MEETING REPORT

Mass Spectrometry and Separation Sciences for Laboratory Medicine: Toward Next Generation Clinical Mass Spectrometry

Steven H. Wong, PhD; Y. Victoria Zhang, PhD; Steven W. Cotten, PhD; R. Brent Dixon, PhD; Saeed A. Jortani, PhD; and Yusheng Zhu, PhD

AACC's fifth annual Mass Spectrometry Conference, held Oct. 1-2, 2015, in Chicago, focused on Mass Spectrometry and Separation Sciences for Laboratory Medicine, and it was the first conference organized by the officers of the newly formed Mass Spectrometry and Separation Science Division (MSSS). The conference was attended by 156 clinical lab professionals, clinicians, pathologists, and IVD industry members.

The Conference Organizing committee included: Steven H. Wong, PhD (conference chair, Wake Forest University School of Medicine); Y. Victoria Zhang, PhD, (Division chair, University of Rochester School of Medicine) Steven W. Cotten, PhD (Ohio State University), R. Brent Dixon, PhD, (Physician's Choice Laboratory Services); Saeed A. Jortani, PhD (University of Louisville School of Medicine); and Yusheng Zhu, PhD (Medical University of South Carolina).

This conference--an intermediate level event built upon the knowledge base of the previous four meetings in the series--examined scientific, technological, and regulatory developments such as high resolution mass spec (HRMS), emerging clinical applications such as tissue imaging, the complementary roles of liquid and gas chromatography, rising concerns regarding implementation of laboratory-developed tests, and the emergence of next generation clinical mass spec tools.

AACC President David Koch, PhD (Emory University), opened the conference and expressed his appreciation for the effort of the Organizing Committee and AACC staff.. He also gave positive marks to a comprehensive meeting program that is intended to be a road map for developing and vetting "Next Generation" clinical mass spectrometry devices and making sure successful breakthroughs are correctly implemented in the clinical laboratory.

In a nice moment, Dr. Koch had the pleasure of introducing Michael Bennett, PhD (Children's Hospital of Philadelphia), who had been notified the night before of his election as AACC President, and was on hand to receive the well-deserved applause of his colleagues at this announcement.

SESSION I - SCOPE OF MASS SPEC TESTING FOR LABORATORY MEDICINE/PATHOLOGY

An opening keynote presentation Prof. Dr. Hans H. Maurer (Saarland University) assessed “High Resolution Mass Spectrometry for Laboratory Medicine in TDM/Tox”. After establishing the HRMS principle, Dr. Maurer pointed to HRMS technologies such as time-of-flight or Orbitrap for offering accurate mass detection given the challenges of drug screening, drug metabolism studies, and drug quantitation and monitoring. Benefits of HRMS methods include smaller samples with less preparation time, easier mass spec optimization, higher sensitivity and selectivity, full scan offering retrospective interpretation, and comprehensive quantitation.

The next conference session was a panel discussion examining issues in laboratory developed tests (LDTs), chaired by Saeed Jortani, PhD (University of Louisville), who outlined the sessions goals as aiming to familiarize participants with the challenges associated with LDTs, and address practical and applied issues such as test development/validation, regulatory issues, and reimbursement considerations. Panel members included Henry Rodriguez, PhD, MBA (National Cancer Institute); Alberto Gutierrez, PhD (U.S. Food & Drug Administration’s Center for Diagnostic and Radiologic Health);. Steven Soldin, PhD, (National Institutes of Health); and. Charles Root, (CodeMap, LLC).

Currently, lab tests for clinical diagnostics are either 1.) Submitted by an in vitro diagnostic company for FDA approval, or 2.) Validated by the labs themselves with validation performed in accordance to CLIA guidelines. And while the FDA recently announced their intention to focus on the second category by exercising its regulatory discretion. Dr. Rodriguez noted that there are numerous cancer diagnostics in the pipeline whose development could become prohibitively expensive due to financial and funding limitations required by the new regulatory path. Despite this outlook, efforts were being made to understand the performance of mass spectrometry for discovery and testing of novel biomarkers for cancer.

Dr. Gutierrez emphasized the need for the new regulatory paradigm, and that laboratories should expect regarding LDTs over the next few years. However, he also noted that FDA would attempt to work with labs to find a proper cost/benefit ratio that would allow them to continue to offer LDTs.

Dr. Soldin discussed the need for higher quality testing methodologies to ensure clinically accurate results and maintain patient safety, noting that many immunoassays did not demonstrate relevance to patient outcome but received FDA approval.

Dr. Root alerted the audience that the latest reimbursement changes were underway from CMS. He advised that familiarity with reimbursement issues was paramount in assuring a successful offering for any test. If the payment of the testing offered was not optimal, the success of any clinical test--LDT or any other mode--would be in doubt.

SESSION II - ESSENTIAL CONCEPTS IN CLINICAL MASS SPEC

Daniel. Holmes, MD (St. Paul's Hospital Providence Health Care) detailed common mistakes and pitfalls with LC/MS/MS and how to avoid them. Using real-world problems from his own laboratory, Dr. Holmes discussed issues that included making calibrators, selecting internal standards, reconstitution volume, chromatography gradients, following published methods, collection tube interferences, and using published reference ranges. He then addressed transcription of results, automation, and scaling up the throughput for a mass spectrometry method.

The next speaker, Brent Dixon, PhD (PCLS), discussed practical sample prep approaches for robust quantitative analysis. He also reviewed solid phase extraction, liquid-liquid extraction, supported liquid extraction, and "dilute-and-shoot," describing their impact on prep time, process complexity, cost, sensitivity, possible interferences, and effect on column life.

Dr. Dixon also detailed for attendees some sample preparation techniques for commonly used specimen types such as urine, serum, and oral fluid in the areas of toxicology, endocrinology, and proteomics.

Victoria Zhang, PhD (University of Rochester Medical Center) engaged the audience with a discussion of finance, personnel, and interface issues related to bringing mass spectrometry into a clinical laboratory. She commented on financing options and capital required for purchasing new instrumentation and how to evaluate the laboratory's return on investment for the purchase. She then transitioned to a discussion of personnel requirements for staffing and resources for training, and ended her presentation with data processing and interfacing issues related to capturing, processing, and reporting mass spectrometry data.

After a networking luncheon, the conference continued with Steven Cotten, PhD (The Ohio State University Wexner Medical Center), giving an overview on method development and validation for certification in accordance with CLSI C62-A and CAP guidelines. Dr. Cotten highlighted some areas for increased focus, including selection of internal standard and LC columns, evaluation of carryover, ion suppression, and matrix effects, as well as verification of linearity/measuring interval, lower limit of detection/quantification, procession, and bias/trueness. And finally, Dr. Cotten advised participants involved in validation studies to closely examine the CAP checklist questions that assess chromatography (calibrator/standard material, quality control), mass spectrometry operation (instrument operation, mass spectrometer tuning, and identification criteria), and matrix effects.

Next up, AACC Past President and Conference Chair Steven Wong, PhD (Wake Forest University School of Medicine), shared his experience in using LC-MS/MS for the measurement of antifungals (voriconazole and posaconazole) for therapeutic drug monitoring. He also provided a primer on the various methods for enantioseparation, using D-/L-methamphetamine, R-/S-fluoxetine, R-/S-methadone as examples to demonstrate how to separate these enantiomers and emphasize the clinical significance of chiral analysis by LC-MS/MS in urine drug abuse testing.

The final Session II speaker, Uttam Garg, PhD (University of Missouri School of Medicine), elaborated on the complementary role of GC-MS in the clinical laboratory. Dr. Garg first emphasized that GC-MS was still in wide use despite LC-MS gaining popularity in clinical laboratories. He went on to describe the functionality of GC-MS, compare GC-MS with LC-MS, and assess the advantages and limitations of both GC-MS and LC-MS. He pointed out clinical applications of GC-MS such as broad spectrum drug screening and metabolic screening, and the role of GC-MS in emerging clinical needs such as metabolomics, biomarker discovery, and environmental biomonitoring.

