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A derivative of imidazobenzimidazole, ML106, inhibits melanin synthesis via p38 MAPK activation

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We investigated the effects of ML106 on melanogenesis in B16F10 melanoma cells. Our results showed that ML106 decreased melanin content and tyrosinase activity in a dose-dependent manner. Interestingly, ML106 did not inhibit microphthalmia-associated transcription factor (MITF) expression, but did decrease tyrosinase expression. Thus, we further investigated the expression and degradation of tyrosinase and related signal transduction pathways. Although ML106 increased glycogen synthase kinase 3 β (GSK3 β) activation, the level of β -catenin level was not affected. Thus, we excluded the involvement of GSK3 β and β -catenin in ML106-induced hypopigmentation. However, ML106 induced the phosphorylation of p38 mitogen-activated protein kinase (MAPK), causing down-regulation of tyrosinase. Thus, we next investigated whether tyrosinase down-regulation was due to proteasomal degradation by p38 MAPK activation. We found that ML106-induced tyrosinase down-regulation was restored by MG132, a proteasome inhibitor. Thus, we propose that ML106 has hypopigmentary activity through tyrosinase degradation *via* p38 MAPK phosphorylation.

1. Introduction

Melanocytes produce melanin in the basal layer of the epidermis, and surrounding keratinocytes receive and distribute melanosomes, thereby regulating human skin color (Yamaguchi et al. 2007; Yamaguchi and Hearing 2009). Melanin synthesis occurs within melanosomes that contain three major melanogenic enzymes: tyrosinase, tyrosinase-related protein 1 (TRP1), and TRP2 (Uyen et al. 2008). Tyrosinase is a key enzyme involved in melanin synthesis, and microphthalmia-associated transcription factor (MITF) is an important transcription factor that regulates tyrosinase (Takeda et al. 2000). Tyrosinase has been shown to undergo post-translational degradation. Tyrosinase down-regulation by degradation can result in decreased melanin synthesis in melanocytes (Francis et al. 2003; Park et al. 2009). Degradation of abnormal proteins misfolded in the endoplasmic reticulum (ER) and short-lived proteins occurs selectively *via* the ubiquitin-proteasome pathway. Proteasomes are multicatalytic proteinase complexes located within cells that selectively degrade ubiquitinated proteins (Hiller et al. 1996; Hochstrasser 1996).

Abbreviations: GSK3 β , glycogen synthase kinase 3 β ; MAPK, mitogen-activated protein kinase; MC1R, melanocortin 1 receptor; MITF, microphthalmia-associated transcription factor; α -MSH, α -melanocyte stimulating hormone; TRP, tyrosinase-related protein; USF-1, upstream stimulating factor-1.

There are discrepancies in the reported effects of glycogen synthase kinase 3 β (GSK3 β) on melanogenesis. First, activation of the Wnt pathway results in activation of Frizzled receptors, inhibition of GSK3 β , and stimulation of β -catenin accumulation (Bellei et al. 2008; Wu et al. 2003). Accumulated β -catenin forms a complex the lymphoid-enhancing factor/T-cell factor (LEF/TCF), and formation of this complex leads to upregulation of MITF (Widlund et al. 2002; Wu et al. 2003). Thus, the GSK3 β pathway can control melanogenesis *via* β -catenin regulation. Second, activation of Akt signaling plays a role in the regulation of melanogenesis through phosphorylation (inactivation) of GSK3 β on serine 9 (Khaled et al. 2002). Therefore, GSK3 β inactivation inhibits MITF phosphorylation at serine 298 and decreases MITF binding affinity to the tyrosinase promoter, leading to (down-regulation) of tyrosinase expression and inhibition of melanogenesis (Khaled et al. 2002). Thus, the GSK3 β pathway can control melanogenesis *via* regulation of MITF phosphorylation.

Mitogen-activated protein kinases (MAPKs), which include extracellular signal-regulated protein kinase (ERK), p38 MAPK, and c-jun N-terminal kinase (JNK), are known to be involved in cell proliferation, differentiation, stress response, and apoptosis (Harper and LoGrasso 2001; Kim et al. 2007). It was reported that the p38 MAPK signaling pathway is also involved in stress-induced melanogenesis (Corre et al. 2004). Moreover, p38 MAPK activated upstream stimulating factor-1 (USF-1) is necessary for UV-induced tyrosinase expression

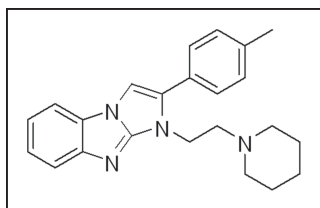


Fig. 1: Chemical structure of ML106.

