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CORRECTION | NOVEMBER 01 2005

**Effects of Bcl-2 levels on Fas signaling-induced caspase-3 activation:
molecular genetic tests of computational model predictions** **FREE**

F. Hua; ... et. al

J Immunol (2005) 175 (9): 6235–6237.

<https://doi.org/10.4049/jimmunol.175.9.6235-b>

CORRECTIONS

Munthe, L. A., A. Os, M. Zangani, and B. Bogen. 2004. MHC-restricted Ig V region-driven T-B lymphocyte collaboration: B cell receptor ligation facilitates switch to IgG production. *J. Immunol.* 172: 7476–7484.

In Table I, in Expt. B^c 4, the B cell donor should be NIP-KLH Id⁻ (i.e., Id negative), not NIP-KLH Id⁺. The corrected table is shown below.

Table I. *Nonlinked Id-driven T-B collaboration, hapten and transfer experiments*

Expt.	Group	B Cell Donor	T Cells	Recipient Mice	Boost	Id ⁺ Ig Anti-NIP (μg/ml) ^a	IgG1 Anti-NIP (μg/ml)
A ^b	1	NIP-KLH Id ⁺	Id-spec Th2	RAG2 ^{-/-}	NIP-BSA	11 (2)	2.5 (0.5)
	2	NIP-KLH Id ⁺	Id-spec Th2	RAG2 ^{-/-}	None	3.0 (2)	0.08 (0.05)
	3	Id ⁺	Id-spec Th2	RAG2 ^{-/-}	NIP-BSA	0.9 (0.5)	0.04 (0.01)
B ^c	1	NIP-KLH Id ⁺	Id-spec Th2	C.B-17	NIP-BSA	20 (5)	19 (16)
	2	NIP-KLH Id ⁺	Id-spec Th2	C.B-17	None	12 (2)	1.3 (1)
	3	Id ⁺	Id-spec Th2	C.B-17	NIP-BSA	<0.06	0.4 (0.2)
	4	NIP-KLH Id ⁻	Id-spec Th2	C.B-17	NIP-BSA	<0.06	<0.1
C ^d	1	NIP-KLH Id ⁺	Id-spec Th2	RAG2 ^{-/-}	NIP-OVA	18 (3)	1.5 (0.5)
	2	NIP-KLH Id ⁺	DO.11.10 Th2	RAG2 ^{-/-}	NIP-OVA	23 (3)	6.3 (1)
	3	NIP-KLH Id ⁺	DO.11.10 Th2	RAG2 ^{-/-}	None	2.0 (0.7)	<0.05

^a Total anti-NIP Ab with V λ 1/2 L chain, irrespective of H chain isotype or allotype.

^b Expt. A: Splenocytes from immunized ((NIP)₆-KLH) or nonimmunized Id⁺ mice were depleted of T cells and injected (10⁷) into RAG2^{-/-} BALB/c mice on day 0 (five mice per group). Id-specific (spec) Th2 cells (6 × 10⁶) and boost (150 μg (NIP)₅-BSA in PBS i.p.) were given on day 1 as indicated. Mean (SD) of anti-NIP Ab in day 15 sera is given, *p* values were calculated by Mann-Whitney Test and are given in main text.

^c Expt. B: Splenic B cells from immunized or nonimmunized Id⁺ or Id⁻ mice were injected (3 × 10⁶) into IgH^b C.B-17 mice (*n* = 5), followed by Th2 cells (5 × 10⁶) and boost as indicated. Ab H chains from transferred B cells were detected by IgG1^a-specific ELISA. Data are from day 6, before immune responses in the unirradiated immunocompetent C.B-17 hosts could contribute to an increased background of λ2⁺ anti-NIP.

^d Expt. C: As Exp. A, but with Id-specific Th2 or DO.11.10 Th2 and (NIP)₆-OVA boost.

