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Rapid, Efficient, and Simple Sequence Confirmation of Synthetic Oligonucleotides Using Confirm Sequence With Targeted and Data-Independent Fragmentation Data

Chris Knowles, Michael Rühl, Güngör Hanci

Waters Corporation, BioSpring GmbH

Abstract

This application note demonstrates the efficiencies gained using the waters_connect™ CONFIRM Sequence application software for sequence confirmation of synthetic oligonucleotides when compared to a manual approach for both QTOF (Vion™ Mass Spectrometer) MS/MS and benchtop TOF (BioAccord™ Mass Spectrometer) MS^E (DIA) data.

Benefits

Automated and rapid sequence confirmation of synthetic oligonucleotides. Minimized risk of user errors with batch analysis compared to manual data processing. 21 CFR Part 11 for product quality control.

Introduction

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Synthetic oligonucleotides have emerged in recent years as a powerful alternative to small molecule and protein therapeutics.[1] Increasing amounts of oligonucleotide drugs reaching the market require analytical methods that can provide reliable and robust quality control.[2,3] The two major categories of synthetic oligonucleotide reaching the market are antisense oligonucleotides (ASOs) and silencing RNAs (siRNAs).[4,5] Both modalities typically employ oligonucleotides smaller than 50 monomers in length.

Mass Spectrometry has proven to be the gold standard approach for characterizing such molecules, especially when modified nucleosides and backbones are utilized.[6-8] Characterizing the sequence of a synthetic oligonucleotide via targeted MS/MS fragmentation is the preferred approach with well understood and annotated fragmentation pathways.[9] Recent investigations into the relationship between oligonucleotide size, precursor charge state and collision energy allow for optimized conditions to generate the sequence confirmation required for regulatory submission.[10]

Two key limitations to this workflow are the manual processing of resulting complex datasets, as well as the limited availability of experienced analysts required to generate high quality MS/MS fragmentation on the mass spectrometers typically used for discovery and early development. Both of these limitations restrict the downstream adoption of MS/MS based sequence confirmation in manufacturing and quality control laboratories.

Here it is demonstrated that the rapid turnaround of high-quality sequence confirmation data on CpG7909, a modified synthetic oligonucleotide therapeutic, using the waters_connect™ CONFIRM Sequence application software.[11] Further demonstration of the potential for routine quality control of synthetic oligonucleotide manufacturing with a benchtop BioAccord™ System (UPLC™-TOF-MS) that was designed for users with limited MS expertise. These results are compared with MS/MS data taken from a QTOF MS (Vion™ MS, an instrument typically used for oligonucleotide characterization.

Manually predicting the expected fragment ions of a synthetic oligonucleotide is challenging. The library features within the CONFIRM Sequence application allow users to create, manage and store custom oligonucleotide sequences using structural information down to the subcomponent level (bases, sugars and linkers). The default monomer entries that come preinstalled with the application are sufficient to create CpG7909, but the library is highly customisable in monomer creation and setting custom fragmentation rules if required.

Several hours of labor-intensive manual processing was reduced to minutes of automated data processing. Reviewing the results was made simple with graphical representation, automated flagging of problematic data areas, and efficient curation of results. The use of a bespoke Targeted Isotope Clustering algorithm in CONFIRM Sequence provides high confidence with detailed fragment ion matching annotated directly on the raw data.

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Experimental

Sample Description

CpG7909, sequence dT*dC*dG* dT*dC*dG* dT*dT*dT* dT*dG*dT* dC*dG*dT* dT*dT*dT* dG*dT*dC* dG*dT*dT (d refers to a deoxyribonucleic acid, * refers to a phosphorothioate backbone modification) was synthesized in house at BioSprings via solid phase synthesis. CpG7909 was diluted with water to a final concentration of 0.5 mg/mL.

LC Conditions

LC system:	ACQUITY™ UPLC™ binary solvent manager
Optical detection:	TUV
Column(s):	ACQUITY UPLC Oligonucleotide BEH™, 130 Å, C_{18} 1.7 µm 2.1 x 100 mm
Column temperature:	60 °C
Injection volume:	2 µL
Flow rate:	0.3 mL/min
Mobile phase A:	7 mM TEA and 80 mM HFIP dissolved in water
Mobile phase B:	3.5 mM TEA and 40 mM HFIP in 50% methanol 50% water
Gradient:	The LC gradient used was as follows: initial conditions 10 %B buffer for 0.2 min, from 0.2 min to 2.0 min from 10 %B to 100 %B, from 2.00 to 2.20 min 100 %B, from 2.20 to 2.30 min from 100

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%B to 10 %B and from 2.30 min to 3.00 min 10 %B. Column temperature was 60 °C with a flow of 0.3 mL/min.