(Corre and Galibert 2005; Park et al. 2010). However, it has also been reported that tyrosinase degradation is related to p38 MAPK activation (Bellei et al. 2010). Thus, the role of p38 MAPK in melanogenesis needs to be investigated in greater detail.

To develop a new skin-whitening agent, we screened 35 compounds from our in-house chemical library. Among these, we selected ML106 (Fig. 1) for further study because it had the best hypopigmentary effects. In the present study, we investigated the effects of ML106 on melanin synthesis and tyrosinase activity using B16 mouse melanoma cells. In addition, we examined the molecular mechanisms by which ML106 regulates melanogenesis.

2. Investigations and results

2.1. Effects of ML106 on cell viability and melanin synthesis

B16F10 cells were treated with ML106 at various concentrations ranging from 0.1 to 10 μM for 24 h. Cell viability was determined using a crystal violet assay. As shown in Fig. 2A, ML106 was not cytotoxic at concentrations of 0.1–10 μM . Therefore, we used concentrations ranging from 0.1 to 10 μM of ML106 for further experiments. First, we measured melanin content after ML106 treatment for 3 days in the presence of $\alpha\text{-MSH}$ (1 μM). Our results showed that ML106 treatment decreased melanin synthesis in a dose-dependent manner (Fig. 2B). Next, we examined tyrosinase activity in cells treated with ML106 and the direct effect of ML106 on tyrosinase activity using mushroom tyrosinase. We found that ML106 treatment decreased $\alpha\text{-MSH}$ -stimulated tyrosinase activity significantly (Fig. 2C).

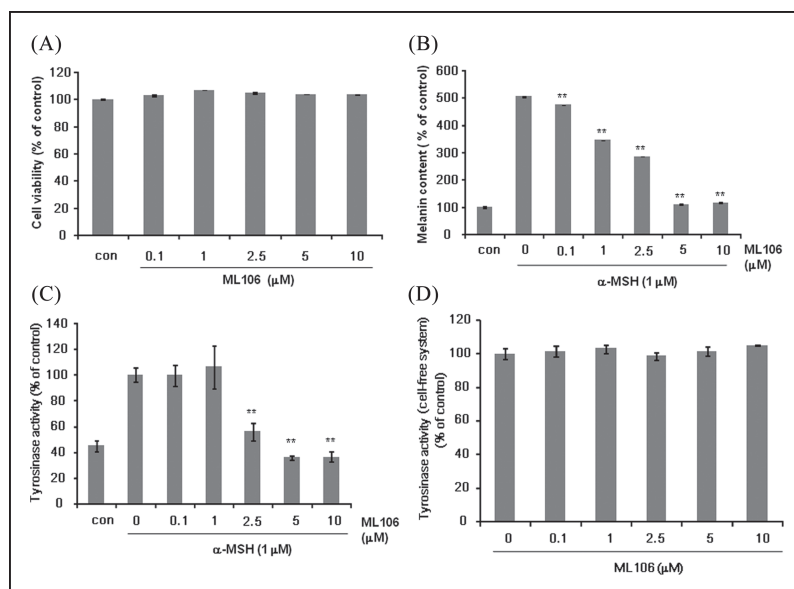


Fig. 2: Effects of ML106 on melanogenesis in B16F10 cells. (A) After serum starvation for 24 h, cells were treated with 0.1–10 μM ML106 for 24 h in serum-free media. Cell viability was determined by the crystal violet assay. Cells were treated with ML106 (0.1–10 μM) in the presence of $\alpha\text{-MSH}$ (1 μM) for 3 days. Melanin content (B), tyrosinase activity (C), and tyrosinase activity in a cell-free system (D) were measured, as described in the Experimental section. Results shown are the averages of triplicate experiments \pm SD. ** $P < 0.01$ versus $\alpha\text{-MSH}$ -treated controls.

