

Staurosporine blocked normal cells at G₁/S boundary¹

WANG Rui-Hong², XUE Shao-Bai³

(Cell Biology Section, Department of Biology, Beijing Normal University, Beijing 100875, China)

KEY WORDS staurosporine; interphase; S phase; thymidine kinase; fibroblasts; cultured cells; stomach neoplasms; flow cytometry; phosphorylation

AIM: To reveal the regulating difference of G₁/S-phase transition between normal and tumor cells by using staurosporine, an unspecific kinase inhibitor.

METHODS: Flow cytometry, Dot blot, kinase activity assay, and electrophoresis. **RESULTS:** A 18-h treatment with staurosporine (5 μg · L⁻¹) blocked normal cell line 2BS cells (normal human embryonic lung fibroblast, 5-20 passages) in G₁ phase, decreased their thymidine kinase (TK) mRNA level and activity, and also dephosphorylated an intracellular 107 kDa protein. Meanwhile, all these effects in 2BS cells disappeared only by washing staurosporine away. Such kind of effects did not occur in tumor cell line BGC-823 cells (human stomach cancer cell). **CONCLUSION:** During the period of G₁/S-phase transition, the kinases involved are more sensitive to staurosporine in normal cells than in tumor cells.

During eukaryotic cell cycle, there are 3 key transition points: G₀/G₁, G₁/S, and G₂/M. The cell cycle control differences between tumor and normal cells appear mainly at G₁/S transition. Tumor cells can free pass this boundary so that they can be immortalized, while the normal cells are controlled very well^[1].

There is a possibility that Retinoblastoma protein (RB) and its family proteins (like p107) and p53 play important roles at G₁/S-phase transition boundary by binding to the transcription factor E2F or affecting the repair of damaged DNA^[2].

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² Now in National Cancer Institute, National Institutes of Health, Bethesda MD 20892, USA.

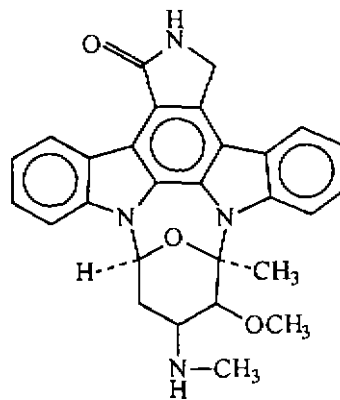
³ Correspondence to Prof XUE Shao-Bai.

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In order to figure out this mechanism, we chose thymidine kinase (TK) as one of our markers. Because TK is a very important kinase for DNA synthesis. It catalyzes the change of thymidine nucleotides to mono-, di-, and triphosphates by transferring the γ-phosphate from ATP to the substrate. Its enzymatic activity and mRNA level are low in G₁ phase cells, but both rise dramatically near the onset of S phase^[3].

Staurosporine, a microbial alkaloid produced by *Streptomyces* sp, 5 μg · L⁻¹ arrested normal cells (eg, foreskin cell, human embryonic fibroblast) in G₁ phase, but had no effect on tumor cells (eg, HL-60 cells)^[4]. In this study, we tried to demonstrate the regulating differences at G₁/S-phase transition between normal and tumor cells.



Staurosporine

MATERIALS AND METHODS

Cell and culture conditions The human embryonic lung fibroblasts (2BS) were maintained in DMEM (Gibco) supplemented with 10 % calf bovine serum, and used within 20 passages. Human stomach cancer cells (BGC-823) were incubated in RPMI 1640 (Gibco) medium with 10 % calf bovine serum.

Staurosporine treatment 2BS or BGC-823 cells were split into 75-cm² flasks at a concentration of 1 · 10⁶ cells/flask. These cells were kept in 37 °C, 5 % CO₂ incubator for overnight. Staurosporine (Sigma) was dissolved with

Me₂SO and added into the cells. The Me₂SO concentration in medium was kept <0.1%. The cells were incubated. For the release of staurosporine, the cells which have been treated were washed 3 times with serum-free medium, then incubated in fresh medium with serum.

Flow cytometric assay Cells were trypsinized, washed with cold PBS for 3 times, and fixed with 75% cold ethanol at 4 °C for overnight. The cells were spun down and the pellets were washed with cold PBS 3 times. The cell pellets were resuspended with PBS containing ribonuclease A (RNase A, free DNase, Sigma) 20 mg·L⁻¹ and left at 37 °C for 30 min. Propidium iodide (PI, in PBS) was added to a final concentration of 50 mg·L⁻¹, and incubated at 4 °C for 1-2 h. All these samples were measured with FACS-440 (B-D Ltd).