MS Conditions

The BioAccord™ System RDa™ was used in full scan with fragmentation mode in the low mass range acquisition range from 50–2000 *m/z*. ESI Polarity was set to negative with a scan rate of 1 Hz. Cone voltage was adjusted to 50 V and the fragmentation cone voltage was varied, starting from 60 or 70 V ramped up to 100 to 120 V. The capillary voltage was set to 0.8 kV, the desolvation temperature to 550 °C and the desolvation gas flow to 800 L/h.

The Vion IMS QTOF was used in ESI negative polarity with standard transmission in the sensitivity mode. Source type was set to ESI with a source temperature of 120 °C, a desolvation temperature of 400 °C, a desolvation gas flow of 800 L/h, a cone gas flow of 50 L/h, a capillary voltage of 2.0 kV, a sample cone voltage of 60 V and a source offset voltage of 100 V. MS/MS acquisition was set in the range of 50 to 2000 *m/z*, a scan time of 0.5 s and low precursor resolution. The following precursor ions (values in *m/z*) were selected: 640.5 (charge state: 12-), 698.7 (charge state: 11-), 768.8 (charge state: 10-), 854.4 (charge state: 9-), 961.2 (charge state: 8-) and 1098.7 (charge state: 7-). The collision energy was varied from between 10, 15, 20, 25, and 30 V for each precursor ion.

Processing Settings

CONFIRM Sequence method settings (MS/MS)

PPM error:	20
Intensity cutoff (counts):	20
Isotope similarity threshold:	65
Isotope intensity threshold:	65

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CONFIRM Sequence method settings (MSe)

PPM error:	30
Intensity cutoff (counts):	200
Isotope similarity threshold:	65
Isotope intensity threshold:	55

Results and Discussion

Sequencing of oligonucleotides using QTOF MS involves charge state selection and collision energy screening for optimal results. Depending on the charge state, the collision energy needs to be optimized to avoid low energy partial fragmentation and high energy over-fragmentation (internal breaks of the sequence and fragmentation of fragments).

For our test molecule CpG7909, an immunostimulatory adjuvant synthetic oligonucleotide therapeutic, the observations of increased energies required for lower charge states made by Gawlig and Rühl (2023) are also seen here for both MS/MS (Table 1) and MSe (Table 2) analysis.[10]

An additional strategy for fragmentation tuning is to target the amount of residual precursor that is present in the fragmentation data. Without residual precursor signal present, it is likely that the molecule has been over fragmented, or that the charge state is unstable in the given conditions. A reduction of %precursor value displayed in CONFIRM Sequence correlates with increasing collision energies in all cases and can also indicate that increased collision energy has caused over fragmentation. Taken together, the presence of a precursor with the highest collision energy for a given charge state can indicate the optimum settings, and the %precursor metric can be used to obtain this optimized result.

With MSe fragmentation, the highest collision energy that provides the minimum amount of residual precursor (5–10%) is optimal in the data shown here. With MS/MS fragmentation the optimum conditions are charge state dependant. Collision energies that show decreased sequence coverage and %precursor compared to a lower

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energy on the same charge state is an indication of over fragmentation. Optimising the conditions for an MS/MS acquisition should attempt to increase the collision energy until the %precursor is below 60%, and continue to increase the energy until the lowest %precursor is obtained that gives increased sequence coverage compared to a lower energy.

Manual processing vs CONFIRM Sequence
Reviewing data from a manual workflow is time consuming and can be prone to user error. The review steps in CONFIRM Sequence are designed to present sequence coverage in a way that is easy to understand and provides features for manually reviewing each fragment ion match directly annotated on the raw data.

Data processing in CONFIRM Sequence is rapid (less than five minutes to process all the data shown here), and can be pre-configured by an expert user to allow for less experienced users to process large datasets under the expert's supervision. Furthermore, the waters_connect™ Software platform is compliance-ready, including the necessary reporting, data integrity controls, and method versioning required for regulatory adherence in quality assurance lab operations.