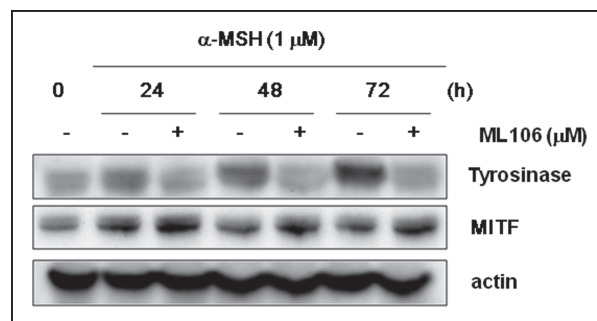


Fig. 3: Effects of ML106 on MITF and tyrosinase protein expression. B16F10 cells were treated with ML106 (5 μM) in the presence of $\alpha\text{-MSH}$ (1 μM) for 24–72 h. Whole cell lysates were then subjected to western blot analysis using antibodies against MITF and tyrosinase. Equal protein loading was confirmed using anti-actin antibody.

However, ML106 did not inhibit tyrosinase activity directly (Fig. 2D). These results suggest that the hypopigmentary activity of ML106 may result from inhibition of the melanogenic pathway involving tyrosinase expression, but not from the direct inhibition of tyrosinase.

2.2. Effects of ML106 on MITF and tyrosinase protein level

Next, we performed western blot analysis to examine MITF and tyrosinase protein levels in $\alpha\text{-MSH}$ -stimulated B16F10 cells treated with ML106 (5 μM). Interestingly, tyrosinase protein expression decreased clearly from 24 h to 72 h, while MITF levels did not change (Fig. 3). These data suggest that ML106 may induce tyrosinase protein degradation.

2.3. Effects of ML106 on signaling pathways involved in melanogenesis

Several reports have indicated that Akt and GSK3 β phosphorylation regulate melanogenesis. Accordingly, we examined whether ML106 (5 μM) induced Akt and GSK3 β phosphorylation in a time course experiment. As shown in Fig. 4A, ML106 inhibited Akt and GSK3 β phosphorylation. The level

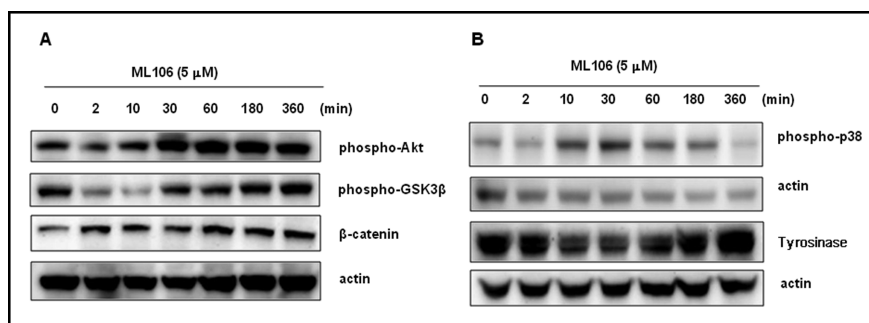


Fig. 4: Effects of ML106 on signal transduction pathways in B16F10 cells. After 24 h of serum starvation, cells were treated with 5 μ M ML106 for the times indicated. (A) Whole cell lysates were then subjected to western blot analysis using antibodies against phospho-specific Akt, phospho-specific GSK3 β , and β -catenin. (B) Western blot analysis was performed using antibodies against phospho-specific p38 MAPK and tyrosinase. Equal protein loading was confirmed using anti-actin antibody.

of β -catenin level did not change. In contrast, we found that ML106 induced phosphorylation of p38 MAPK. The level of p38 MAPK peaked after 30 min (Fig. 4B). In accordance with the increase in p38 MAPK phosphorylation, the tyrosinase level decreased (Fig. 4B).

2.4. ML106 decreases tyrosinase protein expression via proteasomal degradation

Next, we evaluated whether the ML106-induced down-regulation of tyrosinase was due to post-translational degradation of tyrosinase. To accomplish this, we used a proteasome inhibitor, MG132. To inhibit protein synthesis, cycloheximide was added to B16F10 cells. Cells were pretreated with 150 nM of MG132 for 3 h followed by 30 min of ML106 treatment. Tyrosinase levels were then analyzed using western blot analysis. The ML106-induced decrease in tyrosinase level was restored by MG132 pretreatment, but p38 phosphorylation was not affected (Fig. 5). These data indicate that tyrosinase down-regulation is due to proteasomal degradation.