SESSION III
INDUSTRY PERSPECTIVES

The Industry Perspectives session included corporate managers and scientists involved in the mass spectrometry revolution. Matthew Clabaugh represented SCIEX Diagnostics, highlighting the company's instrumentation and opportunities in the clinical space, including toxicology, endocrinology, and forensics. Mr. Clabaugh noted that applications requiring high sensitivity benefit from the technology available to increase ion formation and transmission to the detector. He also remarked on the uptake of mass spec tools in the clinical lab, including for molecular analysis.

Michael Scott, of Agilent Technologies, provided a perspective on change and how industry partners addressed challenges faced by clinical laboratories. He highlighted the need to be more productive or 'go faster'. His company focused on bringing products and tools to the clinical market that facilitate increased productivity with higher (up to 50 fold!) sensitivity. Another example offered by Dr. Scott was 'dynamic MRM' which intelligently changed the dwell times to go faster in acquisition. A natural consequence of 'going faster' on acquisitions was the data review bottleneck , driving iterations of MassHunter platform to reduce the number of data segments an analyst had to review to approve a batch.

Randall Julian, PhD, of Indigo BioAutomation, showed how innovative software solutions could help address data management and provide analytical insight on assay performance. Dr. Julian observed that standardizing data analysis and providing QC tracking results in fewer paper logbooks and checklists. Advanced algorithms supporting streamlined data processing allow for review by exception, further improving peak integration and quality review of chromatograms generated. Automation of chromatographic review and quality inspection enabled a more robust analysis pipeline for growing clinical laboratories.

Sherry Gregory, MBA, of Thermo Fisher Scientific demonstrated how Thermo Fisher Scientific has provided innovative solutions for clinical laboratories including MS integration, robust analyses and throughput to improve sample turn-around time with either a 2-channel and 4-channel multiplexed HPLC system. These are utilized successfully in many major nationwide reference labs, resulting in high throughput and cost effectiveness.

SESSION IV
OPEN FORUM: "CLINICS IN MASS SPEC ANALYSES"

Closing out conference day 1 was an open forum which gave participants an opportunity to with opportunity on technical and management issues from the audience. Discussion ranged from LDTs to translation of proteomic tests for clinical service to development of a list of candidate assays—both clinical and translational biomarkers (and panels)—that are most immediately needed in the clinical lab. This candidate list may inform future efforts to develop a road map for defining and achieving "Next Generation Clinical Mass Spec."

MASS SPEC SURVEY RESULTS
Last fall, AACC's Mass Spectrometry and Separation Sciences Division polled its members on their use of mass spec tools in the clinical and clinical research labs. Click here to see the results of that survey.

SESSION V –Translating Mass Spectrometry Tools to Clinical Practice

Day 2 of the program kicked off with the first Plenary Lecture on the role of assay specificity in improving diagnosis and treatment of endocrine disorders, delivered by Dr. Soldin. Emphasis was placed on the role of assay specificity in improving diagnosis and treatment of endocrine disorders, such as using free T3/T4 result and diagnosis of hypothyroidism. In his example, hypothyroid patients had been under diagnosed due to insufficient analytical sensitivity for immunoassays. Mass spectrometry was a powerful platform to fulfill this role where many immunoassays failed.

Dr. Soldin hammered home the point that correct diagnosis is dependent on reliable and accurate quantitation of disease markers, and in many cases mass spec tools are the most accurate direct detector of theses markers. One more example where the application of mass spectrometry and the expertise of the clinical lab can improve healthcare.

Session V also featured Yusheng Zhu, PhD (Medical University of South Carolina), who discussed the challenges in measuring of water soluble vitamins by UPLC-MS/MS. Water soluble vitamins cannot be stored in human body, being mostly eliminated through urine, and most labs are more accustomed to hydrophilic biological compounds. Dr. Zhu reported that the existing HPLC assays for determining water soluble vitamins remain labor intensive, requiring time consuming derivatization.

The session continued with a second Plenary Lecture, from newly named AACC President-Elect Dr. Bennett, who discussed the application of mass spectrometry in assessment of metabolic

disorders for newborn screening. Aspects related to screening and diagnosis using mass spectrometry were examined, using ornithine transcarbamylase deficiency as an example. Targeted organic acid profiling was used in the diagnosis of a variety of metabolic disorders with complicating issues related to the secondary metabolites from the microbiome and xenobiotics.

Dr. Dixon provided a look at advanced pain management with complementary pharmacogenomics data and conventional toxicology testing. The impact of CYP allele analysis on an individual's pharmacokinetics was discussed. Metabolism, clearance, confirmation rates, for specific alleles were discussed. Examples included drug dosing for warfarin, methadone, and clopidogrel.

Reimbursement expert Dr. Root provided an update on the changing reimbursement landscape for mass spectrometry testing, including regulations for LDTs and their impact on reimbursement. He outlined current codes related mass spectrometry assays then highlight critical changes for 2016. These codes were then contrasted with the G-codes used by Medicare for drug toxicology testing and therapeutic drug monitoring. Dr. Root advised that the advanced diagnostic tests (ADTs) developed and offered by a single laboratory would be coded according to specific CMS billing rules.

SESSION VI
"NEXT GENERATION" MASS SPEC ANALYSES FOR 2020

The final conference session began with a third Plenary Address, where Richard Caprioli, PhD (Vanderbilt University), reviewed tissue imaging as an emerging mass spec application in anatomic pathology.

Dr. Caprioli described a process where, after adding matrix to tissue biopsy, laser ablation of pixel array produces images at single m/z values integrated over all pixels. This can be performed from single cells to whole animal sections such as mouse kidney. Applications include studying the effect of diabetes on renal glomerulus, histology-directed analysis from frozen section and paraffin embedded tissue; and diagnosis of malignant melanoma. Dr. Caprioli suggested that mass spec imaging provides native molecular distribution, a discovery tool, high throughput, and compliments other imaging technologies.

Sean Bendall, PhD (Stanford University School of Medicine), continued the theme of mass spec translational applications with his discussion of massively multiplexed cellular analysis. Dr. Bendall related his lab's work in identifying additional parameters for bioanalysis through measurement of isotopic "tags." He provided an example where single cell proteomics was achieved by applying isotope-enriched lanthanide ions tagged to antibody (Ab) parameters, and then detecting those compounds via flow cytometry. Applications of this technology could include profiling of hematopoietic immune systems (which might correlated with recovery after surgery) or phenotype vs function in disease such as AML, among others. Another recent

development noted by Dr. Bendall is high dimensional imaging using lanthanide as “mass reporters”.

The “next generation” session theme was further emphasized in a presentation by Dr. Zhang, who offered an authoritative review of translational -omics biomarkers. Since biomarker research has been interdisciplinary, she explained, translation to clinical application has been confronted by complexity of human proteome, lack of coherent pipelines, and standardization in sample collection. In moving biomarkers from bench to bedside, pivotal contributions of mass spectrometrists using either MALDI or electro-spray platforms have been integral in the initial processes. Candidate biomarkers can be advanced for expensive and resource-intense validation. Central to successful validation is satisfactory sample quality ensured by addressing pre-analytic issues and intra-/inter-individual variabilities.

As the conference wound down, Dr. Rodriguez offered his observations on linking comprehensive genomics with comprehensive mass spec-based proteomic tools for advancing cancer research and precision medicine. The National Cancer Institute’s Clinical Proteomic Tumor Analysis Consortium, formed in 2012 and led by Dr. Rodriguez, focuses on elucidating proteogenomic complexity of tumors such as colorectal, ovarian and breast cancer. This well coordinated effort by multiple proteome characterization centers has established standardization with samples, supported by community resources – data portal, assay portal and antibody portal, which have been used on a global basis. The consortium has identified proteome subtypes for colorectal cancer by assessing global protein abundance, and used deep-proteomic analysis to show that pathway activation markers in ovarian cancer are correlated with patient survival.