Correale, P., M. G. Cusi, M. T. Del Vecchio, A. Aquino, S. Prete, K. Y. Tsang, L. Micheli, C. Nencini, M. La Placa, F. Montagnani, C. Terrosi, M. Caraglia, V. Formica, G. Giorgi, E. Bonmassar, and G. Francini. 2005. Dendritic cell-mediated cross-presentation of antigens derived from colon carcinoma cells exposed to a highly cytotoxic multidrug regimen with gemcitabine, oxaliplatin, 5-fluorouracil, and leucovorin, elicits a powerful human antigen-specific CTL response with antitumor activity in vitro. *J. Immunol.* 175: 820–828.

The fifth author's name is listed incorrectly. The correct name is Salvatore Pasquale Prete.

There is an error in the grant information. The correct footnote is shown below.

¹This work was supported in part by a grant from "Istituto Superiore di Sanità" no. 1A2/F7 (Research Unit, to E.B.) and in part by a grant of MIUR "Programma di Ricerca Scientifica di rilevante interesse Nazionale" 2004 (coordinator E.B.).

Hua, F., M. G. Cornejo, M. H. Cardone, C. L. Stokes, and D. A. Lauffenburger. 2005. Effects of Bcl-2 levels on Fas signaling-induced caspase-3 activation: molecular genetic tests of computational model predictions. *J. Immunol.* 175: 985–995.

In Table I, in the Reactant B column, Bax should be tBid:Bax₂ for both Cyto.*c* and Smac in the Reactant A^a column. The nongeneral reaction shown in the Comment column for Cyto.*c* (tBid:Bax₂) applies to both this and the Smac (tBid:Bax₂) reactions. The corrected table is shown below.

In Table II, the unit for k10 should be s⁻¹nM⁻¹, instead of s⁻¹. The corrected table is shown below.

In Table III, the unit for ATP should be 10,000 nM. The corrected table is shown below.