TK expression assay Guanidine/acid phenol method was used to isolate the intracellular total RNA, then Dot blot was done and hybridized by TK cDNA probe^[5].

TK activity assay Cells were harvested by trypsinization and washed with cold PBS twice and washing solution (KCl 154 mmol·L⁻¹, thymidine 16 μmol·L⁻¹, β-mercaptoethanol 3 μmol·L⁻¹) twice. The cells were resuspended with cold extracting solution (Tris·HCl 10 mmol·L⁻¹, pH 8.0, thymidine 16 μmol·L⁻¹, β-mercaptoethanol 3 mmol·L⁻¹ to the concentration of 2.5 × 10¹⁰ cells·L⁻¹). The cells were frozen in ethanol-dry ice bath, then thawed at 37 °C for 5 cycles. The cell lysates were spun at 30 000 × g, 4 °C for 30 min. The supernatant was stored at -70 °C. When analyzing TK activity, the following system was used: 30 μL reacting solution (MgCl₂ 15 mmol·L⁻¹, Tris·HCl 30 mmol·L⁻¹, pH 7.5, ATP 30 mmol·L⁻¹), [³H]TdR 10 μL (370 kBq), cell extract 15 μL, and extracting solution 45 μL. The reaction occurred at 37 °C for 20 min, then was stopped by putting the tubes on ice. Spot 80 μL of each reacting mixture onto DE-81 filter. Then the filter was washed with ammonium formate 5 mmol·L⁻¹ 3 times immediately, 15 min each time. The filter was rinsed once with methanol, dried and counted by Liquid Scintillation Analyzer (Packard Tri-Carb 1500).

Intracellular substrate phosphorylation assay The cells were harvested by trypsinization; washed with cold PBS for 3 times, sonicated in cold buffer A (Tris·HCl 20 mmol·L⁻¹, pH 7.5, β-mercaptoethanol 50 mmol·L⁻¹, PMSF 1 mmol·L⁻¹, egtazic acid 0.5 mmol·L⁻¹, edetic acid 2 mmol·L⁻¹, sucrose 0.33 mol·L⁻¹), then spun at 2000 × g, 4 °C for 10 min. Triton X-100 was added into the supernatant to 1%. The supernatants were shaken on ice for 30 min, and spun at 12 000 × g for 30 min. The following reaction was done at 37 °C: protein 100 μg, [γ-³²P]ATP 370 kBq, Tris·HCl 25 mmol·L⁻¹, pH 7.5, MgCl₂ 5 mmol·L⁻¹, CaCl₂ 0.5 mmol·L⁻¹, edetic acid 0.2 mmol·L⁻¹. The total volume was 50 μL. After 30 min, 50 μL 2 × SDS PAGE loading buffer

(with β-mercaptoethanol) was added to stop the reaction. The samples were boiled for 5 min, electrophoresed with 10% SDS-PAGE. The gels were stained with 0.25% Coomassie bright blue R250 in 10% acetic acid/45% methanol/45% H₂O, destained, dried, and exposed to X ray film at -70 °C for 7 d.

RESULTS

Flow cytometry analysis More than 50 samples of 2BS or BGC-823 cells showed: 2BS cells, G₁ phase 56.05 ± 0.01%, S phase 28.12 ± 0.02%, and G₂/M phase 16.43 ± 0.01%; BGC-823 cells, G₁ phase 62.41 ± 0.02%, S phase 28.26 ± 0.02%, G₂/M phase 8.10 ± 0.03%. After treatment with staurosporine 5 μg·L⁻¹ for 18 h, 2BS cells were blocked in G₁ phase, namely 71.11 ± 0.01% cells stayed in G₁ phase, 15.28 ± 0.03% and 13.26 ± 0.03% cells were in S and G₂/M phase, respectively. When these cells were released from staurosporine 5 μg·L⁻¹, they recovered back to the normal: G₁ 61.05 ± 0.01%, S 21.38 ± 0.02%, G₂/M 18.08 ± 0.02%. But under the same kind of treatment, BGC-823 cells basically kept the same cell cycle phase distribution: G₁ phase 62.41 ± 0.02%, S phase 28.26 ± 0.02%, G₂/M phase 8.10 ± 0.03% (Fig 1).