In a final Q&A session with the audience, the program planners asked for thoughts on areas where improvements in mass spec technologies could enable translation of assays from bench to clinical use, and the characteristics of proposed Next Generation Clinical Mass Spectrometry in terms of faster turn-around-time, increased sensitivity and specificity, ease of application partially achieved by automation, harmonization of assays, and data portability via cloud computing.

It was thought that these developments would further enhance routine lab diagnostics as well as the applications for clinical and translational -omic biomarkers, including proteomics, metabolomics, lipidomics, peptidomics, and others. Thus, Next Generation Clinical Mass Spectrometry technologies coupled with innovative companion separation sciences are crucial for propelling the emerging practice of Precision Medicine.

MEETING PROGRAM

AACC/MSSS:

Mass Spectrometry and Separation Sciences for Laboratory Medicine
5th Annual Conference

*October 1-2, 2015 * Doubletree Hotel * Chicago, IL*

Developed in cooperation with AACC's Mass Spectrometry and Separation Sciences Division

DAY 1
Thursday, October 1

SESSION I
SCOPE OF MASS SPEC TESTING FOR LABORATORY MEDICINE/PATHOLOGY

Welcome and Program Open
AACC President David D. Koch, PhD
Emory University School of Medicine (Atlanta, GA)

Conference Overview
Steven H. Wong, PhD
Wake Forest University School of Medicine (Winston-Salem, NC)
Chair, Conference Organizing Committee

KEYNOTE ADDRESS
High Resolution Mass Spectrometry for Laboratory Medicine – Current Status and Perspectives in TDM-Tox
Professor Dr. Hans Maurer
Saarland University (Homburg, Germany)

Panel Discussion: Navigating Development and Implementation of Mass Spec-based LDTs
Saeed A. Jortani, PhD – Moderator
University of Louisville (Louisville, KY)

Henry Rodriguez, PhD, MBA
National Institutes of Health/National Cancer Institute (Bethesda, MD)

Alberto Gutierrez, PhD
U.S. Food and Drug Administration (Silver Spring, MD)

Steven J. Soldin, PhD
National Institutes of Health Clinical Center (Bethesda, MD)

Charles Root, PhD
CodeMap, LLC (Schaumberg, IL)

SESSION II

ESSENTIAL CONCEPTS IN CLINICAL MASS SPEC

Common Mistakes in LC-MS/MS Assay Development – What They Are and How to Avoid Them
Daniel T. Holmes, MD
St. Paul's Hospital Providence Health Care (Vancouver, British Columbia)

Sample Preparation – A Practical Approach for Robust Analyses
R. Brent Dixon, PhD
Physicians' Choice Laboratory Services (Rock Hill, SC)

Bringing Mass Spectrometry to Clinical Practices: Finance, Personnel and Interface Considerations
Victoria Y. Zhang, PhD
University of Rochester Medical Center (Rochester, NY)

Method Development and Validation for Certification in Accordance with CLSI C62-A and CAP Guidelines
Steven W. Cotten, PhD
The Ohio State University Wexner Medical Center (Columbus, OH)

Antifungals, TDM, and DAU Chiral Analysis by LC-MS/MS
Steven H. Wong, PhD
Wake Forest University School of Medicine (Winston-Salem, NC)

Complementary Role of GC/MS in the Clinical Laboratory and Beyond
Uttam Garg, PhD
Children's Mercy Hospitals and Clinics (Kansas City, MO)

SESSION III
INDUSTRY PERSPECTIVES

LC-MS/MS Development for the Clinical Lab – The SCIEX Perspective
Matthew Clabaugh
SCIEX Diagnostics (Framingham, MA)

Agilent Mass Spectrometry: Go Faster
Mike Scott
Agilent Technologies (Santa Clara, CA)

Big Data and Intelligent Algorithms in Diagnostic Testing
Randall Julian, PhD
Indigo BioAutomation (Indianapolis, IN)

Opportunities in Clinical Mass Spec
Sherry Gregory

Thermo Fisher Scientific (West Palm Beach, FL)

SESSION IV
OPEN FORUM: "CLINICS IN MASS SPEC ANALYSES"

End of Day 1

DAY 2
Friday, October 2

SESSION V
TRANSLATING MASS SPECTROMETRY TOOLS TO CLINICAL PRACTICE

PLENARY LECTURE
The Role of Assay Specificity in Improving Diagnosis and Treatment of Endocrine Disorders
Steven J. Soldin, PhD
National Institutes of Health Clinical Center (Bethesda, MD)

Measurement of Water Soluble Vitamins by UPLC-MS/MS
Yusheng Zhu, PhD
Medical University of South Carolina (Charleston, SC)

PLENARY LECTURE
Metabolomic Analysis for Newborn Screening and Diagnosis of Metabolic Disorders
Michael J. Bennett, PhD
Children's Hospital of Philadelphia (Philadelphia, PA)

Advanced Pain Management – Pharmacogenomics Data to Complement Oral Fluid Compliance Testing
R. Brent Dixon, PhD
Physicians' Choice Laboratory Services (Rock Hill, SC)

The Future of Reimbursement for Mass Spec-based LDTs
Charles Root, PhD
CodeMap, LLC (Schaumberg, IL)

SESSION VI
"NEXT GENERATION" MASS SPEC ANALYSES FOR 2020

SPECIAL LECTURE
Emerging Mass Spec Applications in Anatomic Pathology: Tissue Imaging
Richard M. Caprioli, PhD
Vanderbilt University (Nashville, TN)

Translating "-Omics" Biomarkers from Bench to Bedside
Victoria Y. Zhang, PhD
University of Rochester Medical Center (Rochester, NY)

Linking Massive DNA Sequencing with Mass Spec Proteomics for Advancing Cancer Research and Precision Medicine
Henry Rodriguez, PhD, MBA
National Institutes of Health/National Cancer Institute (Bethesda, MD)

Mass Spectrometry-based Single Cell Measurement
Sean C. Bendall, PhD
Stanford University School of Medicine (Stanford, CA)

Panel Discussion
Envisioning "Next Generation" Clinical Mass Spec-based Diagnostics in 2020
Steven H. Wong, PhD– Moderator
Wake Forest University School of Medicine (Winston-Salem, NC)

Richard M. Caprioli, PhD
Vanderbilt University (Nashville, TN)

Saeed A. Jortani, PhD
University of Louisville (Louisville, KY)

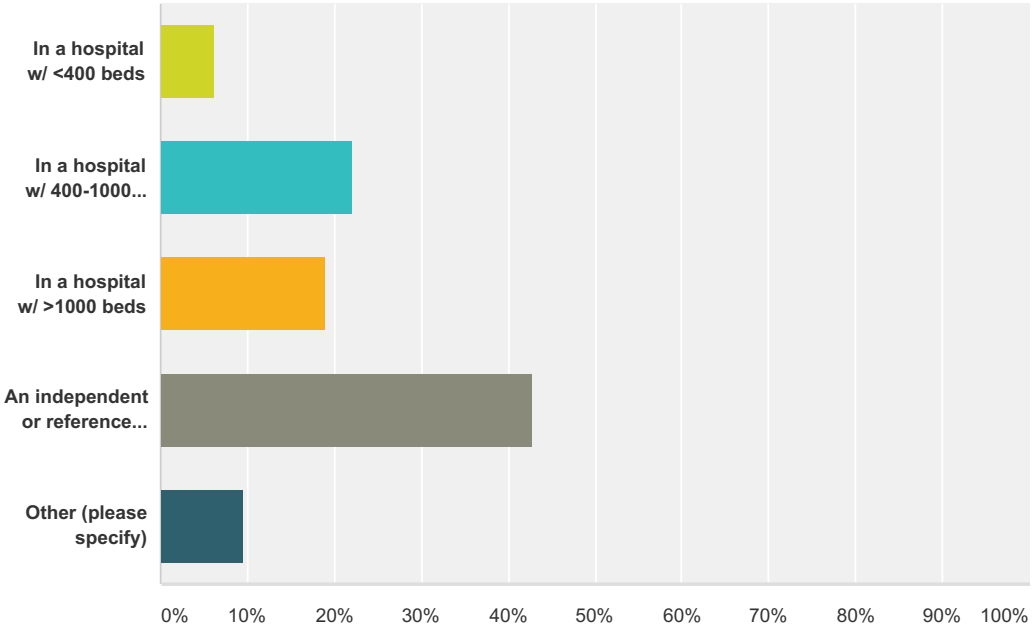
Angella Charnot-Katsikas, MD
The University of Chicago (Chicago, IL)

Henry Rodriguez, PhD, MBA
National Institutes of Health/National Cancer Institute (Bethesda, MD)

End of program

Q1 My lab is...