Table I. *Biochemical reactions*

Reactant A ^a	Reactant B	Reactant C	Forward Reaction Rate	Reverse Reaction Rate	Comment
FasL FasC	Fas FADD	FasC FasC:FADD	k1_f k2_f	k1_r k2_r	Assume noncooperative binding between FADD and Fas, which means that regardless of other molecules in the complex, the FADD-Fas interaction always has the same rate constant.
FasC:FADD FasC:FADD_2 FasC:FADD_2:Casp8 FasC:FADD_2:FLIP FasC:FADD_2:Casp8_2 FasC:FADD_2:Casp8:FLIP FasC:FADD_2:FLIP_2 FasC:FADD:Casp8 FasC:FADD:FLIP FasC:FADD_3	FADD FADD FADD FADD FADD FADD FADD FADD FADD FADD Casp8	FasC:FADD_2 FasC:FADD_3 FasC:FADD_3:Casp8 FasC:FADD_3:FLIP FasC:FADD_3:Casp8_2 FasC:FADD_3:Casp8:FLIP FasC:FADD_3:FLIP_2 FasC:FADD_2:Casp8 FasC:FADD_2:FLIP FasC:FADD_3:Casp8_3	k2_f k2_f k2_f k2_f k2_f k2_f k2_f k2_f k2_f k2_f k3_f	k2_r k2_r k2_r k2_r k2_r k2_r k2_r k2_r k2_r k2_r k3_r	Assume caspase-8 and FLIP have the same binding rate constants for FADD, because their death effector domains (FADD binding domain) have high homology (38).
FasC:FADD_3 FasC:FADD_3:Casp8 FasC:FADD_3:Casp8 FasC:FADD_3:FLIP	FLIP Casp8 FLIP Casp8	FasC:FADD_3:FLIP FasC:FADD_3:Casp8_2 FasC:FADD_3:Casp8_FLIP FasC:FADD_3:Casp8:FLIP	k3_f k3_f k3_f k3_f	k3_r k3_r k3_r k3_r	Similar to binding between FADD and Fas, assume noncooperative binding between FADD and caspase-8 and between FADD and FLIP.
FasC:FADD_3:FLIP FasC:FADD_3:Casp8_2 FasC:FADD_3:Casp8_2 FasC:FADD_3:Casp8:FLIP FasC:FADD_3:Casp8:FLIP FasC:FADD3:FLIP_2 FasC:FADD_3:FLIP_2 FasC:FADD_2 FasC:FADD_2 FasC:FADD_2:Casp8 FasC:FADD_2:Casp8 FasC:FADD_2:FLIP FasC:FADD_2:FLIP FasC:FADD FasC:FADD FasC:FADD_2 FasC:FADD_3:Casp8 FasC:FADD_3:FLIP FasC:FADD_3 Casp8_2_p41	FLIP Casp8 FLIP Casp8 FLIP Casp8 FLIP Casp8 FLIP Casp8 FLIP Casp8 FLIP Casp8 FLIP Casp8 FLIP Casp8_2_p41 Casp8_2_p41 Casp8_2_p41 Casp8_2_p41 Casp8_2_p41	FasC:FADD_3:FLIP_2 FasC:FADD_3:Casp8_3 FasC:FADD_3:Casp8_2:FLIP FasC:FADD_3:Casp8_2:FLIP FasC:FADD_3:Casp8:FLIP_2 FasC:FADD_3:Casp8:FLIP_2 FasC:FADD_3:FLIP_3 FasC:FADD_2:Casp8 FasC:FADD_2:FLIP FasC:FADD_2:Casp8_2 FasC:FADD_2:Casp8:FLIP FasC:FADD_2:Casp8:FLIP FasC:FADD_2:FLIP_2 FasC:FADD:Casp8 FasC:FADD:FLIP FasC:FADD_2:Casp8_2 FasC:FADD_3:Casp8_3 FasC:FADD_3:Casp8_2:FLIP FasC:FADD_3:Casp8_2	k3_f k3_f k3_f k3_f k3_f k3_f k3_f k3_f k3_f k3_f k3_f k3_f k3_f k3_f k3_f k3_f k4 k4 k4 k4	k3_r k3_r k3_r k3_r k3_r k3_r k3_r k3_r k3_r k3_r k3_r k3_r k3_r k3_r k3_r k3_r k4 k4 k4 k4	
Casp8_2* Casp8_2*	Casp3 Casp3*	Casp8_2*:Casp3 Casp8_2*:Casp3	k5 k6_f		$A \xrightarrow{k_f} A^*$ Nongeneral reaction: $A \rightarrow A^*$
Casp8_2* Casp8_2* tBid	Casp3* tBid Bid Bax	Casp8_2*:Casp3 Casp8_2*:Casp3 Cas8_2*:Bid Cas8_2*:Bid tBid:Bax	k6_f k7 k8_f k9_f	k6_r k7 k8_r k9_r	Assume the catalytic reaction rate of caspase_8 is the same regardless of the substrate.
tBid:Bax Smac	Bax tBid:Bax_2	tBid:Bax_2 Smac*	k9_f k10	k9_r	Assume the first Bax and the second Bax binding to tBid have the same rate constants.
Cyto.c	tBid:Bax_2	Cyto.c*	k10		Assume Smac and Cyto.c have the same release rate and nongeneral reaction: $A \xrightarrow{k_f} B$ $A \xrightarrow{k_r} A^*$
Smac* Cyto.c*	XIAP Apaf	Smac*:XIAP Cyto.c*:Apaf:ATP	k11_f k12_f	k11_r k12_r	Nongeneral reaction: $A + B + ATP \xrightleftharpoons[k_r]{k_f} C$
Cyto.c*:Apaf:ATP Cyto.c*:Apaf:ATP:Casp9 Cyto.c*:Apaf:ATP:Casp9 Casp9*	Casp9 Casp9 Casp9* Casp3	Cyto.c*:Apaf:ATP:Casp9 Cyto.c*:Apaf:ATP:Casp9_2 Cyto.c*:Apaf:ATP:Casp9_2 Casp9*:Casp3	k13_f k14_f k15 k16_f	k13_r k14_r k15 k16_r	

