Structure and binding mechanism of vascular endothelial cadherin, a divergent classical cadherin

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Supplementary Material

Supplementary Figure 1: Liposome aggregation by human VE-cadherin ectodomains.
Supplementary Table I: Percent sequence identities between EC1 and EC1-2 domains of VE-cadherin and other classical cadherins.
Supplementary Table II: Root mean square deviations (RMSD) between superposed EC1, EC2 and EC1-2 domains of type I and type II cadherins.
Supplementary Table III: Buried accessible surface area (BSA) for type I and type II cadherin interfaces.

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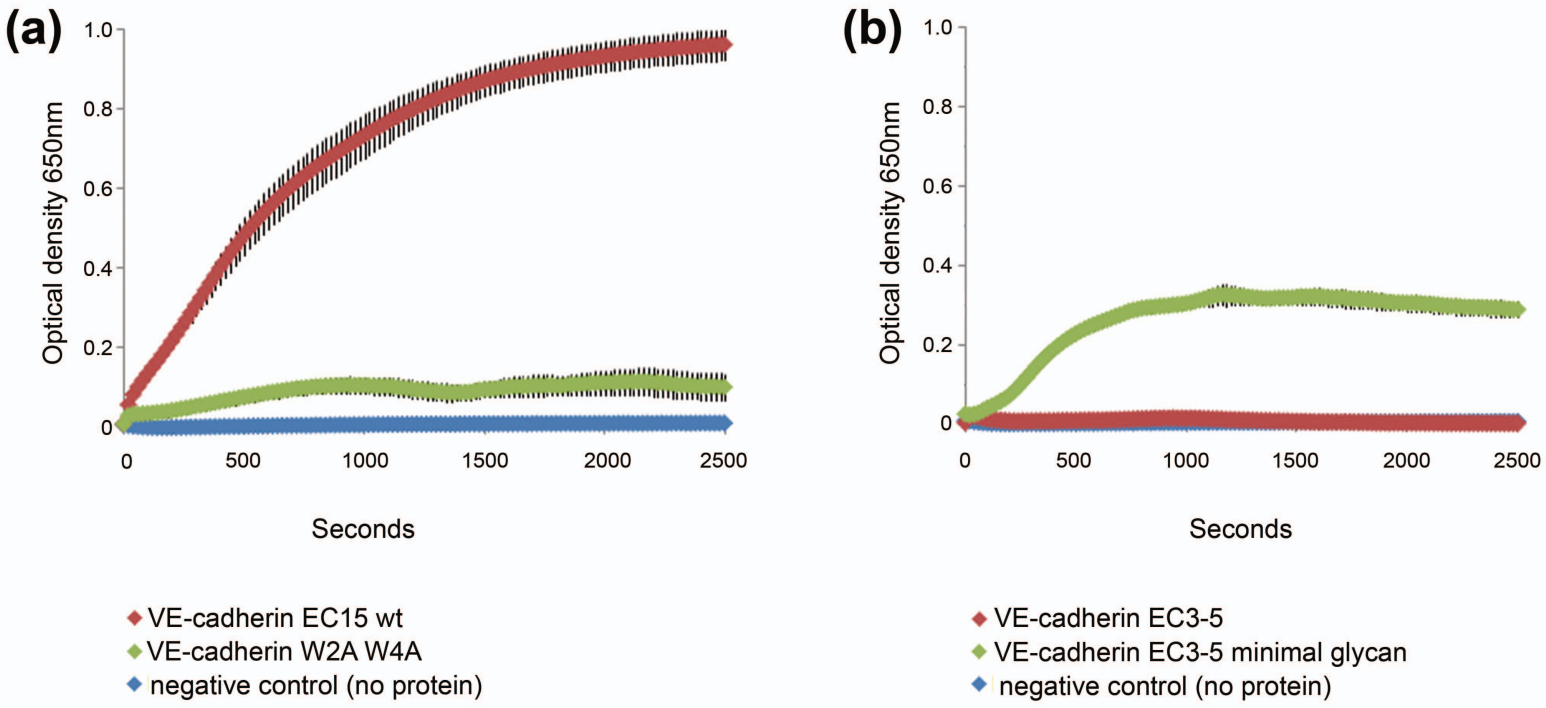

Supplementary Figure 1

Liposome aggregation by human VE-cadherin ectodomains. In consecutive liposome aggregation experiments each spanning a time of 2,500 seconds, the aggregation of liposomes coated with VE -cadherin ectodomain fragments was monitored by light absorption at 650nm. Uncoated liposomes served as negative control (blue trace).(a) Human VE-cadherin ectodomains aggregate liposomes (red trace). Introduction of double strand swap mutation W2A W4A into VE-cadherin strongly diminishes liposome aggregation (green trace). (b) Truncated human VE-cadherin spanning domains EC3-5, which lack adhesive domains EC1-2, fail to aggregate liposomes (red trace). However, identical protein fragments with reduced N-linked glycosylation due to expression in glycosylation deficient HEK 293 GNTI(-) cells are able to aggregate liposomes (green trace).

Supplementary Tables

Supplementary Table 1: Sequence identities given in percent between EC1 and EC1-2 domains of VE-cadherin and other classical cadherins.

EC1 / EC12	**VE**	**11**	**8**	**10**	**9**	**6**	**N**	**E**
VE	100	45	45	38	41	39	/	26
11	47	100	72	64	62	62	35	28
8	45	76	100	59	59	60	35	29
10	43	71	66	100	78	84	32	28
9	45	68	65	82	100	79	32	27
6	43	69	67	84	82	100	34	29
N	34	40	40	38	38	39	100	58
E	31	33	33	33	32	34	/	100

Supplementary Table 2: Root mean square deviations between superposed EC1 (rose), EC2 (purple) and EC12 (blue) domains of type I and type II cadherins.

EC1 EC2 EC12	**VE**	**11**	**8**	**MN**	**E**	**N**	**C**
VE	-	1.16[a]	1.15	1.31	1.52	1.66	1.84
		1.02	1.16	NA [b]	1.09	1.17	1.27
11	1.86	-	0.78	0.55	1.42	1.67	1.67
			0.96	NA	1.01	1.04	1.18
8	1.46	1.65	-	0.80	1.34	1.63	1.62
				NA	1.35	1.35	1.30
MN	NA	NA	NA	-	1.49	1.75	1.75
					NA	NA	NA
E	1.52	2.31	1.87	NA	-	0.94	0.86
						0.73	0.69
N	1.70	2.13	1.83	NA	0.94	-	1.01
							0.80
C	2.01	2.36	2.40	NA	1.14	1.21	-

[a] In case of two molecules present in the crystallographic asymmetric unit, values retrieved by superpositions of chain A only.

[b] Structural data only available for domain EC1.

Supplementary Table 3: Buried accessible surface area (BSA) for type I and type II cadherin interfaces, BSA value for one protomer given.

Protein	BSA [Å²]	pdb ID
EC1-domain		
ck VE-cadherin	913.0[a]	3PPE
m cadherin-8	1264.2	1ZXK
m cadherin-11	1225.8	2A4C
ck MN-cadherin	1254.9	1ZVN
m E-cadherin	817.3	2QVF
m N-cadherin	875.8	2QVI
x C-cadherin	847.6	1L3W
EC12-domains		
ck VE-cadherin	1066.2	3PPE
m cadherin-8	1271.9	2A62
m cadherin-11	1529.2	2S4E
m E-cadherin	817.3	2QVF
m N-cadherin	875.8	2QVI
x C-cadherin	847.6	1L3W

[a] In case of two molecules per asymmetric unit, values given for chain A.