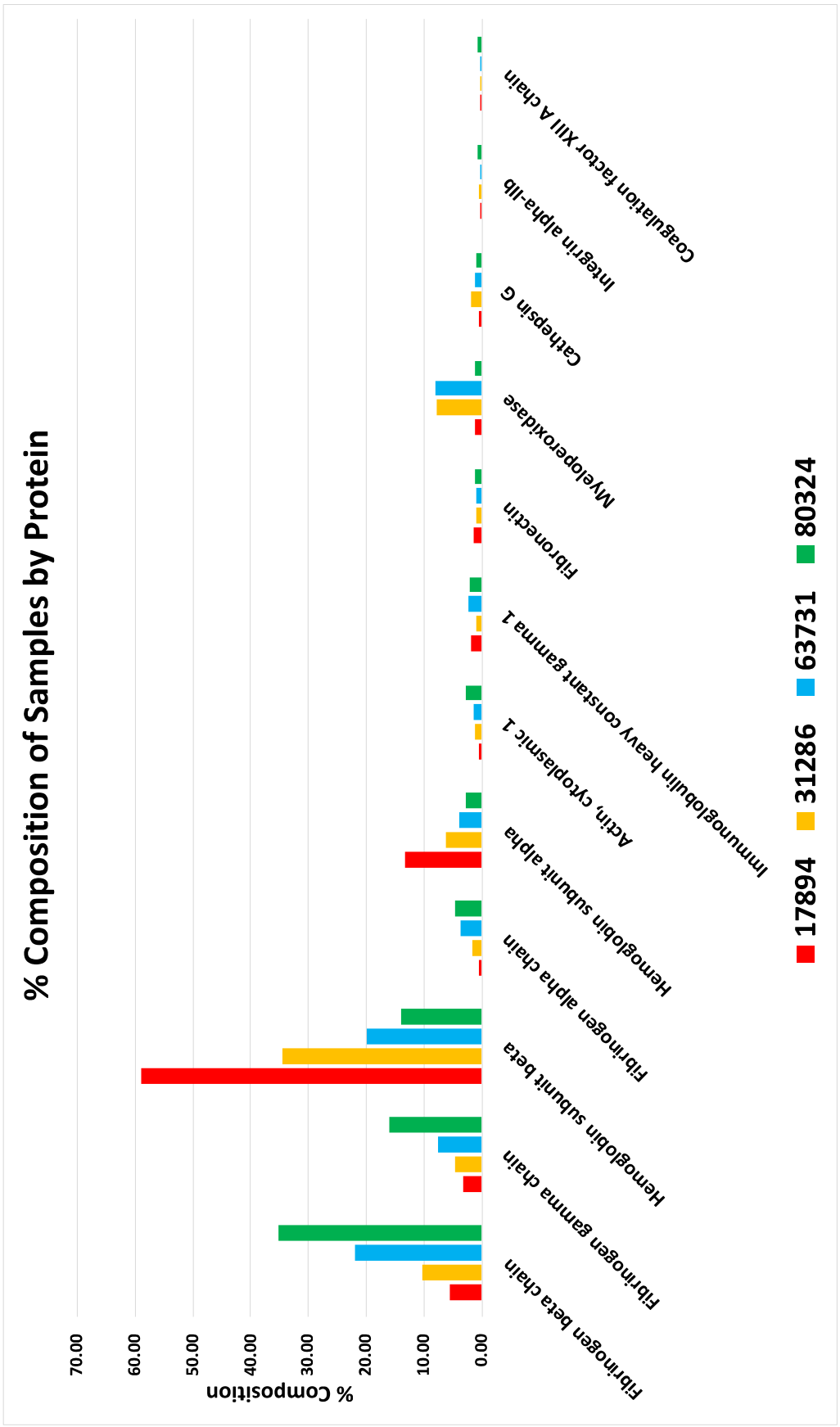


Figure 1: % Composition of Samples by Protein

The proteomics profile differs for each of the four clot samples discussed below. This variation may be partly related to age. There is strong evidence in the literature that the amount of fibrinogen/fibrin in circulation is related to age. Some references suggest an exponential relationship, while others describe it as more linear. Undoubtedly, it is highly variable and most likely multivariate.

Although there appear to be significant differences between the four samples, there is, in fact, much similarity, which is instructive regarding the mechanism of formation. It should be noted that the varying hemoglobin content depends on where the sample was taken from the original clot, as all Hirschman clots have areas where significant red sections are dispersed along the long white sections.

This is likely very significant, as it may indicate cellular damage, perhaps likely due to infection or some other disease mechanism. However, clot retraction is responsible for squeezing out most of the red cells, particularly in white thrombi where they are almost absent.

Proteomics Results for Four Clots

Colour Key for major protein constituents

- **Hemoglobin Beta Chain**
- **Hemoglobin Alpha Chain**
- **Fibrinogen Beta**
- **Fibrinogen Gamma**
- **Fibrinogen Alpha**
- **Fibronectin**
- **Actin**

