

Assessment of light transmission aggregometry on the routine coagulation analyzer Siemens CS-2500 using CE-marked agonists from Hyphen Biomed

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INTRODUCTION

Light transmission aggregometry (LTA) is still considered as the “gold standard” for platelet function assessment but, as a completely manual technology, it is labour intensive. This challenge can be overcome by performing platelet aggregometry in an automated method on a routine coagulation analyzer.

AIM

To compare and correlate results obtained from a traditional manual LTA solution using platelet agonists provided from different manufacturers and realized in our Referent Center with a complete solution including the CS-2500 (Siemens) optimized automated system and CE-marked agonist reagents from Hyphen Biomed.

METHOD

- Platelet rich plasma from patients with suspected platelet disorders, von Willebrand disease or antiplatelet therapy have been assessed using a wide range of agonist concentrations : ADP (0.5- 10 µM), collagen (2 mg/µL), ristocetin (0.625-1.2 mg/mL) or arachidonic acid (1 mM).
- The APACKT-4004 aggregometer (Elitech, France) was used as the reference instrument with platelet agonists provided from different manufacturers.
- We evaluated the CS-2500 analyzer using dedicated software and CE-marked agonists from Hyphen Biomed.
- Results were expressed as Maximal Platelet Aggregation and correlation between the CS-2500 and the APACKT-4004 was analyzed using the Passing and Bablok regression test and the Bland-Altman analysis .

RESULTS

- Between October and December 2017, platelet aggregometry studies were performed in 49 samples (35 samples concerned patients with suspected platelet disorders, 6 samples were RIPA and 8 samples corresponded to antiplatelet therapy tailoring).
- Maximal aggregation response with ADP (0.5-10 µM), collagen (2 mg.mL⁻¹), ristocetin (1.2 mg.mL⁻¹) and arachidonic acid (1 mM) agonists showed significant correlation between the two aggregometers (p<0.01) (Figure 1).
- We observed a more variable response using low doses of ADP (≤ 5 µM).
- We also noted discrepancies with low dose of ristocetin (0.625 mg.mL⁻¹), showing excessive paradoxical agglutination with the CS-2500.
- Bland and Altman plots showed that 95% of the differences were located within acceptable range with most of the agonists, allowing to conclude that the two compared devices could be considered as consistent (Figure 2).
- Eight samples had platelet count in PRP below 150x10⁹ L⁻¹ (range from 34x10⁹ L⁻¹ to 142x10⁹ L⁻¹). In most of these cases, platelet maximal aggregations were consistent between the two systems (Table I).
- One sample of PRP was tested 5 times with 5 µM ADP, showing 1.5% intra-serial imprecision (CV%) of maximal intensity of platelet aggregation assessed with the CS-2500 instrument compared to 6.6% with the APACKT-4004.

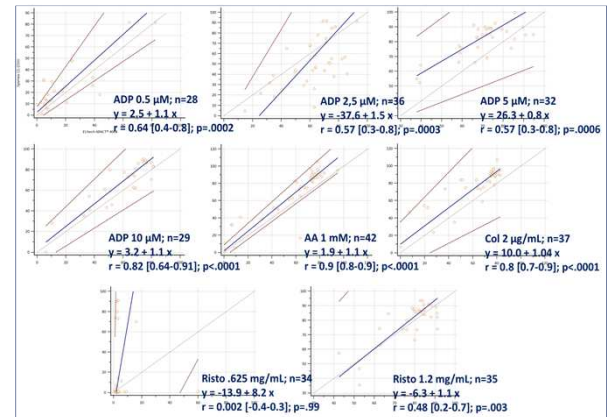


Figure 1. Correlations between the APACKT-4004 and the CS-2500 using the Passing and Bablok regression test (blue lines: fitted regression lines; dotted lines: regression line confidence bands).

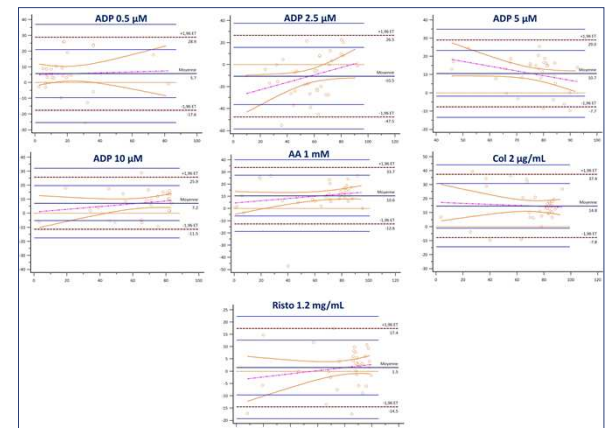


Figure 2. Bland and Altman plots between the APACKT-4004 and the CS-2500 systems.

Table I. Comparison of maximal platelet aggregations between the APACKT-4004 and the CS-2500 systems in eight samples with low platelet count in PRP

Samples	PRP (G/L)	ADP 0,5 µM (%)	ADP 2,5 µM (%)	ADP 5 µM (%)	ADP 10 µM (%)	AA 1 mM (%)	Col 2 µg/mL (%)	Ris 0.6 mg/mL (%)	Ris 1.2 mg (%)
1	96	33	92	72	89	73	NT	NT	NT
2	44	11	21	25	41	NT	NT	43	49
3	34	NT*	NT	51	76	NT	NT	83	74
4	49	NT	NT	NT	NT	0	6	50	45
5	126	25	20	71	71	76	68	NT	75
6	142	NT	NT	NT	NT	46	52	5	9
7	92	23	18	58	63	76	84	70	80
8	141	21	12	44	50	66	58	63	68

* Not tested

Values in red correspond to the CS-2500

CONCLUSIONS

Comparison of platelet aggregometry on the manual APACKT-4004 with the automated CS-2500 platform showed good agreement between the two platforms in a clinical setting. Implementation of LTA in this fully-automated routine coagulation analyzer system should make platelet function testing more widely available and could have the capacity for a high sample throughput.