(Table continues)

Table I. *Continued*

Reactant A ^a	Reactant B	Reactant C	Forward Reaction Rate	Reverse Reaction Rate	Comment
Casp9*	Casp3*	Casp9*:Casp3		k17	
Casp9	XIAP	Casp9:XIAP	k18_f	k18_r	
Casp3*	XIAP	Casp3*:XIAP	k19_f	k19_r	
Equations used for different models					
Bcl_2 binding to Bax alone					
Bcl_2	Bax	Bcl2:Bax	k20_f	k20_r	
Bcl_2 binding to Bid alone					
Bcl_2	Bid	Bcl2:Bid	k20_f	k20_r	
Bcl_2 binding to tBid alone					
Bcl_2	tBid	Bcl2:tBid	k20_f	k20_r	
Bcl_2 binding to both tBid and Bax					
Bcl_2	Bax	Bcl2:Bax	k20_f	k20_r	
Bcl_2	tBid	Bcl2:tBid	k20_f	k20_r	

^a General reaction: $A + B \xrightleftharpoons[k_r]{k_f} C$

Table II. *Reaction rate constants*

Rate Constant	Value	Reference
k1_f	9.09E-05 nM ⁻¹ s ⁻¹	$K_d = k1_r/k1_f = 1.1$ nM from (39)
k1_r	1.00E-04 s ⁻¹	
k2_f	5.00E-04 nM ⁻¹ s ⁻¹	
k2_r	0.2 s ⁻¹	
k3_f	3.50E-03 nM ⁻¹ s ⁻¹	
k3_r	0.018 s ⁻¹	
k4	0.3 s ⁻¹	
k5	0.1 s ⁻¹	
k6_f	1.00E-05 nM ⁻¹ s ⁻¹	
k6_r	0.06 s ⁻¹	
k7	0.1 s ⁻¹	
k8_f	5.00E-03 nM ⁻¹ s ⁻¹	
k8_r	0.005 s ⁻¹	
k9_f	2.00E-04 nM ⁻¹ s ⁻¹	
k9_r	0.02 s ⁻¹	
k10	1e-3 s ⁻¹ nM ⁻¹	
k11_f	7.00E-03 nM ⁻¹ s ⁻¹	$k_{on} = k11_f = 7e6/(M s)$ and $k_{off} = k11_r = 2.21e-3/s$ from (40)
k11_r	2.21E-03 s ⁻¹	
k12_f	2.78e-7 nM ⁻¹ s ⁻¹ nM ⁻¹	
k12_r	5.70E-03 s ⁻¹	
k13_f	2.84E-04 nM ⁻¹ s ⁻¹	
k13_r	0.07493 s ⁻¹	
k14_f	4.41E-04 nM ⁻¹ s ⁻¹	
k14_r	0.1 s ⁻¹	
k15	0.7 s ⁻¹	
k16_f	1.96E-05 nM ⁻¹ s ⁻¹	$K_m = (k16_r + k17)/k16_f = 248 \mu M$ from (41)
k16_r	0.05707 s ⁻¹	
k17	4.8 s ⁻¹	$k_{cat} = k17 = 4.8/s$ from (41)
k18_f	1.06E-04 nM ⁻¹ s ⁻¹	$K_i = k18_r/k18_f = 9.4e-9$ M from (42)
k18_r	1.00E-03 s ⁻¹	
k19_f	2.47E-03 nM ⁻¹ s ⁻¹	$k_{on} = k19_f = 2.5e6/(M s)$ and $k_{off} = k19_r = 2.4e-3/s$ from (43)
k19_r	2.40E-03 s ⁻¹	
k20_f	2.00E-03 nM ⁻¹ s ⁻¹	$K_d = k20_r/k20_f = 1e-8$ M from (44)
k20_r	0.02 s ⁻¹	