The CONFIRM Sequence app provides high fidelity fragment ion matching and removes isobaric fragment assignments from coverage calculations. This leads to fewer false positive assignments and a reduced burden for manual data verification by a user.

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Charge state	Conditions		CONFIRM Sequence results (MS/MS)	
	Set mass	Collision energy (V)	% Coverage	% Precursor
12-	640.5	10	83	10
	640.5	15	46	–
	640.5	20	25	–
	640.5	25	17	–
	640.5	30	13	–
11-	698.7	10	83	37
	698.7	15	67	–
	698.7	20	42	–
	698.7	25	17	–
	698.7	30	17	–
10-	768.8	10	92	72
	768.8	15	92	10
	768.8	20	50	–
	768.8	25	29	–
	768.8	30	17	–
9-	**854.4**	**10**	**100**	**92**
	854.4	**15**	**100**	**47**
	854.4	20	67	–
	854.4	25	38	–
	854.4	30	17	–
8-	961.2	10	38	100
	961.2	15	92	86
	961.2	20	67	26
	961.2	25	38	–
	961.2	30	29	–
7-	1098.7	10	0	100
	1098.7	15	33	98
	1098.7	20	54	63
	1098.7	25	46	–
	1098.7	30	25	–

Table 1. MS/MS sequence confirmation data of CpG7909 processed with CONFIRM

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Sequence. Targeted MS/MS data for charge states 7- to 12- were generated under collision energies ranging from 10 V to 30 V. Data for each acquisition was processed in an automated workflow using raw data matching of predicted isotope clusters via the targeted Isotope Clustering™ algorithm within CONFIRM Sequence. Identification of the precursor in the high energy channel is noted with %precursor value, which indicates fragmentation efficiency. 100% sequence coverage was attained for charge state-9 with collision energies of 10 and 15 V respectively. lower charge states reported higher sequence coverage with increased energy compared to higher charge states. In all cases the highest collision energies reduced the residual precursor below detectable limits, which indicates over fragmentation.

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Conditions	CONFIRM Sequence results (MSe)		
Energy ramp (V)	% Coverage	% Precursor	Charge states found
60–100	83	20	4- 5- 6- 7- 8- 9
60–110	83	15	4- 5- 6- 7- 8- 9
60–120	83	14	4- 5- 6- 7- 8- 9
70–100	83	10	4- 5- 6- 7- 8
70–110	**92**	**8**	**4- 5- 6- 7- 8**
70–120	75	7	4- 5- 6- 7- 8

Table 2. Sequence confirmation data from BioAccord MSe processed in CONFIRM Sequence. MSe data generated using the BioAccord system with various collision energy ramps was processed in an automated workflow using raw data matching of predicted isotope clusters via the targeted Isotope Clustering™ algorithm within CONFIRM Sequence. Identification of the precursor in the high energy channel is noted with the %precursor value. The precursor charge states identified is also shown. The highest coverage (91.67% rounded up to 92% in this table) was found with an energy ramp of 70–110V which has a %precursor of 8%. Increasing the collision energy ramp to 70–120 reduced the % precursor to 7% and sequence coverage to 75%.

Enhanced matching fidelity

Complex fragmentation data of modified synthetic oligonucleotides across a large mass range can take considerable time to deconvolve (up to 20 minutes per spectrum) and requires some expertise to manually investigate the deconvolved results and assign predicted fragments based on mass.

The CONFIRM Sequence app employs an intelligent Targeted Isotope Clustering algorithm to alleviate the challenges of a manual and untargeted approach. CONFIRM Sequence processes data in a targeted fashion, where the predicted isotope clusters for each fragment ion are searched directly against the raw data and matched based on a variety of scoring metrics. Matches to the raw data can be reviewed in the application to support fragment ion assignments.

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Furthermore, a set of logical rules are applied that govern how a set of fragment ions can be used to confirm a monomer assignment. One example of this is with the use of base loss fragmentation ions (*e.g* a-b-ions), where an ion has undergone gas phase ion/ion rearrangements post collision induced dissociation fragmentation that results in a loss of the base component. Because of this loss, it is not reasonable to use only the base loss ion to confirm the presence of a monomer that is directly 5′ to the fragmentation site. The logic in CONFIRM Sequence dictates that it should be used in the n-1 series of fragment ions instead (*e.g*. an a-b3 ion should not be used to confirm the presence of the 3rd monomer, instead it should be used in the [x-]2 ion series). This assignment logic used in CONFIRM Sequence is designed to ensure that the monomers confirmed within the application are based on predictable fragmentation modelling and observable data. There are help files in the software that explain each of the monomer confirmation rules in more detail.