Answered: 63 Skipped: 0

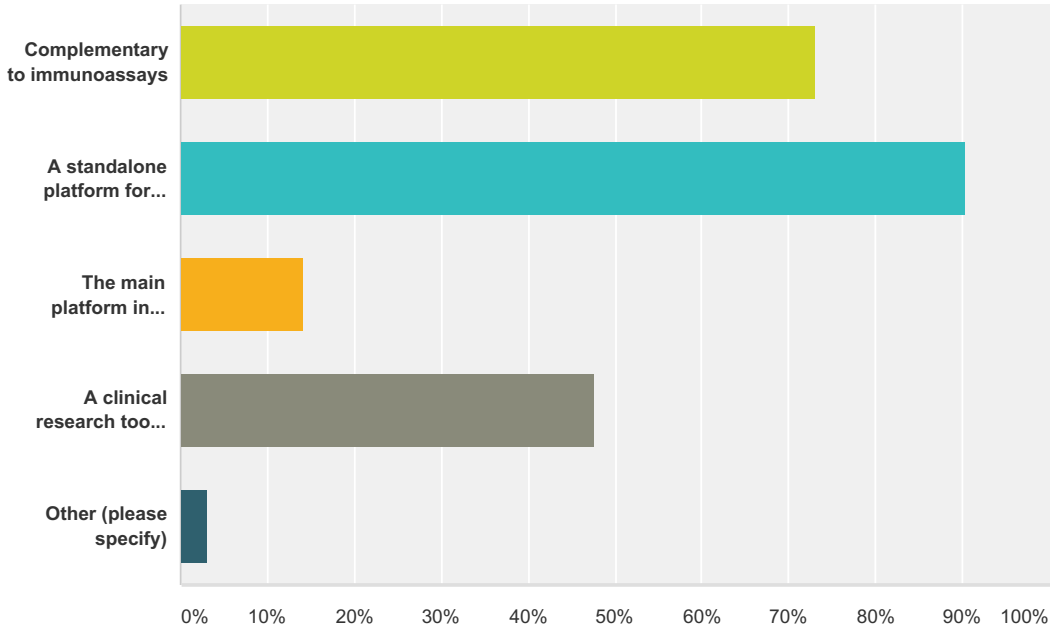


Answer Choices	Responses	
In a hospital w/ <400 beds	**6.35%**	4
In a hospital w/ 400-1000 beds	**22.22%**	14
In a hospital w/ >1000 beds	**19.05%**	12
An independent or reference lab	**42.86%**	27
Other (please specify)	**9.52%**	6
Total		**63**

#	Other (please specify)	Date
1	Off-site hospital core laboratory	9/25/2015 10:22 PM
2	Clinical trials laboratory	9/21/2015 11:28 PM
3	within Pharma	9/21/2015 3:48 PM
4	Instrument Vendor	9/19/2015 4:38 AM
5	Commercial diagnostic R&D	9/18/2015 8:51 PM
6	Contract Research Organization	9/18/2015 5:31 PM

Q2 Currently, do you view clinical mass spec applications being used as… (select all that apply)

Answered: 63 Skipped: 0

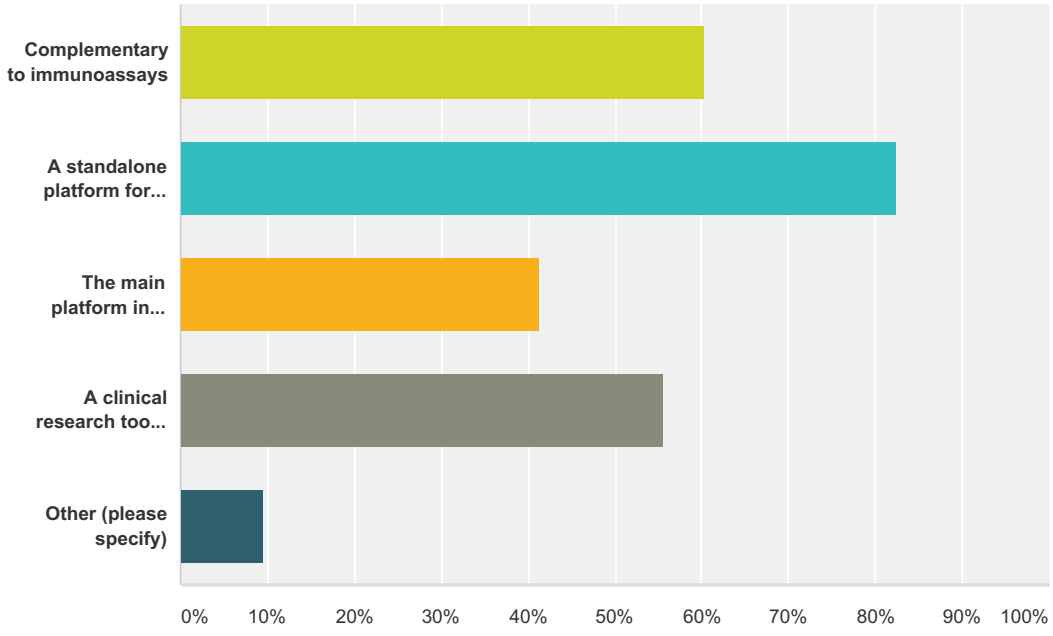


Answer Choices	Responses	
Complementary to immunoassays	**73.02%**	46
A standalone platform for new, lab-developed assays	**90.48%**	57
The main platform in clinical labs	**14.29%**	9
A clinical research tool for Omics investigations (proteomics, metabolomics, lipidomics, peptideomics, etc.).	**47.62%**	30
Other (please specify)	**3.17%**	2
Total Respondents: 63		

#	Other (please specify)	Date
1	Platform for routine testing	9/21/2015 3:48 PM
2	Most promising for TDM	9/18/2015 5:31 PM

Q3 In the year 2020, do you anticipate clinical mass spec applications being used as… (select all that apply)