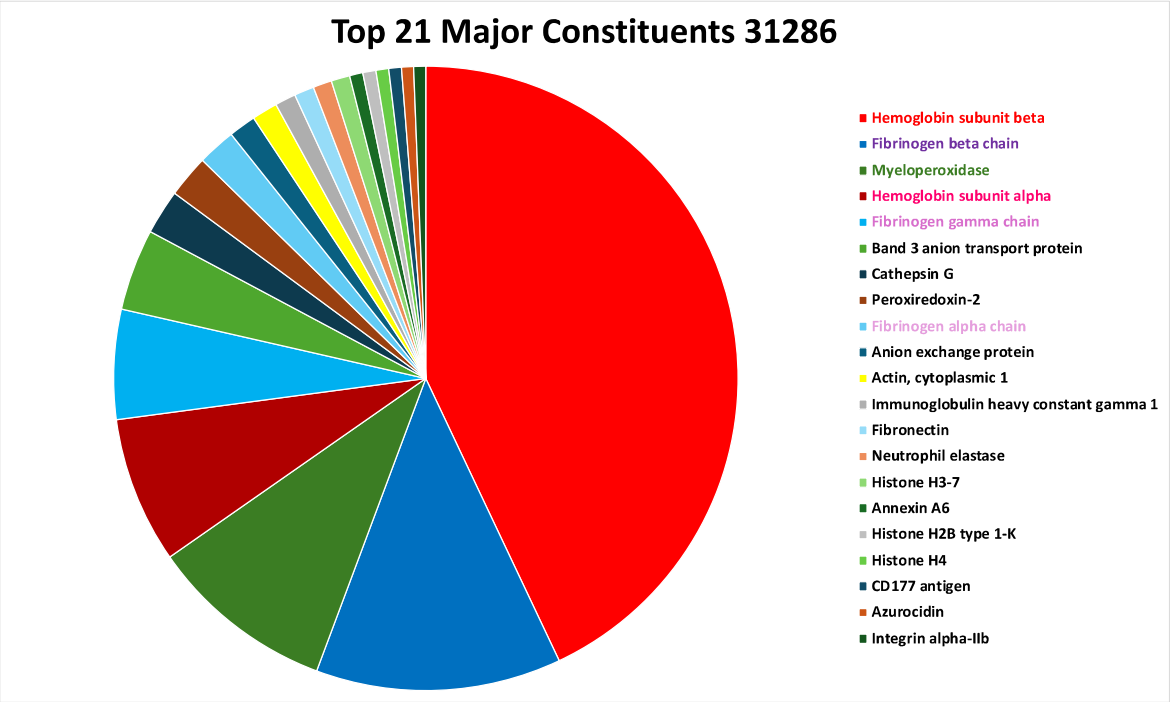


Figure 2: Young Teenage female

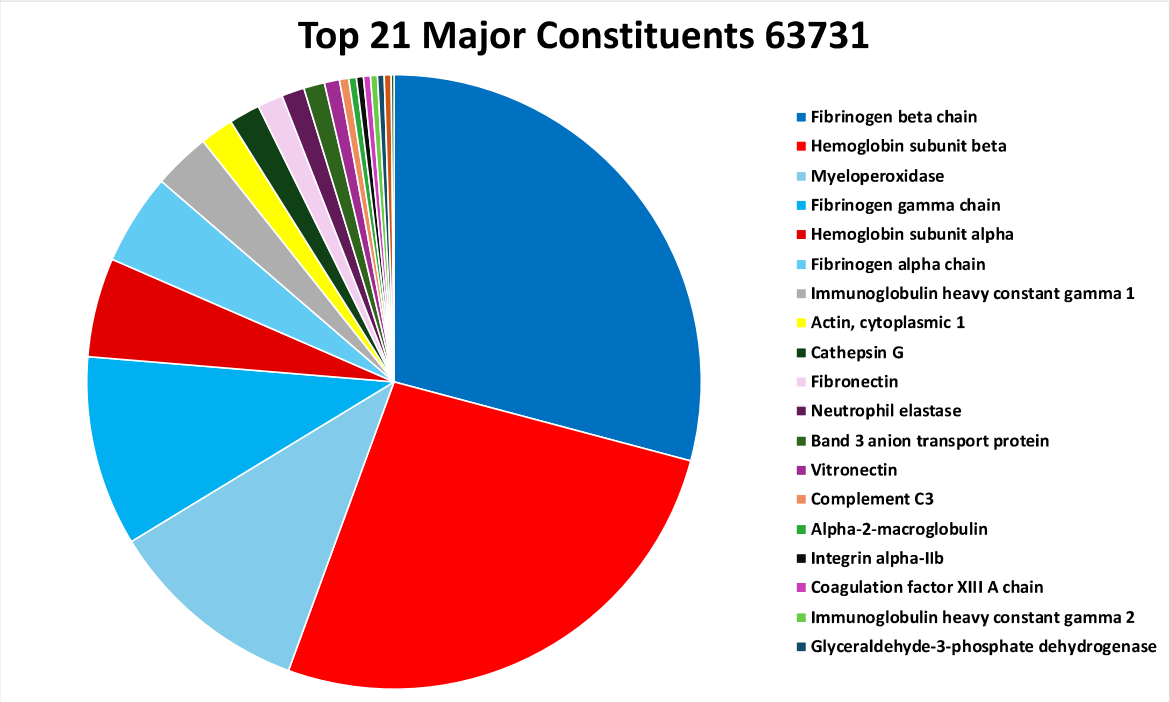


Figure 3: ≈ 25 year old male

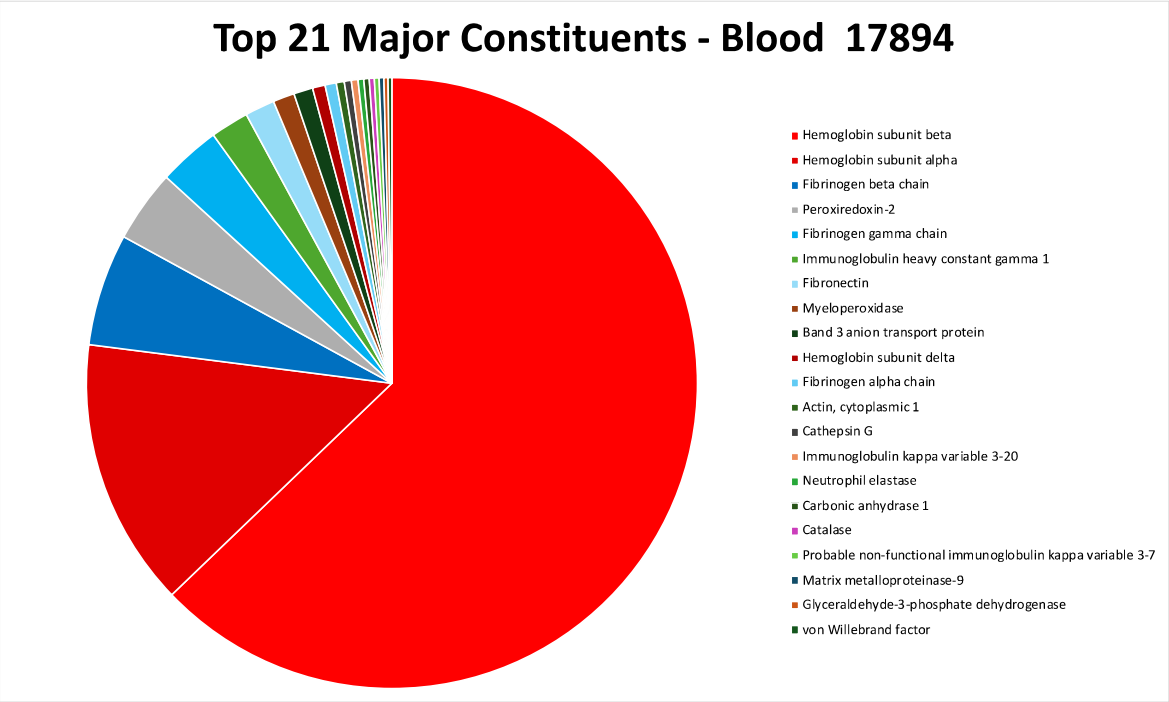


Figure 4: ≈ 40 year old unknown gender

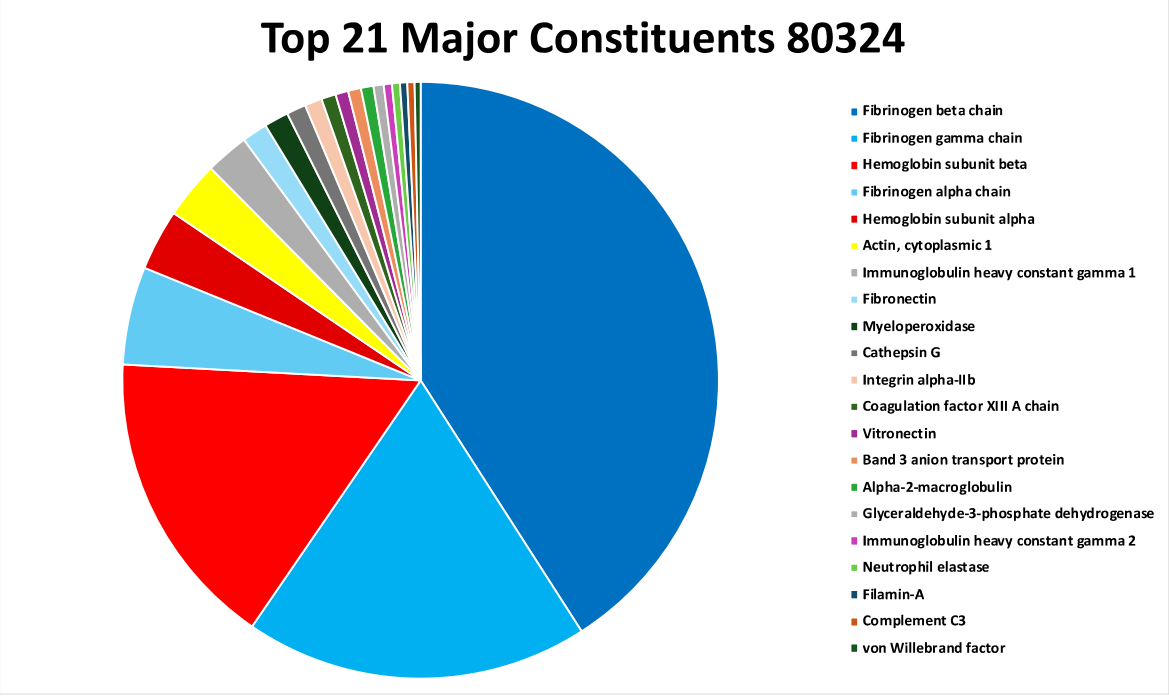


Figure 5: ≈ 70 year old male

Discussion

The Hirschman clots are significantly different in the amount of hemoglobin β chain, which is always dominant, and smaller amounts of hemoglobin α chain. The hemoglobin found in the Hirschman clots results from cellular damage of red blood cells, likely due to infection or another disease mechanism.

It is normal for some blood cells to become trapped in the platelet/fibrin tangle that forms the basis of most blood clots, including both red and white thrombi. However, clot retraction is responsible for squeezing out most of the red cells, particularly in white thrombi, where they are almost always absent. Whole red blood cells do occur, in large numbers, in red-jelly clots and red thrombi, which tend to form primarily in veins. One of the obvious difficulties is that the Hirschman clots are non-uniform in their appearance, with multiple areas of adherence to the endothelial cells lining the blood vessels along the length of the tissue. These areas may contain a small number of erythrocytes trapped within the proteinaceous fibres, but few intact red cells have ever been observed. Mostly the hemoglobin present is therefore from damaged erythrocytes and is free within the clot tissue.

Some of the clots are quite long. Below is a picture of embalmer Richard Hirschman holding a 19-inch clot (approximately 50 cm) in a tube, positioned to indicate where it was located within the deceased body before removal.

The SOS scientists have observed clots even longer than this, with the longest measuring 27 inches (approximately 69 cm). The clot shown in Figure 6, removed by Richard Hirschman, was extracted from an artery in the groin that connected directly to the heart.

Figure 6: 19 inch clot

The most significant finding in proteomics related to these clots is the presence of the fibrin family of proteins. In a normal clot formation, fibrinogen is produced in the liver and circulates in the bloodstream. When thrombin is present, fibrinogen is converted into fibrin. This process involves the removal of two very small fragments from the α and β fibrinopeptide chains, cleaved at the N-terminal end. The removal of these fragments from the alpha chains alters the protein structure, exposing additional binding sites.

Fibrin, which is formed as a result of thrombin activity, is inherently monomeric. This means it has the ability to form long chains by binding end to end, creating structures known as proto-fibrils. The removal of a portion of the α chain exposes new binding sites, facilitating cross-linking that allows the fibrin protomers to join together in a crosswise fashion, resulting in a highly elastic, flexible, and rubbery structure.

Much like a brick wall is constructed, each successive layer of cross-linked fibrin proto-fibrils is linearly displaced by half of a protomer molecule. To understand this process more fully—and as a precursor to the next section, which will explain the proteomics of the Hirschman clots—it is helpful to examine the fibrinogen/fibrin molecule itself.

Essentially, fibrinogen, and thus fibrin, is composed of two sets of three different amino acid chains: α, β, and γ. This information is critical to understanding the structure of the Hirschman clots and why they differ significantly from other types of clots, although they are closely related to the white thrombus. See overleaf for further details.

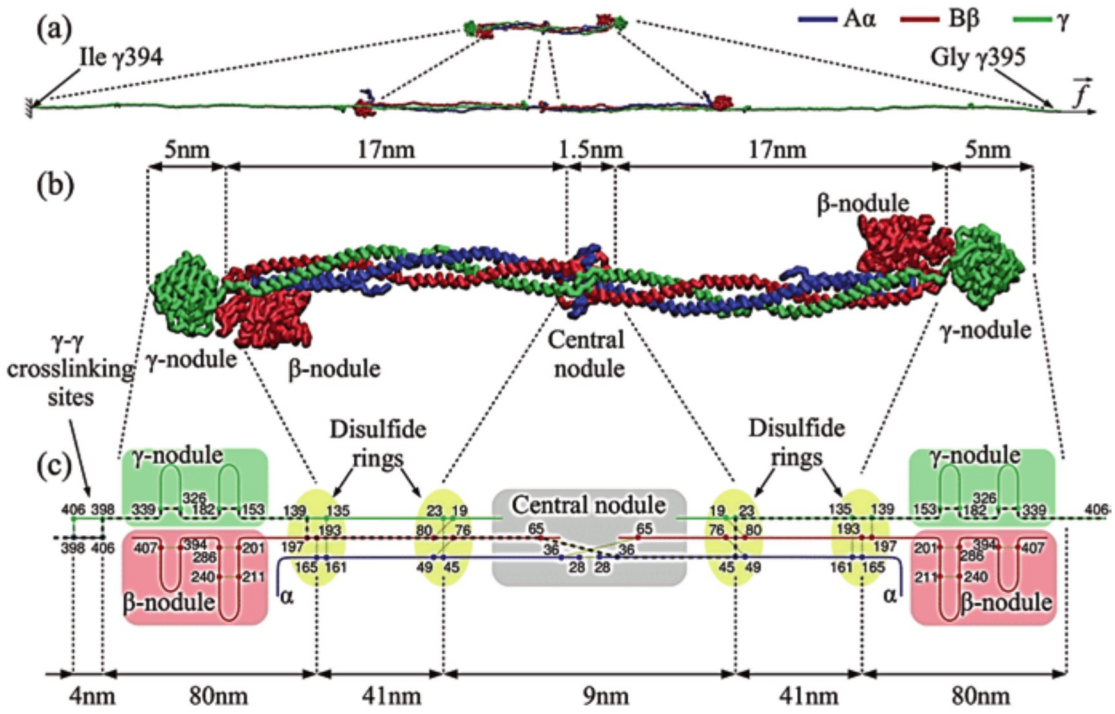


Figure 7: Fibrinogen/fibrin structure

The process of turning fibrinogen into fibrin, and thence into a clot is a complex cascade involving many molecules. See the figure below for a simplified explanation of the brick wall like bonding of fibrin forming a clot.