Ambiguities

CpG7909 has various predicted fragment ions that are isobaric, and using them to confirm multiple sections of the sequence would be disingenuous. CONFIRM Sequence flags these ambiguities and removes them from the initial sequence confirmation set, but provides users the option to add them back in when reviewing the data. As an example, we added back in the w1- ion, which is isobaric with d1- due to the 5′ end and 3′ end monomers being identical. In this case because these monomers are both at the end of the sequence, we reason that allowing for this ambiguous match is acceptable. However, there are multiple isobaric fragment ions within the CpG7909 sequence that cannot be reasonably used to confirm the sequence, making parts of the sequence difficult to cover. This does however highlight the hazard of performing manual sequence confirmation work, where these ambiguities are less easily identified.

Comparing targeted MS/MS to data-independent acquisition (MSe)

CONFIRM Sequence is able to demonstrate 100% sequence coverage in a single MS/MS fragmentation spectra and 92% using data-independent fragmentation based acquisition (DIA) on the BioAccord System. The benefit of MSe (DIA) acquisition is a simplified setup that fragments all precursor ions with a collision energy ramp designed to match the optimized CE settings which have to be pre-determined using targeted MS/MS acquisition. This removes the need to pre-select target precursor charge states and the experimental design to optimize the collision energy.

To assist the optimization of MS/MS experiments the CONFIRM Sequence App presents results for each MS/MS acquisition together in an overview table (Figure 1), where the combined sequence coverage is displayed alongside a table which displays the individual contributions from each spectra. This allows for instant

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determination of the optimum fragmentation conditions across all data, and provides insight on which charge state requires more / less energy to achieve optimum conditions.

Reviewing the fragmentation results for individual analyses in the CONFIRM Sequence app is streamlined with annotated spectra for each fragment ion assignment, which can be navigated through and rejected if necessary (Figure 2). Ambiguous fragment ion assignments are also flagged for review.
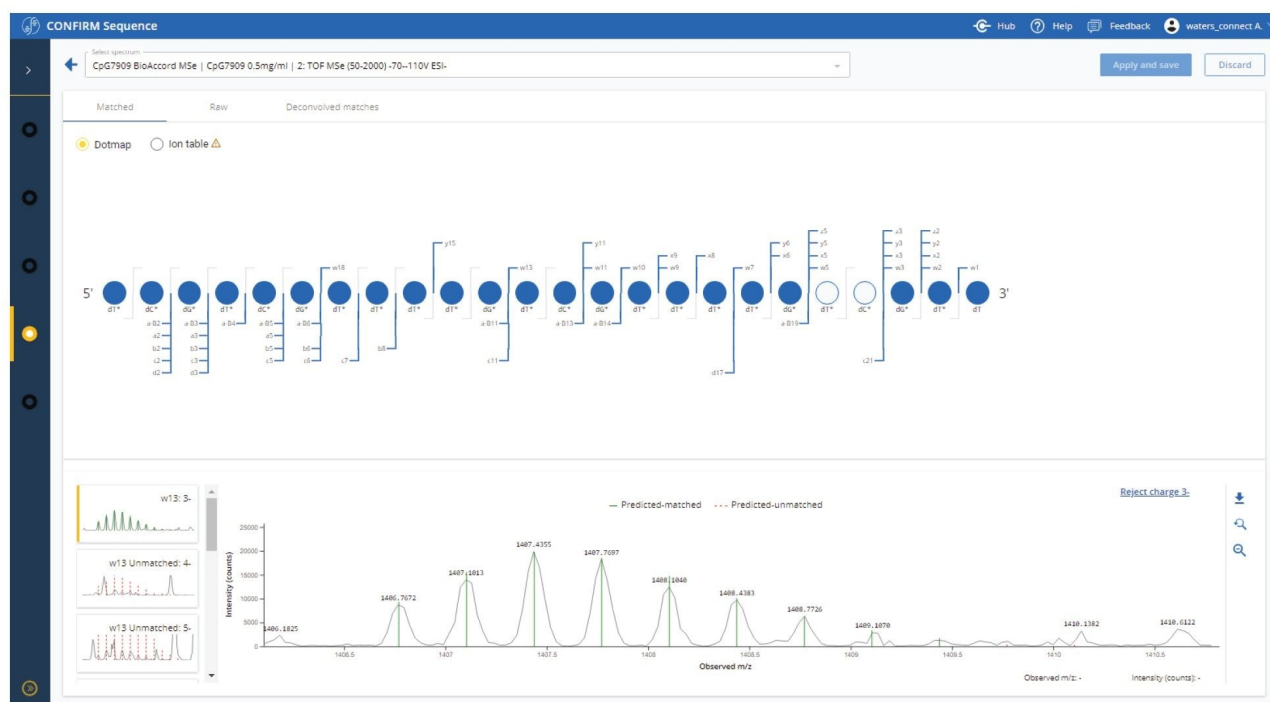
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Figure 1. A screenshot of the CONFIRM Sequence application results overview page, showing the results . The data shown here is the results for an MS/MS experiment on CpG7909 with targeted precursors (m/z) at 640.5 (-12), 698.7 (-11), 768.8 (-10), 854.4 (-9), 961.2 (-8), and 1098.7 (-7). The collision energy was varied from between 10, 15, 20, 25 and 30 V for each precursor ion. An overview of combined sequence coverage is displayed in a Dotmap™ view, where the sequence is represented with colored orbs and fragment ion 'legs', indicating that the monomer is confirmed (blue orb) based on the fragment ions that have been matched in the raw data. Unconfirmed monomers are represented with a white orb.