Answered: 63 Skipped: 0

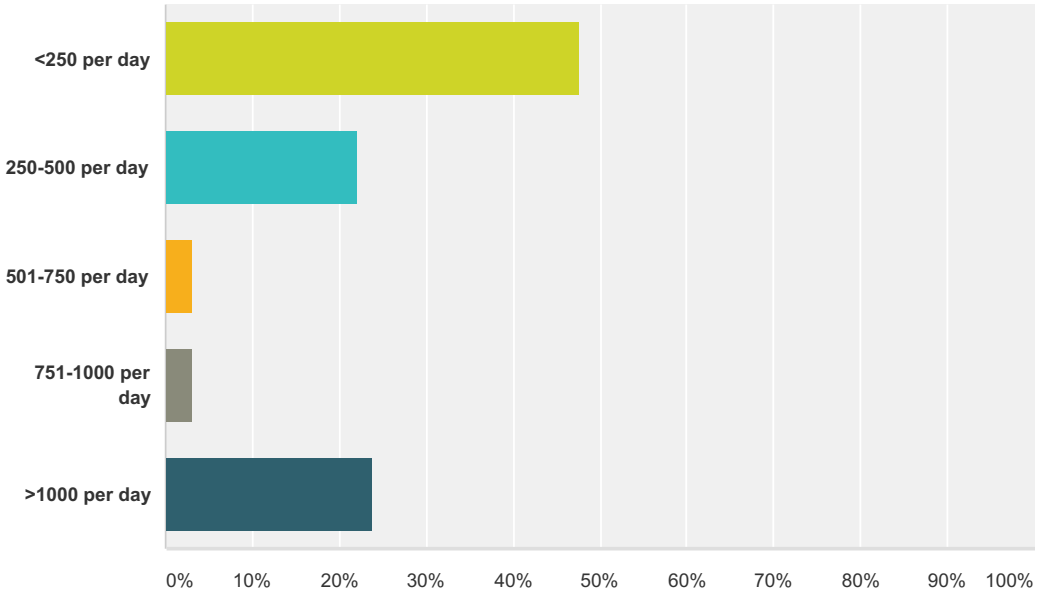


Answer Choices	Responses	
Complementary to immunoassays	**60.32%**	38
A standalone platform for new, lab-developed assays	**82.54%**	52
The main platform in clinical labs	**41.27%**	26
A clinical research tool for Omics investigations (proteomics, metabolomics, lipidomics, peptideomics, etc.)	**55.56%**	35
Other (please specify)	**9.52%**	6
Total Respondents: 63		

#	Other (please specify)	Date
1	maybe one of the main.... I don't think it will replace general chemistry and immunoassays in 5 years.	9/24/2015 12:57 PM
2	Applications in pathology expanded	9/21/2015 11:28 PM
3	One of the two main platforms. The other being molecular deep sequencing.	9/20/2015 10:27 PM
4	Replace immunoassays such as ToF	9/20/2015 12:30 AM
5	Clinic diagnostic omics tool-not just research	9/19/2015 8:34 PM
6	TDM	9/18/2015 5:31 PM

Q4 Currently, what is the total daily volume of assays your laboratory performs on a mass spec platform?

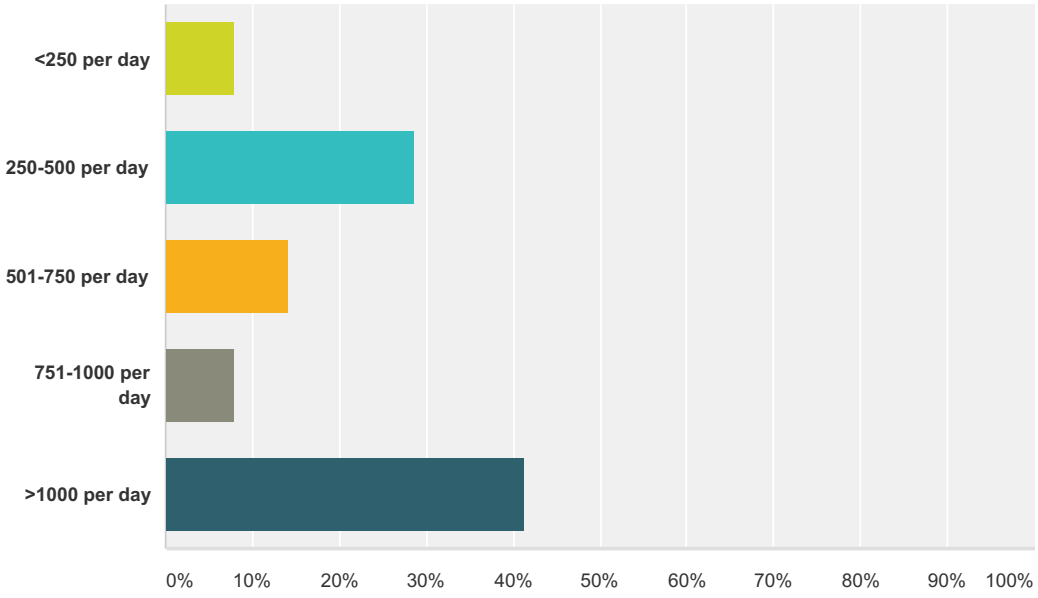
Answered: 63 Skipped: 0



Answer Choices	Responses	
<250 per day	**47.62%**	30
250-500 per day	**22.22%**	14
501-750 per day	**3.17%**	2
751-1000 per day	**3.17%**	2
>1000 per day	**23.81%**	15
Total		**63**

Q5 In the year 2020, what do you anticipate will be the total daily volume of assays your laboratory will perform on a mass spec platform?

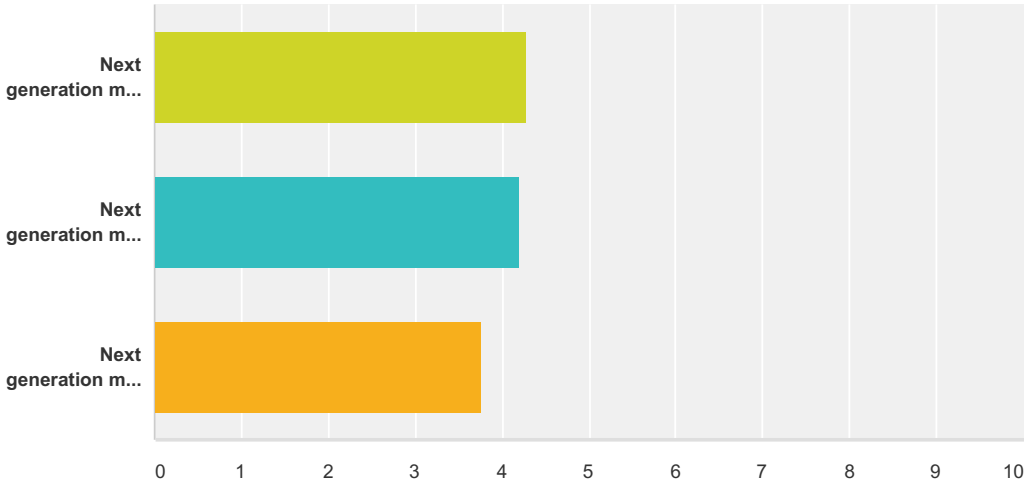
Answered: 63 Skipped: 0



Answer Choices	Responses	
<250 per day	**7.94%**	5
250-500 per day	**28.57%**	18
501-750 per day	**14.29%**	9
751-1000 per day	**7.94%**	5
>1000 per day	**41.27%**	26
Total		**63**

Q6 How important are standardization, harmonization, and comutability in the evolution of mass spec tools for the clinical laboratory?