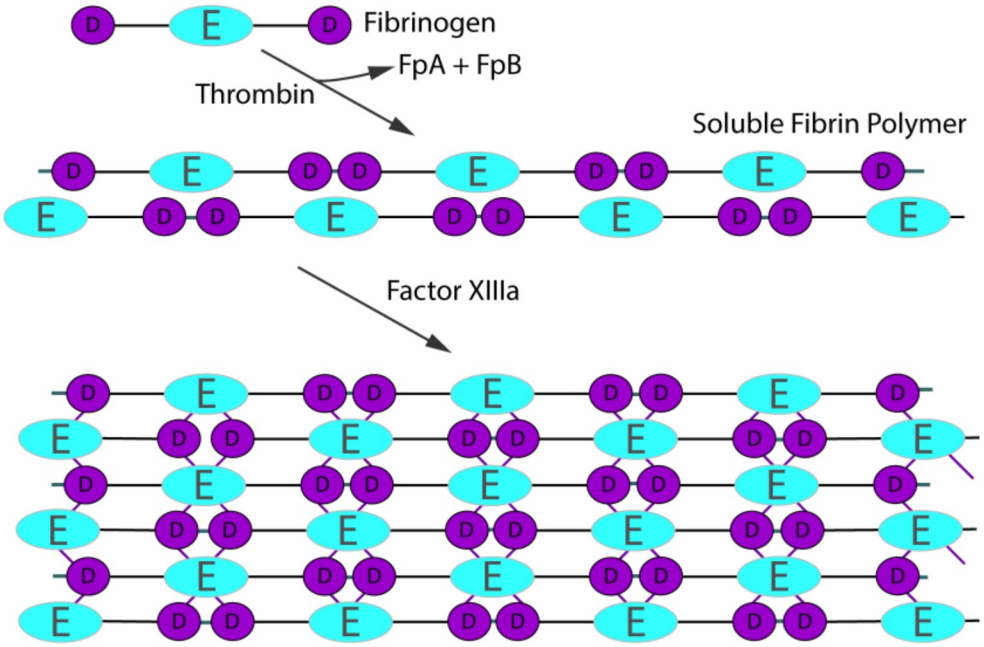


Figure 8: Fibrin protomer binding

When the fibrin protomers cross-link with each other, half a molecule out of phase (see the lower image on the previous page), the center of one fibrin subunit binds to the end of another. In normal clot formation, this interaction creates a very strong structure, which is crucial for its intended function of stemming blood flow from a damaged blood vessel. Failure of a clot can be life-threatening, as it compromises the body's ability to stop bleeding. Conversely, inappropriate clot formation can also lead to death, as seen in conditions like strokes and myocardial infarction.

Another critical finding regarding the Hirschman clots is their excessive phosphorus and sulfur content. These elements are most likely involved in the increased cross-linking responsible for the overly elastomeric physical properties observed. Sulfur is well-known for its role in cross-linking, and phosphorus appears to be involved as well.

It is pertinent to add a footnote to this point: the SOS team was able to easily find a large number of papers in the existing scientific literature that explain the observations related to the Hirschman clots and their formation. These references were not difficult to locate. Relevant papers were traced as far back as 1959, with a significant number published in the last two decades.

Much of the physical chemistry/organic chemistry, and indeed biochemistry, of blood clots was already known prior to 2020, the COVID epidemic and the release of the COVID vaccines. The spike protein associated with both the SARS CoV2 and the COVID vaccines is identified as possibly one of the two catalytic species responsible for creating Hirschman clots. The other chemical catalyst hypothesised is the method of delivery used in the COVID vaccines, the lipid nanoparticle (LNP).

It is known to science that the spike protein and the lipid nanoparticle delivery system used in the vaccines could act as toxins.

Significant Proof

There are several pieces of evidence that distinguish Hirschman clots from all other types of clots, including conventional red thrombi, coagula, and micro-clotting. These differences are particularly evident in the ratios of hemoglobin α and β, as well as the ratios of the three amino acid chains in fibrinogen/fibrin: α, β, and γ.

The first ratio of interest involves hemoglobin α and β. If the hemoglobin ratio is 1:1, this would indicate the presence of intact red blood cells entangled within the clots. However, the observed ratio is 1:5, which clearly suggests a different process involving erythrocyte damage.

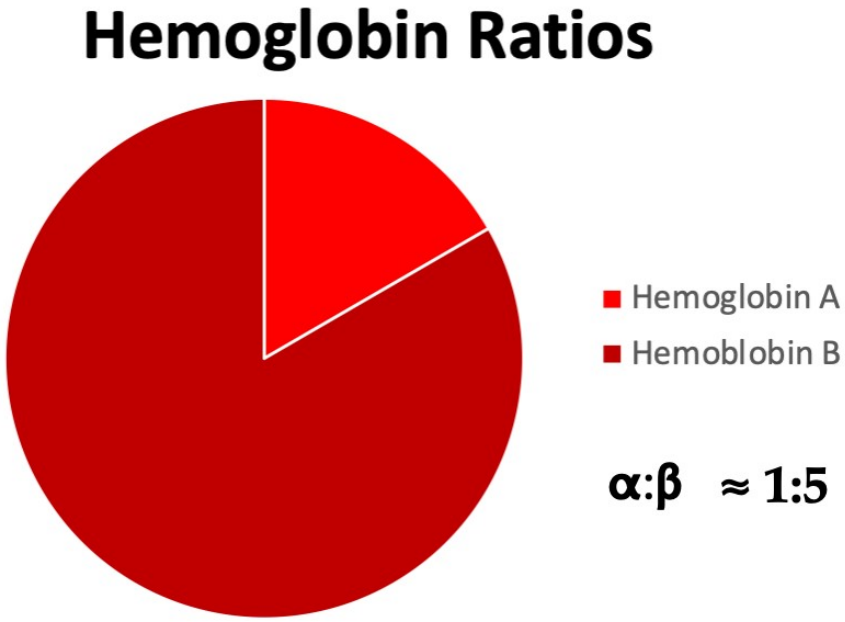


Figure 9: Hemoglobin ratios

In addition to erythrocyte damage, there is a serious imbalance in the fibrin/fibrinogen amino acid chains: α; β; γ. Each fibrinogen, and consequently each fibrin molecule, is composed of two sets of these chains, so the expected ratio in the Hirschman clots should be 2:2:2, or more practically, 1:1:1. However, this is clearly not the case.

Upon analysing the fibrin family amino acid chains in the Hirschman clots, an unusual ratio of 1:3:2 in regard of **α:β:γ** was discovered. See figure below.

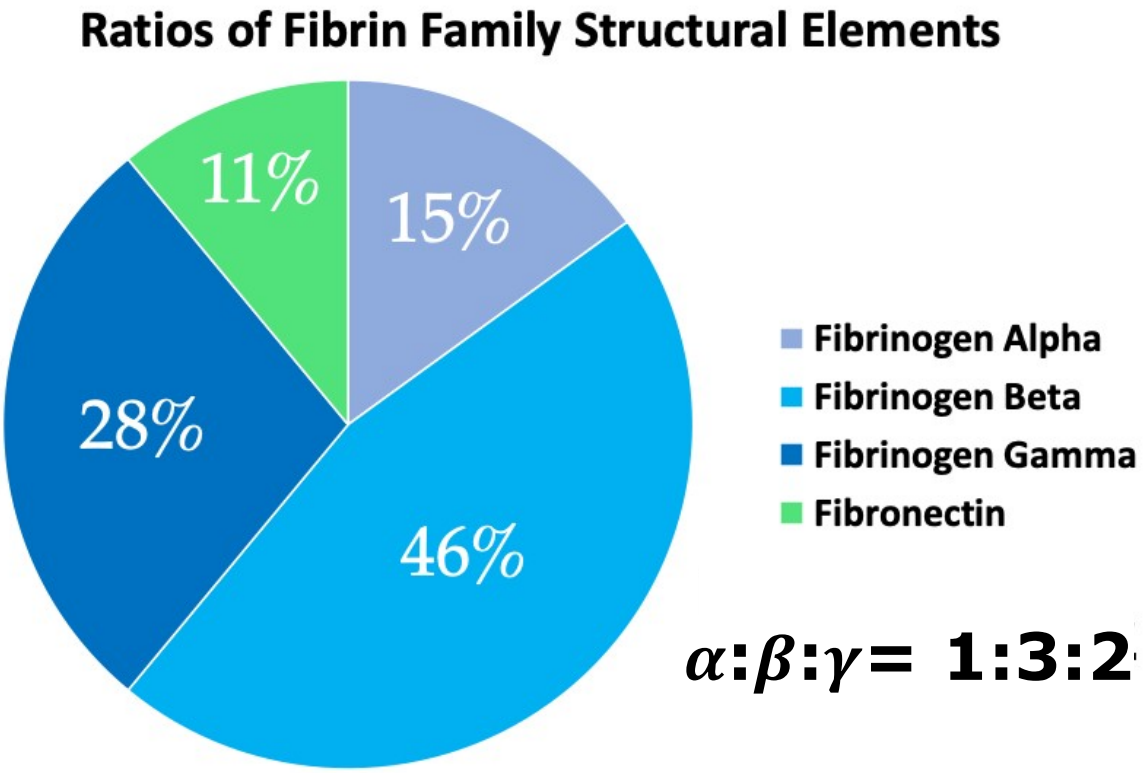


Figure 10: Ratio of Fibrin family proteins, including fibronectin

There is an overabundance of fibrinogen β, followed by a lesser amount of fibrinogen γ, and only a small quantity of fibrinogen α. **It is critical to note that the HPLC-MS results clearly showed fibrinogen chains, not fibrin chains.** This leads to the inescapable conclusion that the major structural elements of the Hirschman clots consist of disassociated, fragmented fibrinogen, not fibrin residues.