Staurosporine 1 or 10 μg·L⁻¹ showed less effect. On the other hand, staurosporine 50 or 75 μg·L⁻¹, arrested both 2BS and BGC-823 cells in G₂/M phase: in 2BS cells, G₂/M phase cell number changed to 38.21 ± 0.02% from 16.43 ± 0.01%; in BGC-823 cells, G₂/M phase cell number increased to 69.06 ± 0.01% from 8.10 ± 0.03%. This effect could not be released.

Dot blot hybridization The Dot blot hybridization with TK probe showed that staurosporine 5 μg·L⁻¹ treatment caused a more dramatic decrease of TK mRNA transcription in 2BS cells than in BGC-823 cells (Fig 2).

TK activity assay TK activity was inhibited in 2BS cells when they were incubated in media containing staurosporine 5 μg·L⁻¹ for 18 h: TK activity dropped from 97.47 kBq·g⁻¹ to 63.10 kBq·g⁻¹ (P < 0.01). Only 67% of the control was left. On the other hand, in BGC-823 cells, there was no change observed, their TK activity of the control group was 234.45 kBq·g⁻¹, of staurosporine

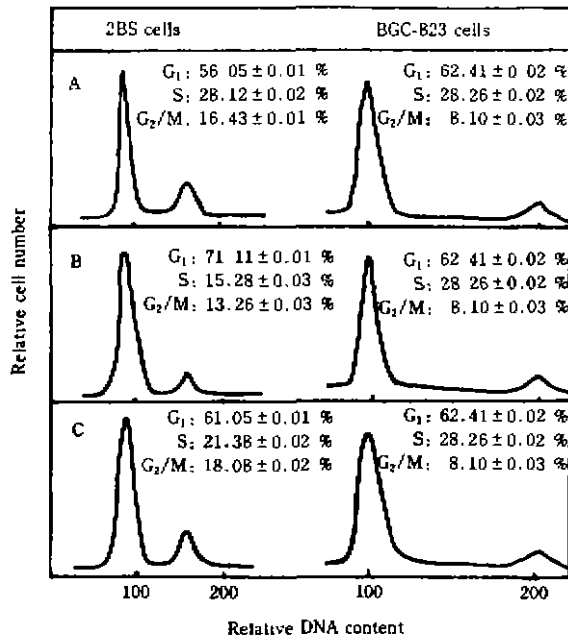


Fig 1. Flow cytometry. A) Control; B) treated with staurosporine 5 µg · L⁻¹ for 18 h; C) released from staurosporine 5 µg · L⁻¹ for 24 h.

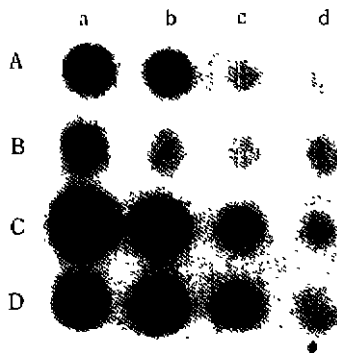


Fig 2. TK expression. A) 2BS cells; B) 2BS cells treated with staurosporine 5 µg · L⁻¹ for 18 h; C) BGC-823 cells; D) BGC-823 cells treated with staurosporine 5 µg · L⁻¹ for 18 h. a) RNA 10 µg; b) RNA 5 µg; c) RNA 1 µg; d) RNA 0.5 µg.

5 µg · L⁻¹ group was 197.42 kBq · g⁻¹, about 84 % of the control was left.

When 2BS cells were released from staurosporine 5 µg · L⁻¹, their TK activity was restored gradually. After 24 h, it went up to 104.76 kBq · g⁻¹, which was near the original level, and no significant difference was found between the control and the released groups. TK

activity of BGC-823 cells did not change from the beginning to the end (Tab 1).

Tab 1. Effect of staurosporine 5 µg · L⁻¹ on TK activity in 2BS and BGC-823 cells. n = 5, $\bar{x} \pm s$.

^aP > 0.05, ^cP < 0.01 vs control.

