

Main specifications for the DS3000

Main unit specifications

Item	Details
Number of capillaries	4
Capillary length	36 cm
Sample format	8-tube strip × 4
Device control	Touch panel PC
Number of Dyes	6
Application	Sequencing analysis / Fragment analysis
Size	400 (W) × 600 (D) × 600 (H) mm
Weight	45 kg
Performance guarantee temperature	15 – 30°C
Performance guarantee humidity	20 – 80% RH (no condensation)
Power input	100 – 240 ±10% VAC, 50/60 Hz
Rated power	260 VA
Supported secondary analysis software	<ul style="list-style-type: none"> <li>• Mutation Surveyor (SoftGenetics, LLC, sold separately)</li> <li>• GeneMarker (SoftGenetics, LLC, sold separately)</li> <li>• GeneMarker HID (SoftGenetics, LLC, sold separately)</li> </ul>

Run module specifications

Run Module	Application	Polymer type	Contiguous Read Length*1 (bp, QV20 CRL)	Average run time (minutes)
Fast_Sequence36_Polymer7	Sequencing analysis	Polymer7	≥600	≤32
Standard_Sequence36_Polymer7	Sequencing analysis	Polymer7	≥700	≤60
BDx_Fast_Sequence36_Polymer7	BDx sequencing analysis	Polymer7	≥600	≤32
BDx_Standard_Sequence36_Polymer7	BDx sequencing analysis	Polymer7	≥700	≤60

Run Module	Application	Polymer type	Average run time (minutes)	Sizing precision*2 (bp, 50 – 400 bp)
Fragment_Analysis36_Polymer7	Fragment analysis	Polymer7	≤35	NA
Fragment_Analysis36_Polymer4	Fragment analysis	Polymer4	≤44	<0.16

\*1 Contiguous Read Length (bp, QV20 CRL) is measured with BigDye® Terminator v3.1, Sequencing Standard Kit (Thermo Fisher Scientific, sold separately)

\*2 Sizing precision (bp, 50-400 bp) is measured with PowerPlex™ ES17 Fast Allelic Ladder and WEN ILS 500 ESS, (Promega®, sold separately)

• BigDye is a registered trademark of Thermo Fisher Scientific Inc.

• Promega, PowerPlex is a registered trademark of Promega Corporation.

Consumables specifications

Product name	Part number	Details	Remarks
Capillary Cartridge 36 cm	613-0330	1 pcs	Storage temperature: 15 – 30°C
Buffer	613-0252	Anode Buffer × 2 cartridges Cathode Buffer × 2 cartridges	Storage temperature: 2 – 10°C
Polymer7	613-0251	4 cartridges	Storage temperature: 2 – 10°C
Polymer4	613-0250	4 cartridges	Storage temperature: 2 – 10°C
Septa for Cathode Buffer Cartridge	613-7231	10 pcs	
Retainer for Cathode Buffer Cartridge	613-7233	4 pcs	
Septa for 8 well tubes	613-7230	24 pcs	
Base and Retainer for 8 well tubes	613-7232	4 pcs	
Anode Electrode Assembly	613-7263	1 pcs	

Specifications in this catalog are subject to change with or without notice, as Hitachi High-Tech Corporation continues to develop the latest technologies and product for its customers.

CAUTION: For correct operation, follow the instruction manual when using the instrument.

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Hitachi High-Tech Corporation

Tokyo, Japan  
[www.hitachi-hightech.com/global/science/](http://www.hitachi-hightech.com/global/science/)  
 Toranomom Hills Business Tower, 1-17-1 Toranomom, Minato-ku,  
 Tokyo 105-6409, Japan  
[customercenter.ev@hitachi-hightech.com](mailto:customercenter.ev@hitachi-hightech.com)



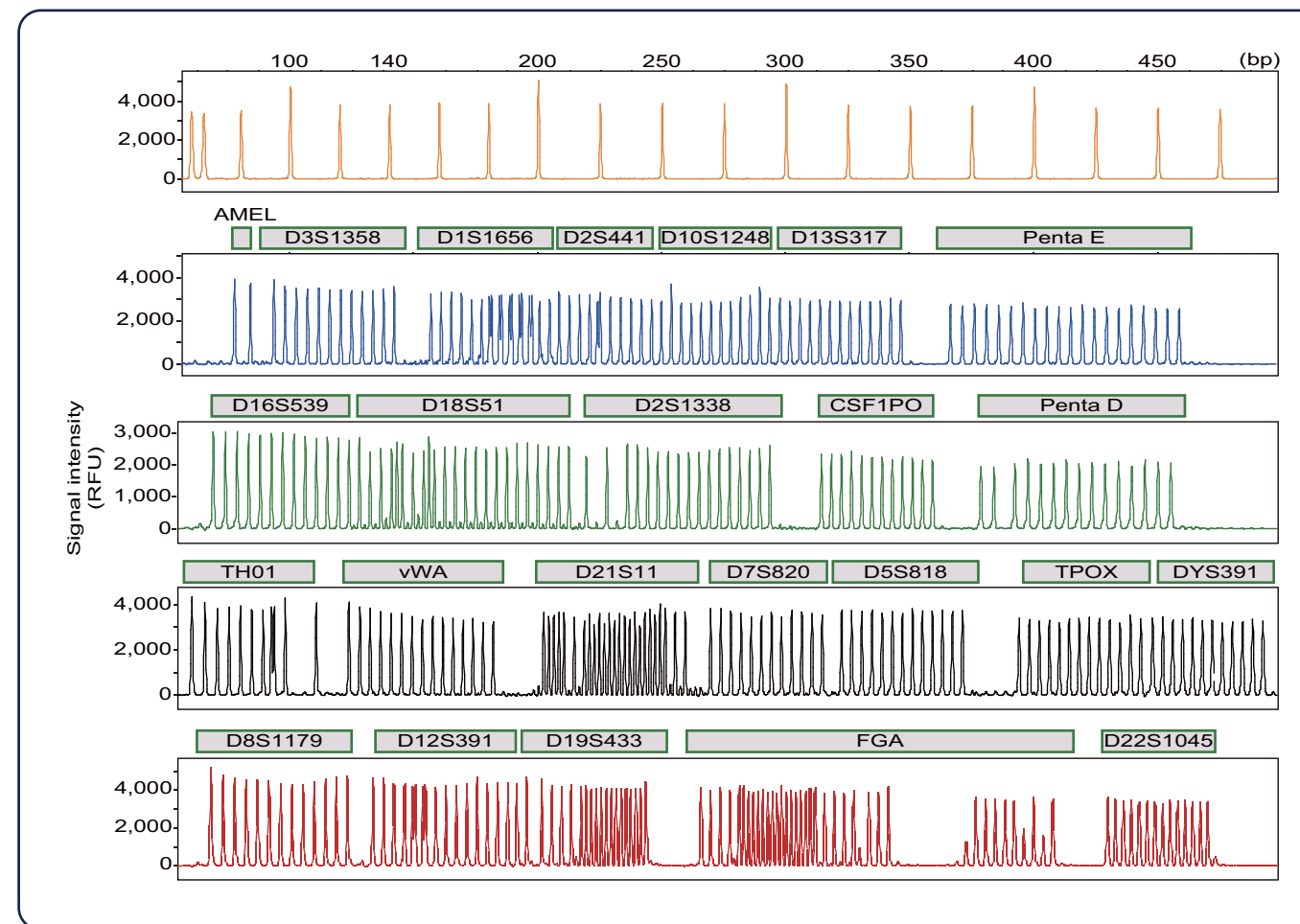
Fragment analysis using Polymer7 with DS3000 Compact CE Sequencer