The table presents results for individual MS/MS spectra and includes information on the Injection / channel name, the retention time, acquisition details, precursor observed mass, precursor charge states identified, the residual %precursor ions detected and the % coverage supplemented with a simplified Dotmap™ representation of confirmed monomers. Ordering this table by sequence coverage showed that two individual MS/MS conditions were able to produce 100% sequence coverage (charge state -9 at 10V and 15V collision energy). The % precursor drops from 91.62% at 10V to 46.81% at 15V. The precursor was not detected for this charge state when 20v was used, which indicates that over fragmentation has occurred at this energy.

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Figure 2. A screenshot of the CONFIRM Sequence application results drilldown page from MSe experiments on CpG7909. The drilldown is presenting results from the optimum MSe conditions at 70–110 that produced 91.67% sequence coverage. Individual ions on the Dotmap™ can be selected to display annotated chromatograms of matching in the the raw data. In this example the w13- ion is selected and the matched charge state 3- is displayed. Green lines indicate the expected profile of matched fragment isotopes. All charge states between -1 and -10 are viewable, with red dotted lines indicate the expected profile of unmatched isotopes. Each fragment ion charge state can be reviewed and rejected if necessary. The data can also be displayed as a table, an annotated chromatogram for the raw data or as an annotated deconvolved mass chromatogram. CpG7909, sequence dT*dC*dG* dT*dC*dG* dT*dT*dT* dT*dG*dT* dC*dG*dT* dT*dT*dT* dG*dT*dC* dG*dT*dT (d refers to a deoxyribonucleic acid, * refers to a phosphorothioate backbone modification).

Conclusion

The CONFIRM Sequence waters_connect™ application works well for both targeted MS/MS and data-

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independent fragmentation data.

Manual deconvolution and fragment assignment for synthetic oligonucleotide sequence confirmation is time consuming, more prone to user error, and highly dependent on user experience. In contrast, the automated CONFIRM Sequence workflow produced comparable results to manual workflows, but includes the benefits of automated fragment matching, matching directly on the raw data, improved processing speed, and consideration of isobaric ambiguities in the sequence coverage results.

The BioAccord extends the usability of the automated data processing for regulated manufacturing and quality labs, by providing a small footprint and cost-effective LC-MS system designed for non-MS experts on a compliance-ready platform. The CONFIRM Sequence App is capable of processing and annotating the DIA fragmentation data from BioAccord System and enabling high confidence assignments in an automated workflow. Good quality high energy data obtained from this TOF MS system makes it an attractive alternative to QTOF or other high-end mass spectrometry.

QTOF systems that possess greater fragmentation control and ultimate sensitivity for the initial characterization of a molecule may prove overkill for such routine sequence confirmation challenges. The utility of the CONFIRM Sequence App for supporting both workflows, enables a reduced training burden and for smoother transitions of molecules and methods from development to manufacturing and QC organizations.

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Acknowledgements

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