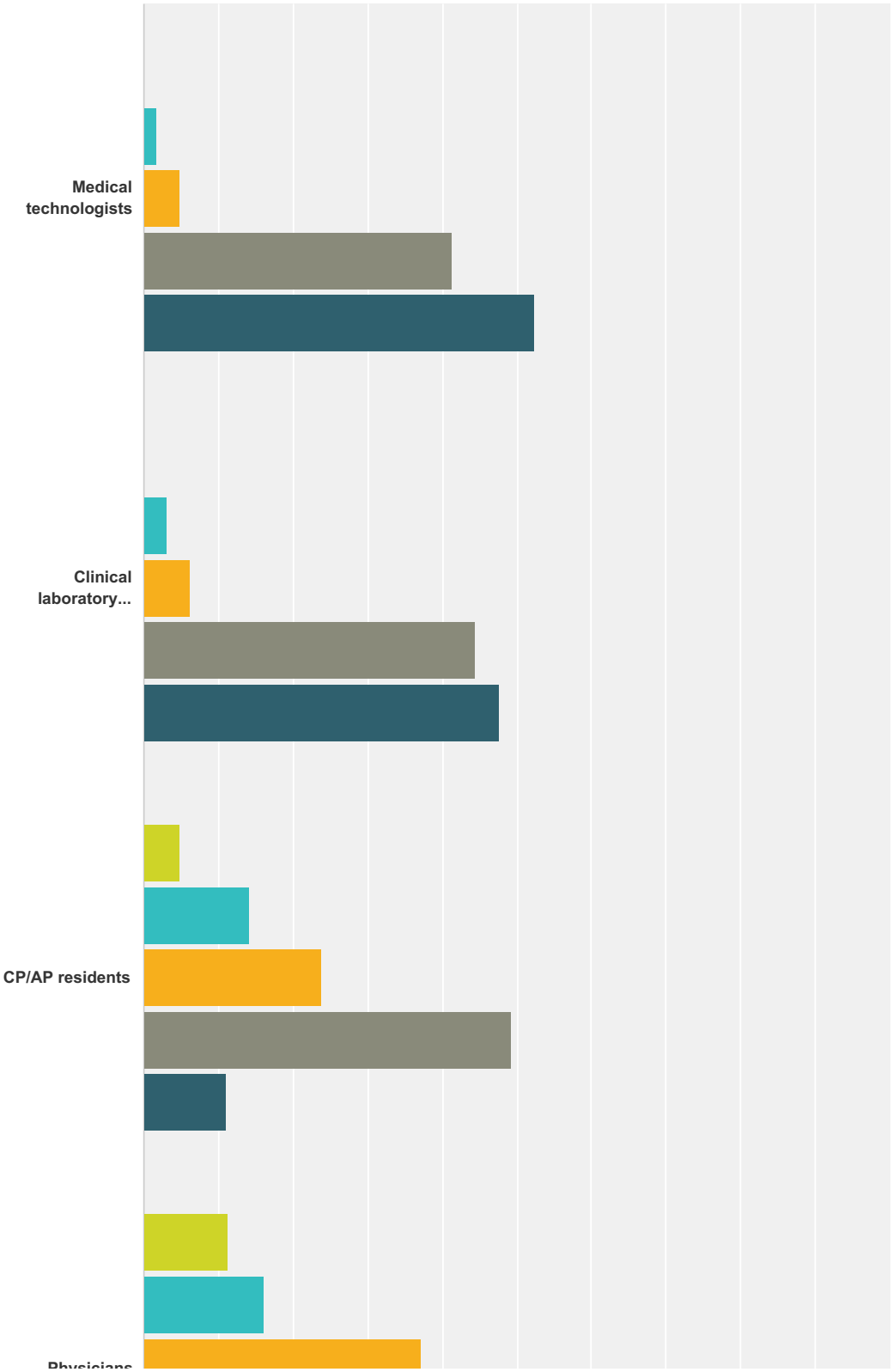
Answered: 63 Skipped: 0

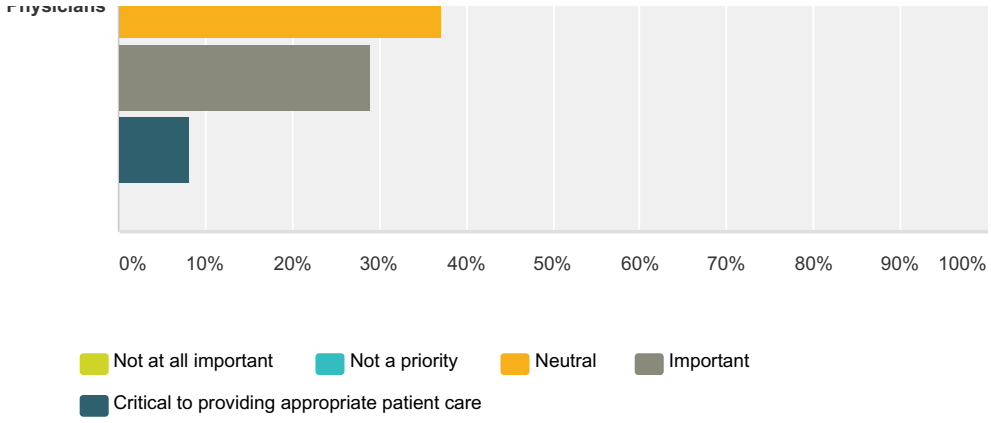


	Not at all important	Not a priority	Neutral	Important	Critical to providing appropriate patient care	Total	Weighted Average
Next generation mass spec tools should demonstrate minimal variability between platforms	**4.76%** 3	**0.00%** 0	**1.59%** 1	**50.79%** 32	**42.86%** 27	63	4.27
Next generation mass spec tools should address inter-laboratory variability	**1.59%** 1	**4.76%** 3	**4.76%** 3	**50.79%** 32	**38.10%** 24	63	4.19
Next generation mass spec tools should address the differences between data sets in biomarker discovery efforts	**1.59%** 1	**9.52%** 6	**25.40%** 16	**39.68%** 25	**23.81%** 15	63	3.75

Q7 How important is specialized training among the following groups to the adoption and proper operation of mass spec tools in the clinical laboratory?

Answered: 63 Skipped: 0



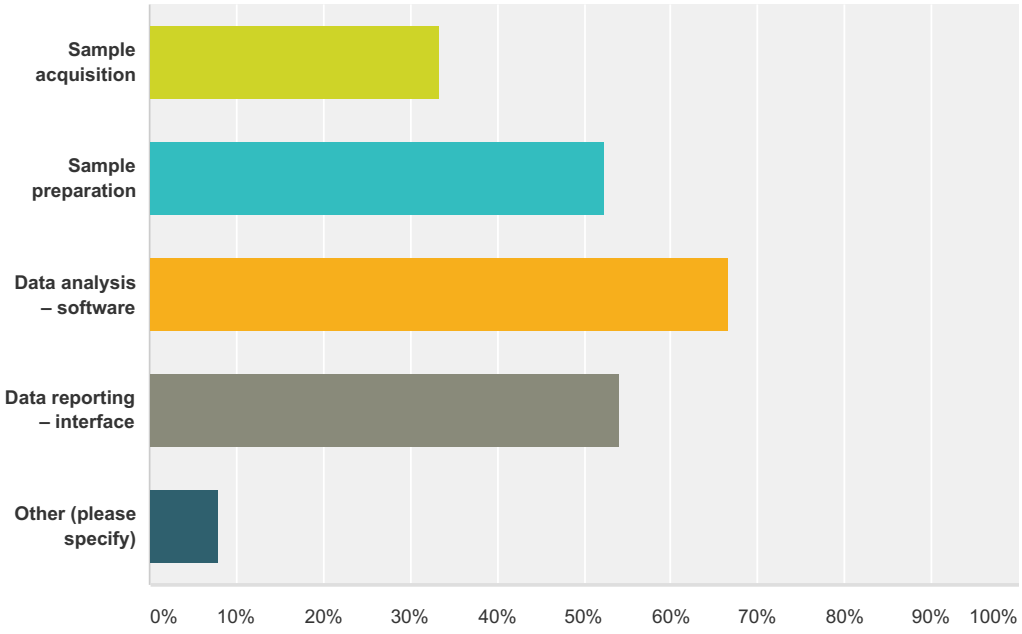


	Not at all important	Not a priority	Neutral	Important	Critical to providing appropriate patient care	Total Respondents
Medical technologists	**0.00%** 0	**1.59%** 1	**4.76%** 3	**41.27%** 26	**52.38%** 33	63
Clinical laboratory fellows	**0.00%** 0	**3.17%** 2	**6.35%** 4	**44.44%** 28	**47.62%** 30	63
CP/AP residents	**4.76%** 3	**14.29%** 9	**23.81%** 15	**49.21%** 31	**11.11%** 7	63
Physicians	**11.29%** 7	**16.13%** 10	**37.10%** 23	**29.03%** 18	**8.06%** 5	62

#	Other (please specify)	Date
1	AP\CP are in denial about changes in the future...	9/21/2015 2:06 PM
2	Training or knowledge of MS for MLTs is urgent. It is difficult to find adequate experience to not slow down insourcing mass spec assays to the lab.	9/21/2015 11:42 AM

Q8 Currently, which of the following laboratory processes are automated on your mass spec testing line? (select all that apply)