Table III. *Initial conditions*

Parameter	Value (nM)	Reference
Fas	10.00	
FasL	2.00	Equivalent to 100 ng/ml FasL
FADD	16.67	Unpublished observations
Flip	81.00	
Casp8	33.33	(45)
Casp3	200.00	(45)
Bid	25.00	
Bcl2	75.00	
Bax	83.33	
Cytoc	100.00	
Smac	100.00	
XIAP	30.00	(45)
Casp9	20.00	(41)
ATP	10,000.00	
Apaf	100.00	

Grueter, B., M. Petter, T. Egawa, K. Laule-Kilian, C. J. Aldrian, A. Wuerch, Y. Ludwig, H. Fukuyama, H. Wardemann, R. Waldschuetz, T. Möröy, I. Taniuchi, V. Steimle, D. R. Littman, and M. Ehlers. 2005. Runx3 regulates integrin α_E /CD103 and CD4 expression during development of CD4⁻/CD8⁺ T cells. *J. Immunol.* 175: 1694–1705.

In the **Abstract**, in the third sentence, the word “rust” should have been published as “runt.” The correct sentence is shown below.

The transcription factor Runx3/AML-2 (Runx, runt dominant factor; AML, acute myeloid leukemia) is expressed specifically during the development of CD8 single-positive (SP) thymocytes, where it silences CD4 expression.

Straathof, K. C., A. M. Leen, E. L. Buza, G. Taylor, M. H. Huls, H. E. Heslop, C. M. Rooney, and C. M. Bollard. 2005. Characterization of latent membrane protein 2 specificity in CTL lines from patients with EBV-positive nasopharyngeal carcinoma and lymphoma. *J. Immunol.* 175: 4137–4147.

In Table I, the HLA restrictions for two of the LMP2 epitopes are incorrect. The correct HLA restriction for TVCGGIMFL in the sixth row should be A*0201/06 and for LLWTLVVL in the seventh row should be A*0201. The corrected table is shown below.

Table I. LMP2-specific T cell populations in patient CTL lines^a

Minimum Epitope	Amino Acids	HLA Restriction	No. Responding/ No. Tested	SFC/10 ⁵ CTL (range)
CLGGLTMV	416–434	A*0201/06/07/09	4/12	84 (19–236)
GLGTLGAAI	293–301	A2	1/12	459
LTAGFLIFL	453–461	A2	0/12	
FLYALALLL	356–364	A*0201	7/12	381 (7–1990)
LIVDAVLQL	257–265	A*0204 or A*0217	1/12	651
TVCGGIMFL	243–251	A*0201/06	2/12	198 (175–222)
LLWTLVVL	329–337	A*0201	2/12	19 (14–24)
FTASVSTVV	144–152	A68	2/6	38 (23–53)
SSCSCPLSKI	340–350	A11	3/3	43 (8–90)
TYGPFVMSL	419–427	A24	2/5	58 (16–101)
PYLFWLAAI	131–139	A23/24	3/6	462 (12–1132)
ILLARFLY	349–358	A29	1/2	6
RRWRRLTVC	237–245	B*1402	1/1	41
RRRWRRLTV	236–244	B*2704/05/09	1/2	16
RRLTVCGGIMF	240–250	B27	1/3	129
MGSLEMVPM	1–9	B*3501	1/5	880
LPVIVAPYL	125–133	B53	1/2	5
IEDPPFNSL	200–208	B60	1/2	918
DYQPLGTQDQSLYL	73–87	DR4 or DR16	1/1	57

^a Listed are the amino acid sequence of newly identified (in bold) as well as previously described LMP2 epitopes (27, 29–33); their location in the LMP2 molecule; HLA restriction; the number of CTL lines from NPC, HL, and NHL patients in which responses to these epitopes were identified; and the strength of these responses. When responses to the indicated epitope were found in more than one patient, CTL line average response and range are shown.