The presence of small amounts of fibronectin suggests adhesion points between the Hirschman clots and the glycocalyx of the endothelial cells lining the blood vessels, which contain connective tissue and adhesive proteins.

The staggering conclusion is that the Hirschman clots are distorted white thrombi, where the conversion of fibrinogen to fibrin did not occur. Furthermore, the SOS researchers were unable to find any significant quantity of thrombin in any of the samples tested. The further implications of this will be discussed in a future press release.

The SOS team quickly established that the ratio of fibrinogen chains corresponds almost exactly to their level of chemical reactivity. The organic chemistry is very clear. From an energetic perspective, the most reactive fibrinogen chain is the β chain, followed by the fibrinogen γ chain. The extremely low chemical bonding energy of the α chain results in very little of it being incorporated into the growing, distorted thrombus known as the Hirschman Clot.

The subject of chemical bond energy and reactivity is a critical component in understanding the formation of Hirschman clots.

Hypothesis to explain our findings

The authors suggest that, for the first time in history, large numbers of aberrant white thrombi have been found in cadavers shortly after death. These aberrant white Hirschman clots must be forming in the arteries and veins of living people.

Histology of Hirschman Clots

While chemical analysis can provide valuable information about the elemental and molecular makeup of Hirschman clots, it does not offer significant insights into their actual tissue-like structure. In general, there is a scarcity of available micrographs detailing thrombi. However, a few examples are provided below for comparison to the Hirschman clots (Figures 11–15).

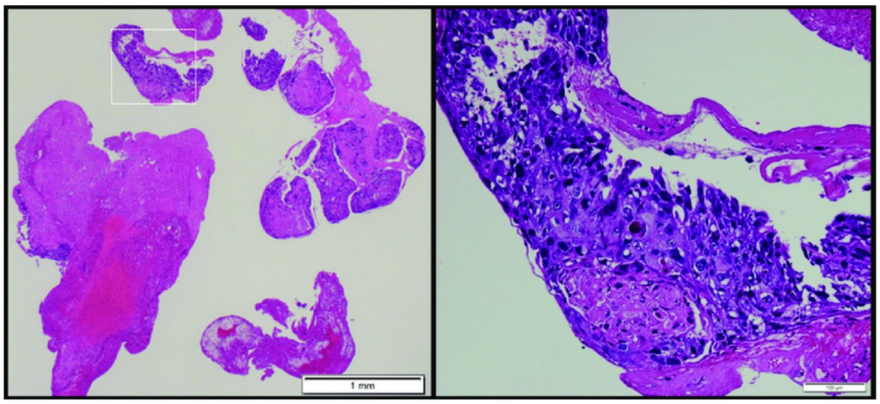


Figure 11: Histopathology of thrombus composed of fibrin and squamous cells stained with hematoxylin and eosin

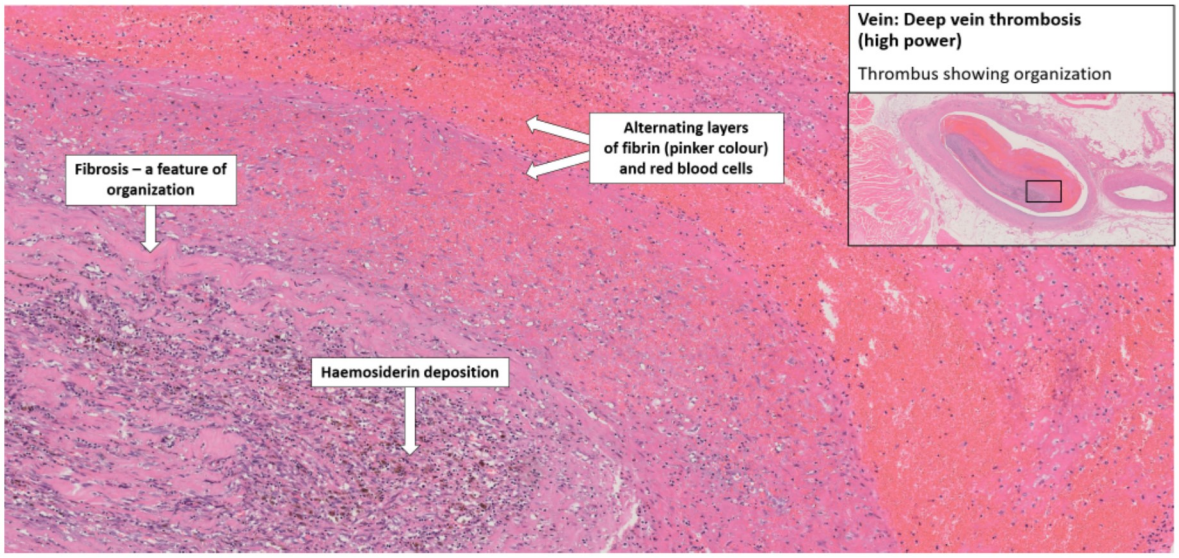


Figure 12: Deep vein thrombosis

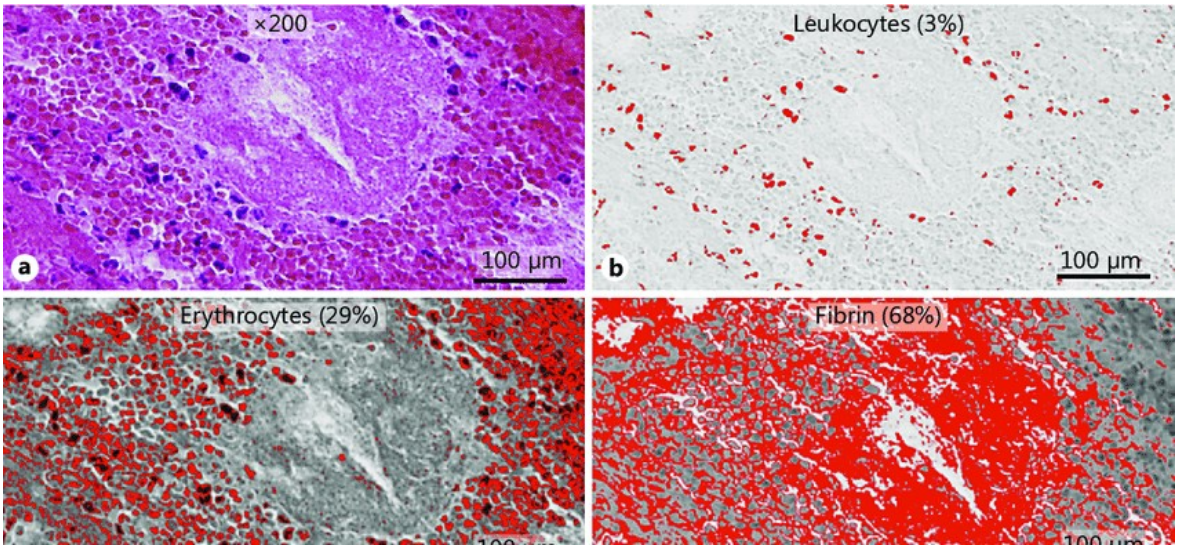


Figure 13: Histopathology of a red thrombus

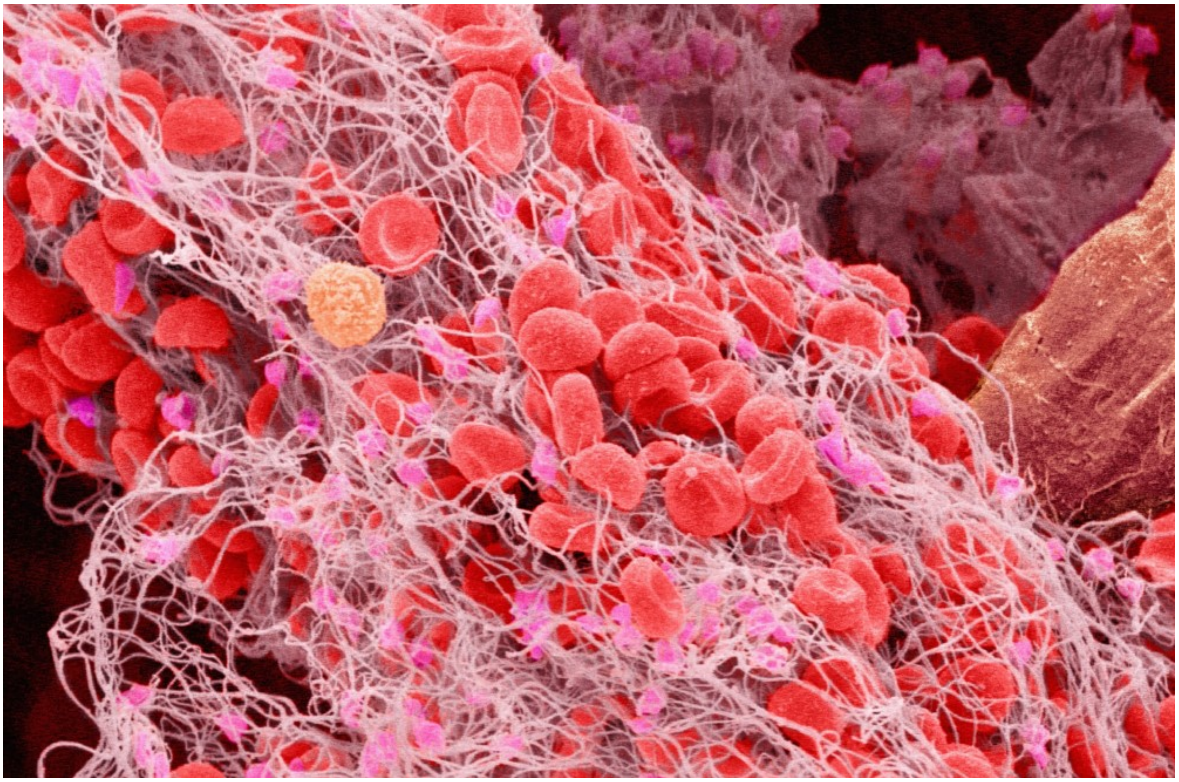


Figure 14: Autopsy finding of platelet-rich multi-organ red thrombi (electron microscope image, artificially coloured for clarity)

Note in Figure 14 above, the complex network of fibrin fibers entangling red blood cells (erythrocytes) and light pink platelets.