Drug time/h	Release time/h	TK Activity/kBq · g ⁻¹	
		2BS	BGC-823
0	0	94.2 ± 0.8	234.4 ± 5.5
2	0	113.0 ± 0.7	202.0 ± 2.3
4	0	86.6 ± 1.2	197.5 ± 1.1
18	0	63.1 ± 0.9 ^c	197.4 ± 6.5 ^a
18	24	104.8 ± 0.6 ^a	196.6 ± 6.0
18	2	86.6 ± 0.8	188.4 ± 0.7
18	4	120.4 ± 0.5	210.6 ± 0.8

Intracellular protein phosphorylation test

There was no change of protein phosphorylation level in 2BS and BGC-823 cells treated with staurosporine 5 µg · L⁻¹ for 1 - 4 h, but treated with staurosporine 5 µg · L⁻¹ for 18 h, the phosphorylation of a 107 kDa protein in 2BS cells disappeared, and it was rephosphorylated again if the staurosporine was washed out for 24 h. BGC-823 cells behaved in a different way. Compared with the control, the phosphorylation level of this 107 kDa protein had no change after either treated with staurosporine 5 µg · L⁻¹ or released from it for 24 h (Fig 3).

All these suggested the phenomenon that staurosporine 5 µg · L⁻¹ treatment inhibited the phosphorylation of an intracellular 107 kDa protein was specific in 2BS cells, and such a kind of effect could be released.

DISCUSSION

Our contribution about staurosporine reported here is consistent with the Crissman's^[3]. The transcription of TK is controlled by transcription factor E2F^[6], and generally, E2F is negatively regulated by intracellular RB family (retinoblastoma gene product RB and p107 etc). TK activity is able to be restored when E2F-RB or E2F-p107 complex has been destroyed. In normal cells, the efficient way to break this is to phosphorylate RB or p107^[7]. Considering the data we got in 2BS cells treated with staurosporine 5 µg · L⁻¹ together with

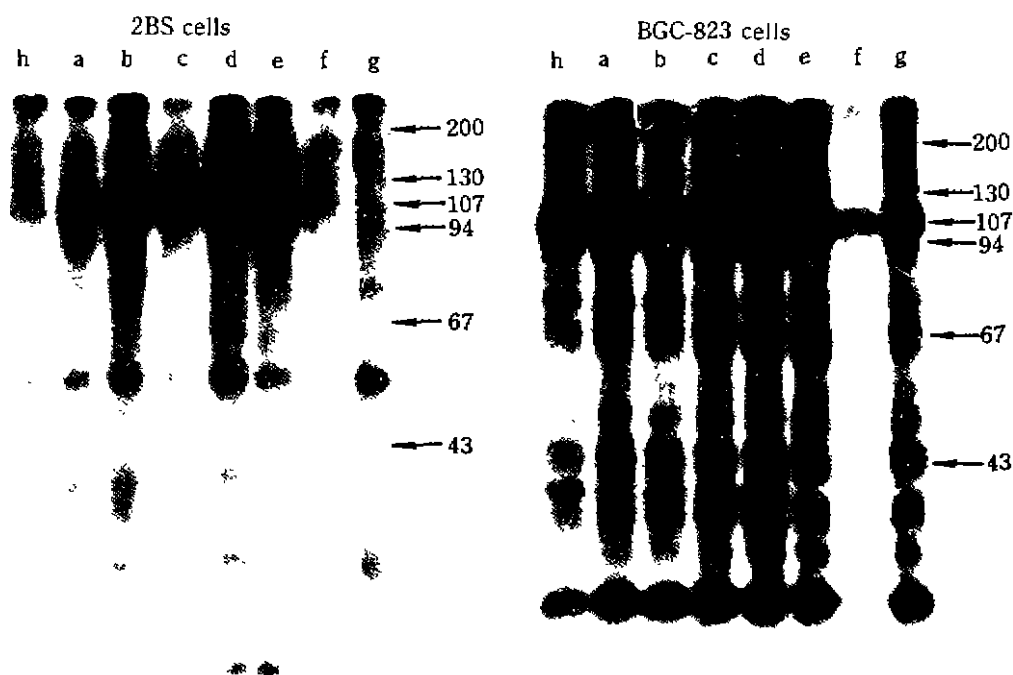


Fig 3. Intracellular substrates phosphorylation. a) Control; b) Cells treated with staurosporine $5 \mu\text{g} \cdot \text{L}^{-1}$ for 1 h; c) 2 h; d) 3 h; e) 4 h; f & g) 18 h; h) Cells released for 24 h after 18-h treatment with staurosporine $5 \mu\text{g} \cdot \text{L}^{-1}$.

these facts, it is quite possible that the 107 kDa protein is p107, and kinase affected by staurosporine might be cyclin A-cdk2^[8-9].

On the basis of our results, we suggest that there is a reversible proliferating regulation point at G_1/S -phase boundary. This kind of regulation functions by directly affecting E2F function. In the view of the expression time differences between the genes regulated by E2F, this control point should be the result of the long process regulated by all kinds of involving kinases.