Answered: 63 Skipped: 0

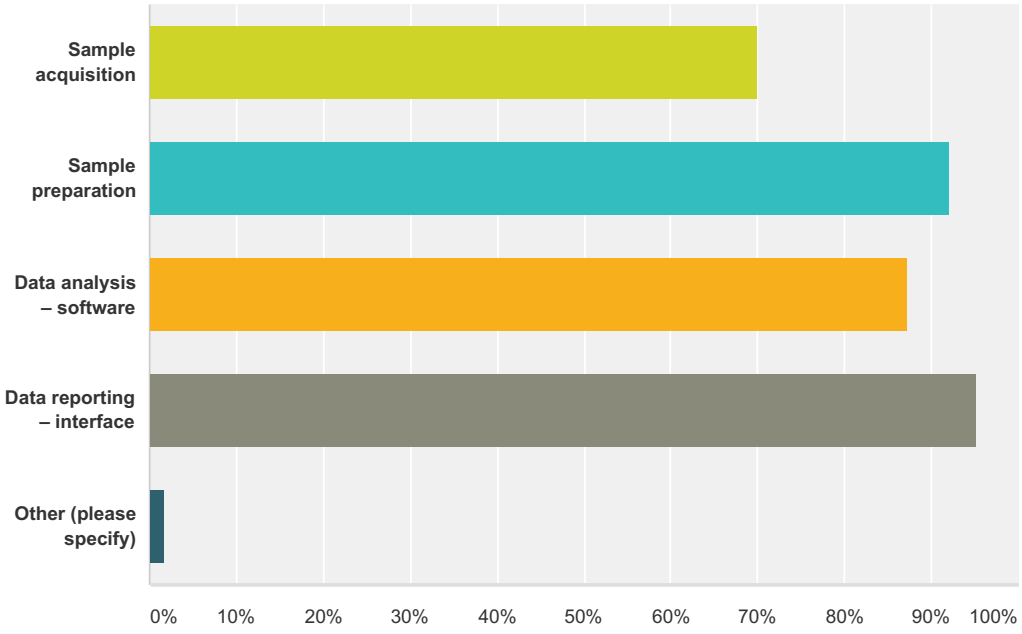


Answer Choices	Responses	
Sample acquisition	**33.33%**	21
Sample preparation	**52.38%**	33
Data analysis – software	**66.67%**	42
Data reporting – interface	**53.97%**	34
Other (please specify)	**7.94%**	5
Total Respondents: 63		

#	Other (please specify)	Date
1	none	9/23/2015 6:44 PM
2	Sent out for analysis	9/20/2015 8:01 PM
3	None	9/19/2015 11:44 AM
4	some data analysis	9/19/2015 1:52 AM
5	Don't have a mass spec in-house	9/18/2015 5:10 PM

Q9 In 2020, which of the following laboratory processes would you anticipate will be automated on your mass spec testing line? (select all that apply)

Answered: 63 Skipped: 0

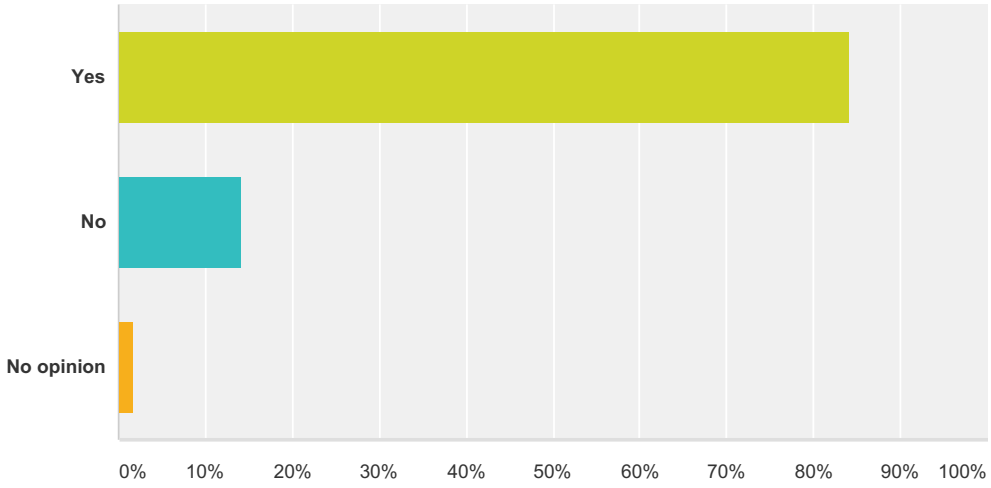


Answer Choices	Responses	
Sample acquisition	**69.84%**	44
Sample preparation	**92.06%**	58
Data analysis – software	**87.30%**	55
Data reporting – interface	**95.24%**	60
Other (please specify)	**1.59%**	1
Total Respondents: 63		

#	Other (please specify)	Date
1	Integration with LIS	9/21/2015 11:28 PM

Q10 In your opinion, would increased choices for automation and data management accelerate the adoption of mass spec tools for the clinical laboratory?

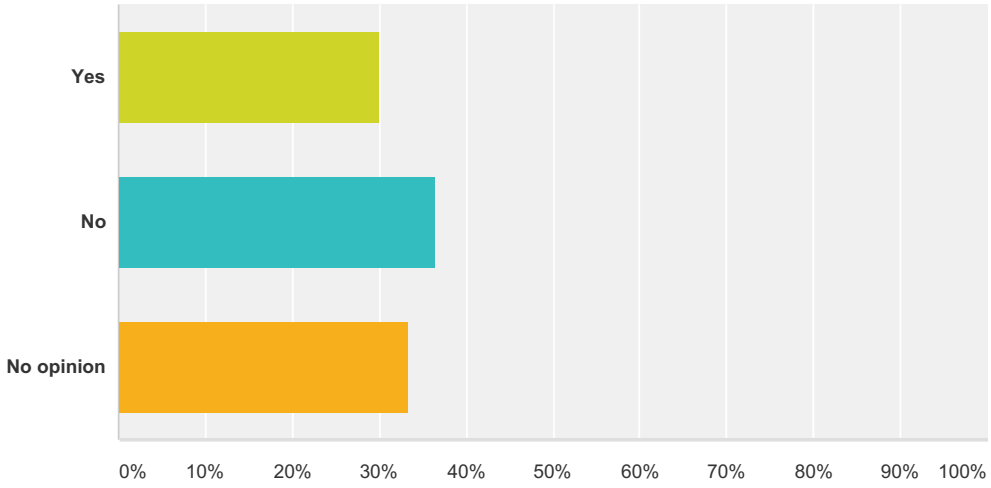
Answered: 63 Skipped: 0



Answer Choices	Responses	
Yes	**84.13%**	53
No	**14.29%**	9
No opinion	**1.59%**	1
Total		**63**

Q11 In your opinion, would cloud-based data management accelerate the adoption of mass spec tools for the clinical laboratory?