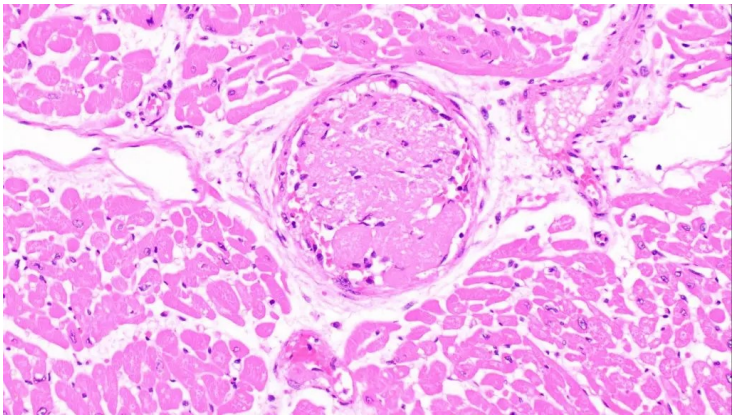


Figure 15: Blood clot in the heart of a COVID patient

Hirschman Clots ex-Embalmers

Hirschman clots are significantly different to conventional blood clots normally found in humans. They tend to be very long, thin, fibrous, elastomeric in physical character and have polymeric structure. They resemble elastic bands that can be variously flat (thalloid) or round. Some typical Hirschman clots are show in photographs taken by embalmers.

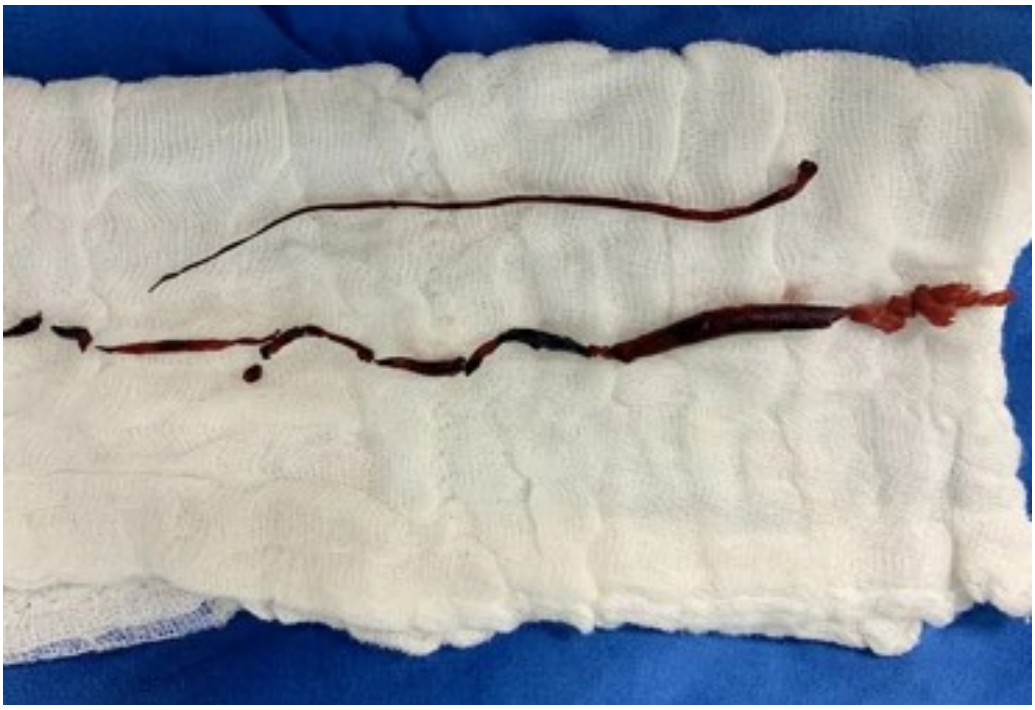


Figure 16: Fibrous clot from a COVID patient

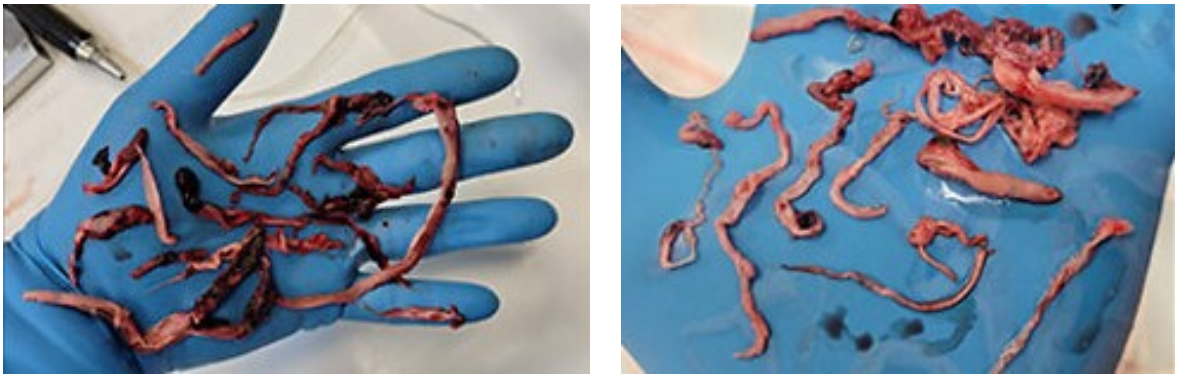


Figure 17: Hirschman's clots

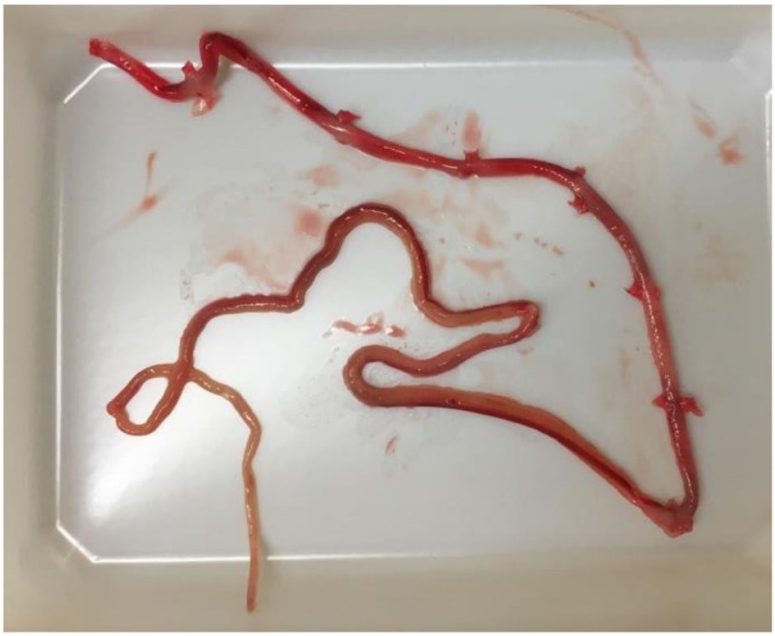


Figure 18: Worm-like fibrous clot from a patient who died from COVID disease

Note that the worm-like clot in Figure 18 is very round and smooth, with red inclusions that may represent either intact erythrocytes or the hemoglobin from damaged red cells. This appearance is totally unlike the classic "chicken-fat", softer clots or emboli (embolisms) typically found by embalmers in deceased bodies.

The clots obtained by the SOS scientists vary widely in form, though they all share certain characteristics in shape and texture. Often, these clots are more thallus-like, or flat, rather than merely round, worm-like structures. The flat, thallus-like clots are

found in both arteries and veins, where they appear rolled up, potentially allowing some blood flow to persist. An example of the typical size of clots found in deceased bodies during embalming is illustrated in Figure 18.

Figure 19: Fibrous clot from COVID diseased patient

Figure 20, shows one of the flat thallus shapes, which are found in both arteries and veins and are often rolled up, presumably still allowing some blood flow.

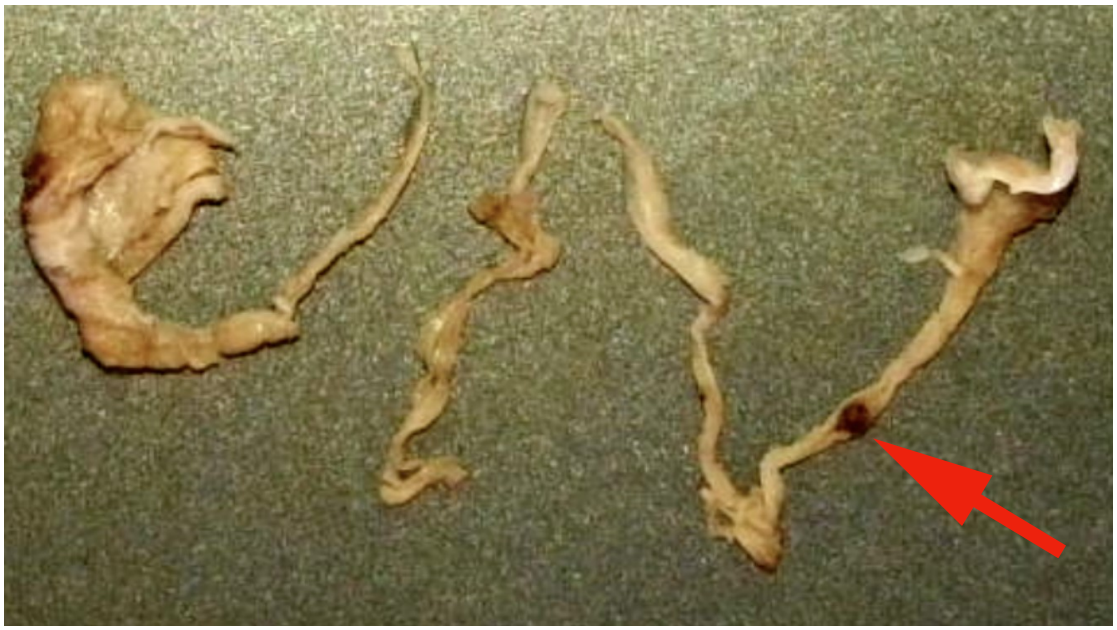


Figure 20: Unfurled thallus clots from a patient who died with COVID disease

Hirschman Clots - Histology

One of the most common histological stains is hematoxylin and eosin (H&E). Hematoxylin is a basic dye that binds to acidic components, primarily nucleic acids in the cell nucleus. It stains the nuclei of cells a deep blue or purple, making the genetic material within and outside the cells clearly visible.