Our data confirmed that staurosporine $5 \mu\text{g} \cdot \text{L}^{-1}$ was able to block normal cells in G_1 phase, and had nothing to do with the tumor cells. The difference of proliferation control between normal and tumor cells came from their sensitivities to staurosporine $5 \mu\text{g} \cdot \text{L}^{-1}$ during G_1/S -phase transition. The loss of sensitivity of tumor cells to staurosporine $5 \mu\text{g} \cdot \text{L}^{-1}$ means all their kinases involved in this regulation process get resistance to staurosporine $5 \mu\text{g} \cdot \text{L}^{-1}$ at some extent, and this would make E2F function continuously at anytime so that the tumor cells can synthesize DNA and divide immortally.

At the same time, according to the information we got on the other several kinds of cell lines, such as NIH3T3, tsRSVNIH3T3-LA90 (33 °C, the transformed phenotype), C3H10T1/2, and transformed C3H10T1/2, HEP2, we think staurosporine $5 \mu\text{g} \cdot \text{L}^{-1}$ can retain many kinds of normal cells in G_1 phase, and this is very helpful for the medicine combination which is being used to cure the patients carrying cancers.

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Staurosporine 阻断正常细胞于 G₁/S 时相的边界

王瑞虹, 薛绍白

R977

(北京师范大学生物系细胞研究室, 北京 100875, 中国)

关键词 staurosporine; 核分裂间期; S期; 激酶抑制剂; 胸腺嘧啶核苷激酶; 成纤维细胞; 培养的细胞; 胃癌; 流式细胞光度术; 磷酸化

目的: 通过使用非特异性激酶抑制剂 staurosporine (5 μg·L⁻¹), 揭示正常与肿瘤细胞之间在 G₁/S 时相过渡阶段调控的不同。方法: 流式细胞光度术, 点杂交, 激酶活性分析, 电泳。结果: 18 小时 staurosporine (5 μg·L⁻¹) 的处理, 可以阻断正常细胞系 2BS 细胞(人胚胎肺成纤维细胞, 5-20 代)于 G₁ 期, 降低其胞内胸腺嘧啶核苷激酶(TK)的转录和活性水平, 同时也去磷酸化胞内一个 107 kDa 的蛋白。在 2BS 细胞系中, 所有以上现象在洗去 staurosporine 后都可以得到逆转。但是, 所有以上结果在 BGC-823 细胞内(人胃癌细胞)未曾出现。结论: 在 G₁/S 时相过渡阶段, 正常与肿瘤细胞的调节存在差别。在正常细胞中, 参与这一调节的激酶对 staurosporine (5 μg·L⁻¹) 比在肿瘤细胞内的激酶敏感得多。

Effects of dexamethasone and ibuprofen on LPS-induced gene expression of TNF_α, IL-1β, and MIP-1α in rat lungQIU Hai-Bo, PAN Jia-Qi¹, ZHAO Yong-Qiang¹, CHEN De-Chang(Department of Critical Care Medicine, ¹Department of Hematology, Peking Union Medical College Hospital, Chinese Academy of Medical Sciences. Beijing 100730, China)

KEY WORDS Wistar rats; lipopolysaccharides; tumor necrosis factor; interleukin-1; gene expression; dexamethasone; ibuprofen; respiratory distress syndrome

AIM: To study the kinetics of tumor necrosis factor α (TNF_α), interleukine-1β (IL-1β), and macrophage inflammatory protein-1α (MIP-1α) gene expression in rat lung after ip lipopolysaccharides (LPS) and the effect of dexamethasone (Dex) and ibuprofen (Ibu) on the cytokines gene expression. **METHODS:** The

amount of Evans blue in lung was measured by fluorescence method. The mRNA levels of TNF_α, IL-1β, and MIP-1α in rat lung were assessed by slot blot analysis. **RESULTS:** The mRNA levels of TNF_α, IL-1β, and MIP-1α in rat lung after ip LPS increased in a dose-dependent manner, and peaked at 2, 6, and 12 h, respectively. Both Dex 50 mg·kg⁻¹ and Ibu 90 mg·kg⁻¹ injected at 1 h before ip LPS markedly decreased the content of Evans blue in lung at 1 h after ip LPS. After Dex or Ibu pretreatment, the peak levels of TNF_α, IL-1β, and MIP-1α mRNA decreased markedly compared with LPS alone. **CONCLUSION:** The gene expression of TNF_α, IL-1β, and MIP-1α in rat lung increased