Abstract

When using the DS3000 Compact CE Sequencer, the operator can choose the optimal polymer for the analysis from Polymer4 or Polymer7. Polymer7 is mainly used for sequencing analysis, but can also be used for fragment analysis. Here, we describe the performance of Polymer7 for fragment analysis using the GenePrint™ 24 System (Promega®).

Detecting closely spaced peaks

The allelic ladder is a standard sample used for DNA profiling and contains all possible alleles in the target short tandem repeat (STR). In the GenePrint™ 24 System, there are 388 peaks between 60 and 500 bases with an interval of 1 to 4 bases. As shown in Figure 1, DS3000 have correctly detected all peaks in a total of 80 tests in this study.



Legend

Figure 1: Electropherogram of GenePrint™ 24 Allelic Ladder Mix

Electropherogram obtained using GeneMarker HID. The color and width of the lines have been changed for better viewing. The green border around marker names indicates that all the expected peaks for that marker were detected.

### Comparison with performance using Polymer4

The performance using Polymer7 and Polymer4 was compared using different indicators. The GenePrint™ 24 System, which was used for Polymer7, is not recommended for use with Polymer4 in the DS3000 Compact CE Sequencer.

Instead, we used the PowerPlex™ ESI 17 Fast Allelic Ladder Mix to evaluate the performance using Polymer4.

The results of 80 tests are shown in Table 1.

### Electrophoresis Quality

The electrophoresis quality (EQ) represents the maximum base length for which two peaks with a difference in base length of 1 base can be separated. The EQ is displayed on the results screen each time a fragment analysis is completed. There was no significant difference in performance using Polymer7 or Polymer4. Note that EQ is not related to CRL in the sequencing analysis.

### Migration time for 500-base fragment

This represents the time required to detect signals from 500 bases using the size standards WEN ILS 500 (Promega®) for Polymer7 and WEN ILS 500 ESS (Promega®) for Polymer4. The results show that the peak migration time is shorter for Polymer7 than for Polymer4, indicating that the electrophoresis process can be completed faster with Polymer7.

### Sizing precision

This represents the variation in the estimated fragment size across four capillaries. The sizing precision is estimated as the standard deviation in the fragment size for each detected peak. The results show that the sizing precision for both polymers is less than 0.16 bases, which is recommended for DNA profiling [1].

**Table 1: Comparison of the analytical performance**

Polymer type		Polymer 4	Polymer 7
Allelic ladder		PowerPlex™ ESI 17 Fast System	GenePrint® 24 System
No. of replicate		80	80
EQ(bp)	mean	506.8	500.8
	S.D.	7.04	6.35
Migration time of signal of 500 bases (min)	mean	25.5	18.7
	S.D.	0.11	0.04
Max. sizing precision(bp)		< 0.16	< 0.16

### Materials and Methods

The allelic ladder included in each kit was electrophoresed using the protocol in Table 2. The GeneMarker HID ver. 2.9.0 (SoftGenetics, LLC) was used for allele calling and fragment size calculation.

**Table 2: Assays used in this report**

Polymer	Assay	Run voltage
Polymer 4	Promega_5Dye_WENILS_36_P4	13 kV
Polymer 7	Promega_5Dye_WENILS_36_P7	13 kV

#### Caution

- DS3000 Compact CE Sequencer is for Research Use Only and not intended for diagnostic procedures.
- This document shows an example of verification under limited samples and environments.
- It does not guarantee that data equivalent to those in this document can be obtained with every sample under every environment.

#### Reference

1. Lazaruk, K., Walsh, P., Oaks, F., Gilbert, D., Rosenblum, B., Menchen, S., Scheibler, D., Wenz, H., Holt, C., and Wallin, J. Genotyping of forensic short tandem repeat (STR) systems based on sizing precision in a capillary electrophoresis instrument, *Electrophoresis* (1998)19:86–93