Eosin is an acidic dye used to stain the cytoplasm and extracellular matrix. It binds to basic components, such as proteins in the cytoplasm and extracellular matrix, staining these structures in various shades of pink to red.

These two stains are used together to provide contrast and detail in microscopic tissue slides. H&E staining is routinely employed in medical diagnostics, particularly in pathology, to identify and study tissue abnormalities, such as cancer, inflammation, and other diseases.

The combination of hematoxylin and eosin in the H&E stain offers a comprehensive view of tissue structure, making it indispensable in both research and clinical settings. The SOS scientists used this staining technique in the initial stages to determine the nature of the clot tissue.

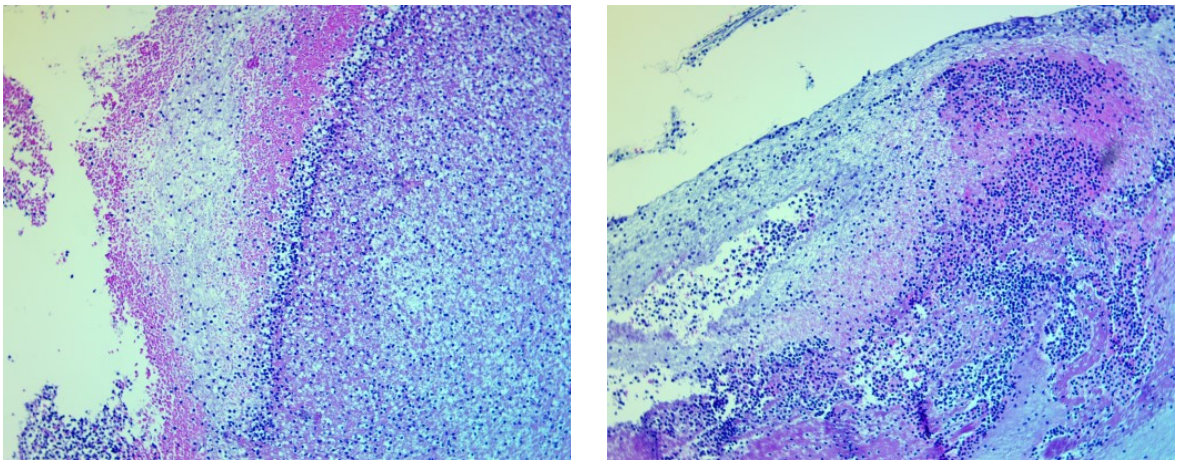


Figure 21: H&E 100X of a clot from a 70 year old male

Figure 21 shows two images of transverse sections of the same clot extracted from a 70-year-old male. Note the cellular nature of the tissue, evidenced by the myriad of small purple dots, which are lymphocytes. The areas of pink staining represent the extracellular matrix of fibers that form the scaffolding of the clot, in which various white blood cells (leukocytes) are entangled.

An image of the same clot (Figure 22), taken at 400X magnification, clearly reveals the cellular nature of the clot, with large leukocytes trapped within the mesh of what we now understand to be damaged fibrinogen molecules, rather than intact fibrin protomers.

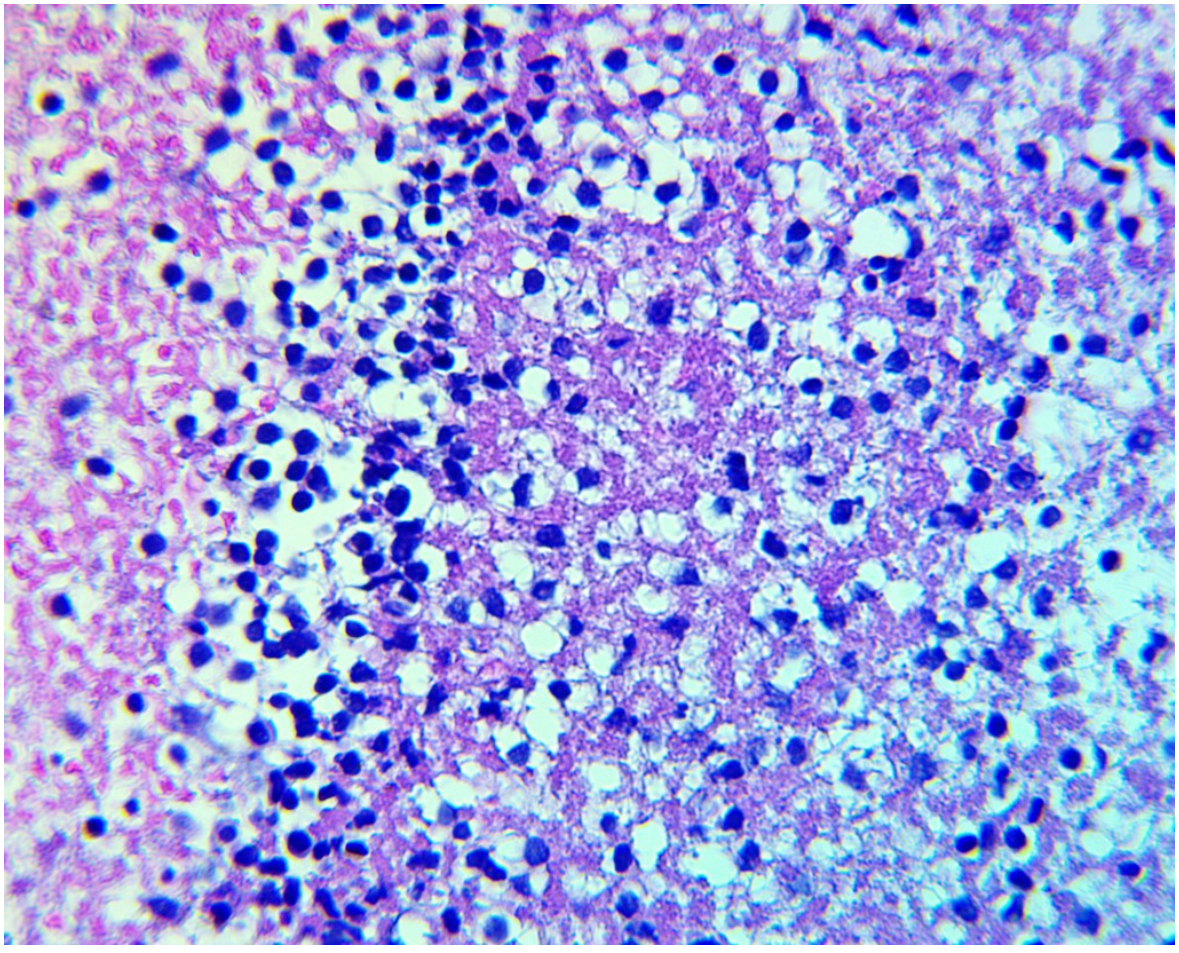


Figure 22: H&E 400X of a clot from a 70 year old male.

While some of the leukocytes are round, many exhibit rather strange, distorted nuclei, which may indicate damage due to disease or another factor. The extracellular fibers are clearly visible in a jumbled network that entraps cells. Note the absence of intact erythrocytes (red blood cells), which could be due to the process known as contraction, a natural part of white thrombus formation.

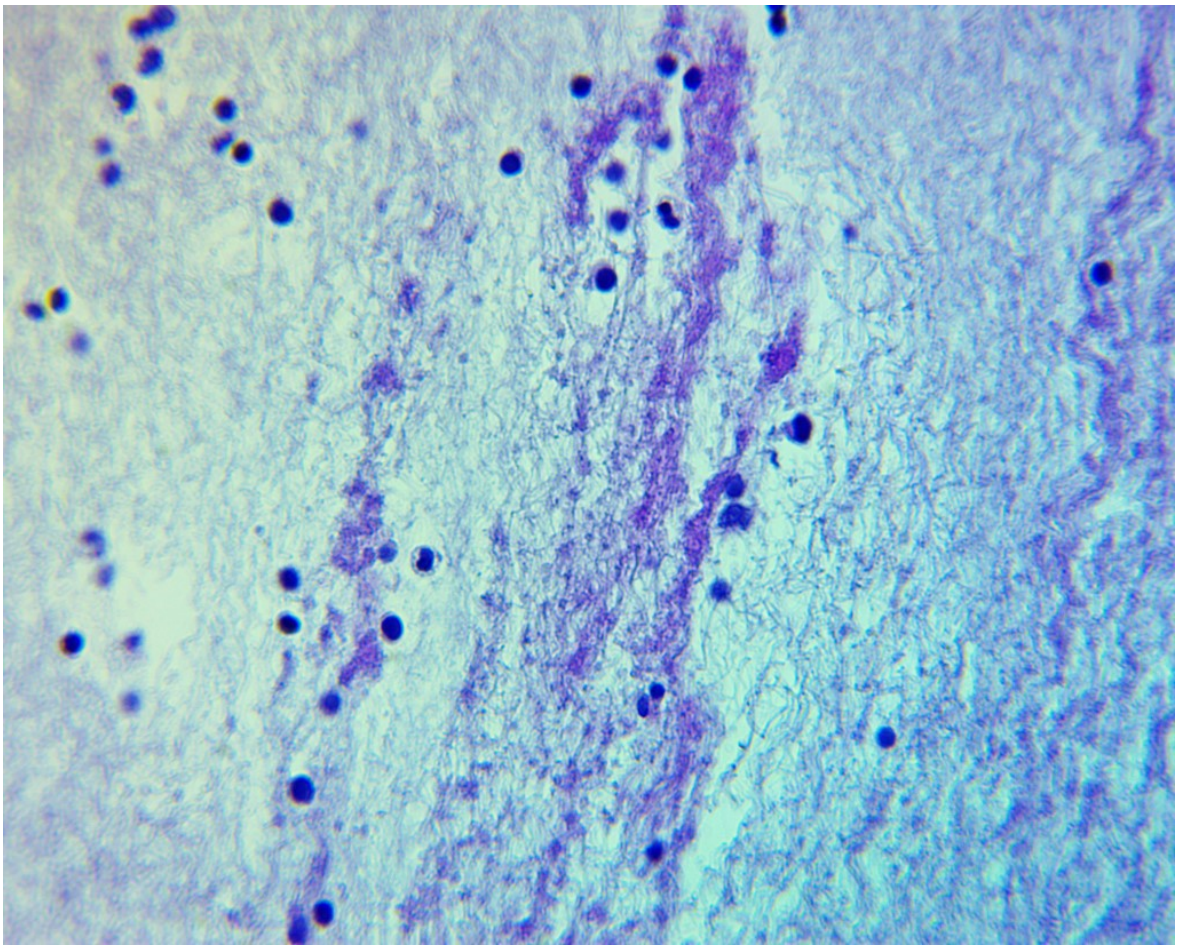


Figure 23: H&E 400X of a clot from a 70 year old male.