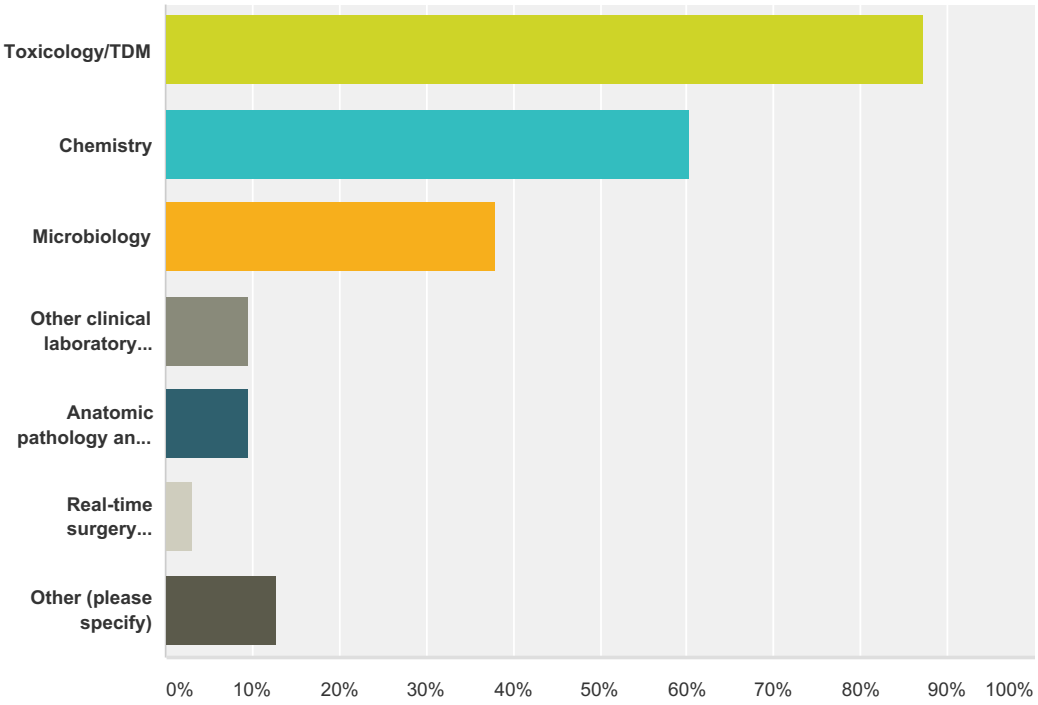
Answered: 63 Skipped: 0



Answer Choices	Responses	
Yes	**30.16%**	19
No	**36.51%**	23
No opinion	**33.33%**	21
Total		**63**

Q12 In which clinical environments does your facility currently use mass spec-based tools? (select all that apply)

Answered: 63 Skipped: 0



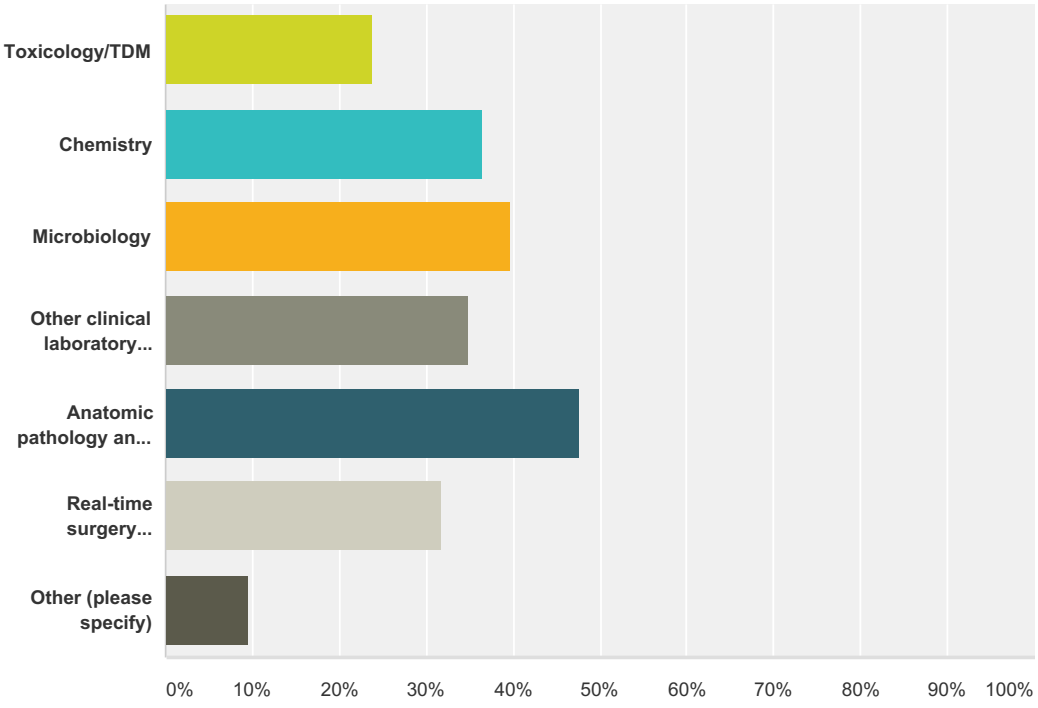
Answer Choices	Responses	
Toxicology/TDM	**87.30%**	55
Chemistry	**60.32%**	38
Microbiology	**38.10%**	24
Other clinical laboratory medicine – hematology and blood bank	**9.52%**	6
Anatomic pathology and tissue imaging	**9.52%**	6
Real-time surgery monitoring	**3.17%**	2
Other (please specify)	**12.70%**	8
Total Respondents: 63		

#	Other (please specify)	Date
1	immunoglobulins	9/24/2015 12:57 PM
2	Immunology	9/23/2015 4:44 PM
3	Endocrinology	9/21/2015 2:03 PM
4	PK sample analysis	9/21/2015 2:02 PM
5	metabolic disease	9/19/2015 8:34 PM
6	Protein panels	9/19/2015 11:23 AM

7	In the 3 areas checked, we collaborate with several other institutions, medical schools, companies	9/18/2015 5:31 PM
8	Don't use it	9/18/2015 5:10 PM

Q13 Of the environments where mass spec tools ARE NOT currently in use, which one(s) would you like to see this technology take hold by 2020? (select all that apply)

Answered: 63 Skipped: 0



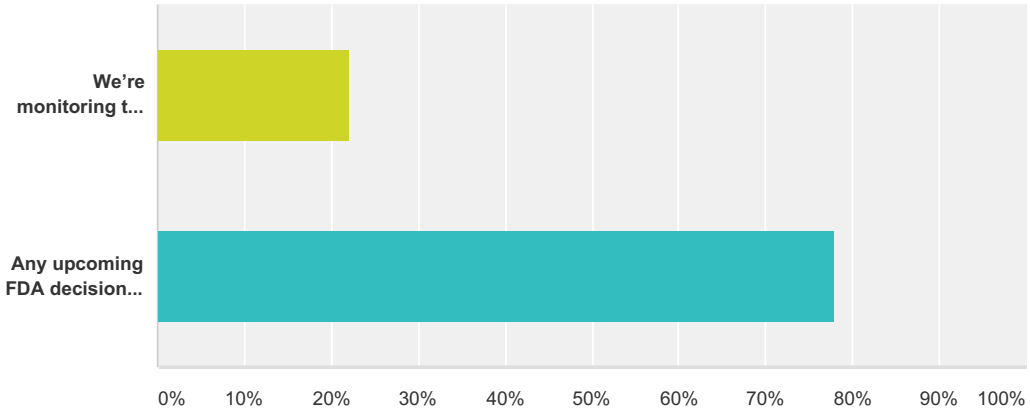
Answer Choices	Responses	
Toxicology/TDM	**23.81%**	15
Chemistry	**36.51%**	23
Microbiology	**39.68%**	25
Other clinical laboratory medicine – hematology and blood bank	**34.92%**	22
Anatomic pathology and tissue imaging	**47.62%**	30
Real-time surgery monitoring	**31.75%**	20
Other (please specify)	**9.52%**	6
Total Respondents: 63		

#	Other (please specify)	Date
1	More immunoglobulins work	9/24/2015 12:57 PM
2	Protein analysis	9/23/2015 4:44 PM
3	Peptide determinations	9/21/2015 2:14 PM
4	large molecule bioanalysis	9/21/2015 2:09 PM
5	comment for micro- AST instead of just ID	9/18/2015 5:58 PM

6	We would really value "random access" to allow for more stat apps v. large sample batches	9/18/2015 5:31 PM

Q14 Which of the following statements most suits your institution's stance toward potential FDA regulations regarding mass-spec IVDs?

Answered: 63 Skipped: 0



Answer Choices	Responses
We're monitoring the situation and will wait to see what happens in the next 12-24 months before deciding whether to expand our lab offerings in this area.	22.22% 14
Any upcoming FDA decisions may cause us to alter our processes, but we will continue to expand applications for our mass spec lab tools and will adapt accordingly to any new regulations.	77.78% 49
Total	63