Figure 23 shows another part of the same clot depicted in Figure 22, this time in an area with far fewer cells. Here, the skeletal formation of damaged fibronectin and distorted proto-fibrils, which form the basis of the actual Hirschman clot, are clearly visible. Note that some of the lymphocytes (white blood cells) have distorted nuclei. Erythrocytes (red blood cells) are notably absent, hence the "White Thrombus" description. This image is both diagnostic of and typical for a Hirschman clot.

Assembly of Hirschman Clots

At the injury site, platelets accumulate, appearing as octopus-shaped cells that bridge the area of injury. They form a virtual mesh, serving as the skeleton for what should become a life-saving plug to stem the flow of blood. Platelets send out chemical signals to increase the liver's production of fibrinogen, which, under normal circumstances, is converted into fibrin by the enzyme thrombin.

The fibrin protomers, or fibrils, surround and enmesh the platelets, ultimately forming a clot. Various other cells, including red blood cells, are entrapped during this process. As the clot matures, the platelets contract their 'tentacles,' drawing the tissue's sides together to reduce the number of stem cells required to redifferentiate into the various cell types that make up blood vessels.

During this contraction process, red blood cells are literally squeezed out, so a mature white thrombus is largely white, due to the paucity of erythrocytes. This process differs from that of red thrombi, which generally form in veins at low blood pressure and flow rates. In these clots, many red blood cells remain trapped in the fibrin matrix, making the clots appear more red.

A unique feature of Hirschman clots is that they form in both arteries (high blood pressure and flow rate) and veins (low blood pressure and flow rate). Hirschman clots are not homogeneous in terms of the cells entrapped in the matrix. Instead, they consist of random collections of proto-fibrils anchored together in heterogeneous bundles that tend to have a growth axis and direction.

The cross-linking that holds this fibrinous 'bird's nest' of fibers together is due to the increased prevalence of disulfide bonds and the promiscuous bonding of excess phosphorus. As a result, raised levels of phosphorus and sulfur are present in Hirschman clots, as evidenced by ICP-MS (mass spectrometry) analysis. This

cross-linking by excess phosphorus and sulfur gives the conglomeration elastomeric properties, resembling a rubber band.

These highly flexible yet surprisingly strong clots appear to be anchored at the nucleation site on the endothelial lining of the blood vessel. The authors hypothesise that this may occur as a result of damage to the endothelium, potentially caused by SARS-CoV-2 viral entry through the lipid bilayer of endothelial cells.

After being synthesized in the cytosol by the host's ribosomes, the Spike Protein is transferred to the outer surface of each cell, marking it as a target for attention by the host's immune cells. If the immune cells detect and destroy or damage the cell displaying the foreign Spike Protein on its surface, the destruction of that cell may release excess free phosphorus. This phosphorus could then become available to incorporate into fibrinogen amino acid chains during the initiation of clot formation.

The cellular disruption itself may be sufficient to act as the nucleation site for the formation of a new Hirschman clot. The authors suspect that Hirschman clots are composed primarily of fibrinogen that has not been converted to fibrin by the action of thrombin.

Because the three polypeptide chains (α, β, γ) that normally comprise fibrinogen/fibrin are partially dissociated, their ratio of incorporation into Hirschman clots as the main structural components is driven by their available bond energy. Accordingly, in Hirschman clots, the beta chain, with its high bonding energy, constitutes 50% of the clot, while the gamma chain accounts for 30%, and the alpha chain makes up the remaining 20%.

Due to this distorted ratio of the three polypeptide chains (α, β, γ), Hirschman clots are not typical white thrombi.

Additionally, because of the relative lack of red blood cells and fibrin, they do not resemble conventional red thrombi either.

Thus, Hirschman clots appear to represent a completely new class of thrombus, forming in both arteries and veins—a novel disease. Consequently, the natural clot-busting enzyme, plasmin, is unable to disassemble them.

It seems likely that the Hirschman clotting cascade is initiated either by viral infection or by COVID vaccines containing lipid nanoparticles and their subsequent spike protein production.

From our observations, Hirschman clots appear capable of growing unrestricted along the length of the blood vessel lumen. The original point of damage in the endothelial lining serves as both the nucleation site for clot formation and the attachment point.

In cases of genuine COVID infection, clot formation as a result of cellular destruction (inflammation) may be caused by the host's own immune system. However, no such mechanism of clot formation from viral attack is described in the medical literature, as far as the authors can ascertain.

In cases where COVID vaccines appear to be the triggering event, the authors suspect that the lipid nanoparticles within the vaccine and/or the subsequent Spike Protein production may cause endothelial damage, leading to the initiation of Hirschman clotting.

A distinctive feature of Hirschman clots is the relative lack of fibrin and the apparent lack of thrombin to convert fibrinogen to

fibrin. It is currently unknown whether thrombin is absent, present but somehow disabled, or otherwise inhibited.

In the hypothetical case of synthetic (iatrogenic) clot causation as a result of COVID vaccines, the Spike Protein (produced by the host cells) and the lipid nanoparticles may act as the initiators of the clotting cascade. In the absence of functional thrombin, the clotting cascade may instead utilise partially disassociated fibronectin rather than fibrin, resulting in a long, rubbery clot. This clot will have at least one attachment point to the endothelial lining of the blood vessel and will grow into the lumen, extending downstream from the attachment point or nucleation site.

Denouement

The sudden appearance of long, white fibrous clots in the deceased was first observed by embalmers after the COVID vaccines were rolled out.

These rubbery clots did not resemble the normal clots, such as red thrombi or chicken fat clots, normally seen in deceased bodies.

These clots resemble white thrombi, but unlike normal white thrombi they are found in veins as well as arteries.

The elemental analysis provides evidence of increased phosphorus, sulphur and tin, each of which contributes to the new clotting phenomenon.

The sudden rise in these aberrant white clots, post-COVID vaccines rollout, in subjects undergoing surgery is further evidence of a causal link that needs to be urgently investigated.

To date, as of the time of writing, medical professionals and their organisations, including public health bodies, are continuing to

deny the existence of these unique, anomalous white thrombi. The fact that there is very strong pressure not to conduct autopsies in those dying suddenly is further evidence of a dangerous coverup undertaken by health authorities worldwide.

Evidence from whistleblowers and brave health professionals who are not afraid to speak up provide a sinister backdrop to what may constitute the greatest public health emergency ever seen. That officials continue to deny the reality of these unique clots can only lead the observer to the conclusion that a vast, worldwide coverup is in force.

Failure of authorities to act professionally and responsibly, in the best interests of public health, can only signal a health crisis of unprecedented proportions.

If this situation is not addressed in the very near future, there exists a potential for what can only be described as an existential crisis for the species Homo sapiens sapiens.

May God have mercy upon humanity.

APPENDIX

Inductively Coupled Plasma Mass Spectrometry

ICP-MS is a powerful analytical technique used to detect and quantify trace elements and isotopes in various samples, including environmental, biological, geological, and industrial materials. It combines the ionisation capabilities of an inductively coupled plasma with the mass analysis capabilities of a mass spectrometer, offering high sensitivity and precision.

Step-by-Step Process

Sample Introduction:

The process begins with the introduction of the sample, which can be in the form of a liquid, solid, or gas. In most cases, samples are dissolved in an appropriate solvent, typically an acid, to create a solution that can be nebulized.

The solution is then introduced into the ICP-MS system using a nebulizer, which converts the liquid sample into a fine aerosol.

Nebulisation and Aerosol Formation:

The aerosol produced by the nebulizer is transported into the plasma torch by a flow of argon gas. The aerosol consists of tiny droplets containing the sample's analyte elements.

Inductively Coupled **Plasma** (ICP) Generation:

The plasma is generated in a quartz torch by passing a stream of argon gas through a high-frequency radio frequency (RF) coil. The RF coil creates an oscillating magnetic field, which ionises the argon gas, forming a high-temperature plasma (approximately 6,000 to 10,000 K).

As the aerosol enters the plasma, the intense heat causes the solvent to evaporate, and the sample particles are vaporised and atomised. The atoms are then ionised, forming positively charged ions.

Ion Extraction:

The ions produced in the plasma are extracted from the high-temperature plasma region and directed into the mass spectrometer. This is achieved through a series of cones (sampler and skimmer cones) that create a vacuum environment and focus the ion beam into the mass spectrometer.

Mass Spectrometry:

Once the ions enter the mass spectrometer, they are separated based on their mass-to-charge ratio (m/z). This is typically done using a quadrupole, time-of-flight, or sector field mass analyzer.

The mass spectrometer rapidly scans across a range of m/z values, detecting the ions corresponding to different elements and their isotopes.

Detection and Quantification:

The ions are detected by an ion detector, such as an electron multiplier or Faraday cup, which measures the intensity of the ion signal.

The intensity of the signal is proportional to the concentration of the element in the sample. The ICP-MS system then converts this signal into quantitative data, allowing for the determination of element concentrations at trace and ultra-trace levels (often down to parts per trillion, ppt).

Data Analysis:

The data collected by the detector is processed by a computer system, which generates a mass spectrum. This spectrum shows the presence and abundance of elements in the sample.

Calibration with known standards is performed to ensure accurate quantification, and various corrections may be applied to account for potential interferences or matrix effects.

Advantages of ICP-MS

High Sensitivity: ICP-MS can detect elements at extremely low concentrations, making it one of the most sensitive analytical techniques available.

Multi-element Capability: It can simultaneously detect and quantify multiple elements in a single analysis.

Isotopic Analysis: ICP-MS can distinguish between different isotopes of the same element, allowing for isotopic ratio studies.

Wide Dynamic Range: The technique can accurately measure elements across a wide range of concentrations, from trace levels to major constituents.

Applications of ICP-MS

ICP-MS is widely used in various fields, including:

Environmental Monitoring: Analysis of trace metals in water, soil, and air.

Clinical and Biomedical Research: Trace element analysis in biological samples like blood, urine, and tissues.

Geochemistry: Determination of elemental composition in rocks and minerals.

Food Safety: Detection of heavy metals and contaminants in food products.

Pharmaceuticals: Quality control and trace element analysis in drug formulations.

Conclusion

ICP-MS is a versatile and highly sensitive analytical technique that plays a critical role in various scientific and industrial applications. By combining the high-temperature ionisation capabilities of an inductively coupled plasma with the precise mass analysis of a mass spectrometer, ICP-MS provides accurate and reliable data for trace element analysis.

HPLC-MS in Proteomics: A Detailed Explanation

1. Overview of HPLC-MS

High-Performance Liquid Chromatography (HPLC): HPLC is a chromatographic technique used to separate complex mixtures into individual components based on their interactions with a stationary phase (usually a packed column) and a mobile phase (a solvent or mixture of solvents). In proteomics, HPLC is used to separate peptides and proteins in a sample, facilitating their subsequent identification and quantification.

Mass Spectrometry (MS): Mass spectrometry is a technique used to measure the mass-to-charge ratio (m/z) of ions. In proteomics, MS is used to identify peptides and proteins by measuring the masses of peptide fragments generated by enzymatic digestion (commonly with trypsin) and comparing them to known peptide mass databases.

2. The Workflow of HPLC-MS in Proteomics

Sample Preparation:

Protein Extraction: Proteins are extracted from biological samples (e.g., cells, tissues, or biofluids) using various lysis methods.

Protein Digestion: The extracted proteins are digested into smaller peptides using a proteolytic enzyme like trypsin, which cleaves at specific amino acid residues, usually after lysine (K) or arginine (R).

Peptide Purification: The resulting peptide mixture is often purified to remove salts, detergents, or other contaminants that could interfere with HPLC or MS.

HPLC Separation:

Peptide Separation: The peptide mixture is injected into the HPLC system, where it is separated based on differences in hydrophobicity, charge, or size. This separation typically occurs in a reverse-phase column (C18) under gradient elution, where the mobile phase composition changes over time to elute peptides with different properties.

Fractions Collection: The separated peptides elute from the HPLC column at different times (retention times) and are directed into the mass spectrometer for analysis.

Mass Spectrometry Analysis:

Ionisation: The separated peptides enter the mass spectrometer and are ionised, usually by electrospray ionisation (ESI). ESI generates charged ions from the peptides in solution, which are then introduced into the mass analyzer.

Mass Analysis: The mass analyzer (e.g., quadrupole, time-of-flight (TOF), or orbitrap) measures the mass-to-charge ratio (m/z) of the ionised peptides. This produces a mass spectrum, which displays the detected ions as peaks with specific m/z values.

MS/MS (Tandem Mass Spectrometry): To identify the peptides, the mass spectrometer can perform a second stage of analysis (MS/MS), where selected precursor ions are fragmented into smaller ions (product ions) within the mass spectrometer. The resulting fragment ions provide a unique pattern (fragmentation spectrum) that can be used to deduce the peptide's amino acid sequence.

Data Analysis:

Peptide Identification: The MS/MS fragmentation spectra are compared against protein or peptide databases (e.g., UniProt, NCBI) using bioinformatics software to identify the peptides and their corresponding proteins.

Quantification: Peptide abundances can be quantified based on the intensity of the ion signals. Techniques such as label-free quantification, isotope labelling (e.g., SILAC, TMT), or spectral counting can be used for this purpose.

Protein Inference: Identified peptides are mapped back to their parent proteins. This process helps determine which proteins are present in the sample and in what quantities.

3. Applications of HPLC-MS in Proteomics

Protein Identification: HPLC-MS is used to identify proteins in complex biological samples, such as cell lysates, tissues, or plasma. It is crucial for discovering novel proteins and understanding their functions.

Quantitative Proteomics: By comparing peptide abundances across different conditions or samples, HPLC-MS can be used for quantitative analysis, providing insights into differential protein expression, which is essential for biomarker discovery and understanding disease mechanisms.

Post-translational Modifications (PTMs): HPLC-MS is highly effective in detecting and characterising post-translational modifications (e.g., phosphorylation, glycosylation) on proteins, which play critical roles in regulating protein function and signaling pathways.

Protein-Protein Interactions: HPLC-MS can analyse protein complexes, providing information about protein-protein interactions and network dynamics within cells.

Biomarker Discovery: In clinical proteomics, HPLC-MS is employed to discover and validate protein biomarkers associated with diseases, facilitating early diagnosis and personalised medicine.

4. Advantages and Challenges

Advantages:

High Sensitivity: HPLC-MS can detect proteins and peptides at low concentrations, making it ideal for analysing complex biological samples.

Specificity: The combination of chromatographic separation and mass spectrometric analysis provides high specificity in identifying proteins and their modifications.

Versatility: HPLC-MS can be applied to a wide range of proteomic studies, from basic research to clinical applications.

Challenges:

Complexity of Data Analysis: The large datasets generated by HPLC-MS require sophisticated bioinformatics tools for analysis and interpretation.

Dynamic Range: The wide dynamic range of protein concentrations in biological samples can be challenging, potentially leading to the underrepresentation of low-abundance proteins.

Sample Preparation: Proper sample preparation is crucial, as impurities can affect both chromatographic separation and mass spectrometric detection.

Conclusion

HPLC-MS is a cornerstone technology in proteomics, enabling the detailed analysis of proteins in complex biological systems. By combining the strengths of liquid chromatography and mass spectrometry, HPLC-MS provides a powerful platform for identifying, quantifying, and characterising proteins, offering deep insights into the molecular mechanisms underlying biological processes and diseases. Despite the challenges, advancements in HPLC-MS technology and data analysis continue to push the boundaries of proteomics, making it an indispensable tool in modern biology and medicine.

Matrix-Assisted Laser Desorption/ Ionisation

MALDI-TOF (Matrix-Assisted Laser Desorption/Ionisation - Time of Flight) Mass Spectrometry is a powerful analytical technique used to identify and characterise large biomolecules, such as proteins, peptides, and polymers. Here's a concise explanation:

Sample Preparation: The sample is mixed with a matrix, a small organic compound that absorbs laser energy, and this mixture is applied to a metal target plate.

Laser Desorption/Ionisation: A laser beam is directed at the sample, causing the matrix to absorb the energy and vaporise. This process transfers energy to the sample molecules, causing them to ionise without breaking down.

Ion Acceleration: The ionised molecules are accelerated in an electric field within the mass spectrometer. Since all ions receive the same energy, their velocity depends on their mass-to-charge ratio (m/z).

Time of Flight (TOF) Detection: The ions travel through a flight tube to the detector. Lighter ions reach the detector faster, while heavier ions take longer. The time taken for ions to reach the detector is measured, and this "time of flight" is used to calculate the m/z ratio.

Data Analysis: The resulting data is plotted as a mass spectrum, displaying peaks corresponding to the m/z ratios of the ions. This spectrum is used to identify the sample components based on their mass.

Advantages:

High Sensitivity: Capable of detecting minute amounts of material.

Rapid Analysis: Provides quick results, especially useful in clinical diagnostics and proteomics.

Minimal Sample Preparation: Requires relatively simple sample preparation compared to other mass spectrometry techniques.

Disadvantages

Matrix Interference:

The matrix used in MALDI can sometimes produce background signals or interfere with the analysis, particularly when analysing low-mass compounds, making it difficult to distinguish between the sample ions and matrix ions.

Limited Quantification:

MALDI-TOF is less effective for quantitative analysis. The ionisation efficiency can vary between samples, making it challenging to obtain accurate quantification without extensive calibration.

Fragmentation Issues:

While MALDI is generally gentle and minimises fragmentation, some large biomolecules might not ionise well, leading to incomplete or inefficient fragmentation. This can complicate the interpretation of the mass spectrum, especially for complex mixtures.

Sample Preparation Variability:

The quality of the MALDI spectrum can be highly dependent on the sample preparation technique. Inconsistent sample-matrix crystallisation can lead to variability in results, affecting reproducibility.

Mass Range Limitations:

MALDI-TOF is generally effective for analysing large biomolecules like proteins and peptides, but it may not perform as well with very small molecules or compounds with a low mass-to-charge ratio (m/z).

Sample Spotting:

The technique relies on spot-to-spot consistency on the target plate, which can be difficult to achieve. Variations in sample deposition can lead to inconsistent results, especially in high-throughput applications.

High Initial Cost:

The equipment for MALDI-TOF is expensive, and maintaining the system, including the cost of lasers and other components, can also be high. This can be a barrier for smaller laboratories.

Limited Structural Information:

While MALDI-TOF is excellent for identifying molecules based on their mass, it provides limited structural information compared to other techniques like tandem mass spectrometry (MS/MS), which can provide more detailed fragmentation data.

Despite these disadvantages, MALDI-TOF remains a widely used and valuable tool in many fields, particularly when the advantages outweigh the potential drawbacks.

In conclusion:

MALDI-TOF is widely used for identifying microorganisms, protein analysis, and detecting biomarkers in clinical samples due to its accuracy, speed, and ability to handle complex mixtures.