3. Discussion

Human skin pigmentation is regulated by complex and intricate interactions between melanocytes and keratinocytes in the epidermis (Choi et al. 2010). Many studies have focused on developing new therapeutic agents to prevent hyperpigmentation. Therefore, we investigated whether ML106 inhibited hyperpigmentation induced by α -MSH in B16F10 melanoma cells. Moreover, we focused the mechanistic basis of ML106 regulation of melanogenesis.

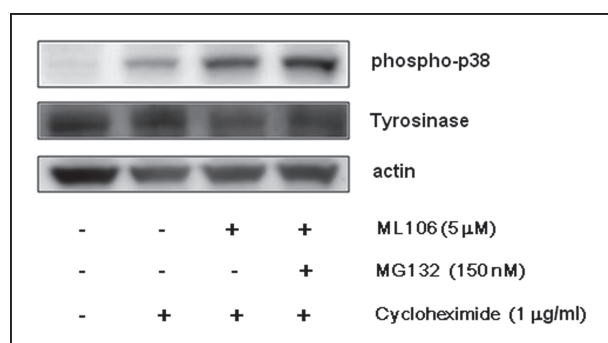


Fig. 5: Effects of inhibition of proteasomal degradation on melanogenesis. Following serum starvation for 24 h, cells were pretreated with 1 μ g/ml of cycloheximide for 1 h and with 150 nM MG132 for 3 h as indicated, after which they were treated with 5 μ M ML106 for 30 min. Whole cell lysates were then subjected to western blot analysis with antibodies against phospho-specific p38 MAPK or tyrosinase. Equal protein loading was confirmed using anti-actin antibody.

MITF is a major transcriptional regulator of melanogenic enzymes such as tyrosinase and TRP1 (Bentley et al. 1994; Busca and Ballotti 2000; Kim et al. 2003). Several reports have suggested that Akt inhibition and subsequent GSK3 β activation stimulate MITF binding to the M-box of the tyrosinase promoter *via* MITF phosphorylation at serine 298, thereby up-regulating melanogenic protein expression and inducing melanogenesis (Kang et al. 2011; Lin et al. 2012; Takeda et al. 2000). For example, we reported that GSK3 β inactivation by KHG25855 reduced MITF binding affinity and subsequently decreased tyrosinase expression (Kim et al. 2011). However, we showed in the present study that ML106 did not stimulate melanin synthesis, even though it inhibited Akt and activated GSK3 β . It has also been reported that activation of GSK3 β can cause β -catenin degradation, leading to decreased melanin synthesis (Bellei et al. 2008; Wu et al. 2003). However, the level of β -catenin was not altered by ML106 treatment. Instead, ML106 reduced tyrosinase protein expression without decreasing MITF protein expression (Fig. 3). These results indicate that GSK3 β activation is not related to ML106-induced hypopigmentation.

As mentioned in the introduction, the ERK and p38 MAPK pathways are involved in the regulation of melanin synthesis (Hirata et al. 2007; Smalley and Eisen 2000; Tsang et al. 2012). In our experiment, however, ERK levels did not change after ML106 treatment (data not shown). Rather, ML106 induced p38 MAPK phosphorylation. On the one hand, p38 MAPK has been shown to increase tyrosinase expression with the concomitant accumulation of melanin (Jiang et al. 2009; Lee et al. 2011). On the other hand, the phosphorylation of p38 MAPK is related to tyrosinase degradation (Bellei et al. 2010). The major pathways of protein degradation in eukaryotic cells include proteolysis in proteasomes and lysosomes. Tyrosinase could be degraded in proteasomes *via* ER-associated protein degradation after the post-Golgi stage, as reported in linoleic acid-treated melanoma cells (Ando et al. 2007, 2006), or it could be degraded *via* the endosomal/lysosomal degradation system, as reported in phenylthiourea-treated melanoma cells (Hall and Orlow 2005). To investigate tyrosinase degradation, we treated cells with the proteasome inhibitor MG132 and evaluated changes in the levels of tyrosinase expression by western blot analysis. As shown in Fig. 5, the ML106-induced decrease in tyrosinase level was restored by treatment of cells with MG132. These results indicate that ML106-induced tyrosinase down-regulation is due to tyrosinase degradation by the proteasomal pathway.

In summary, our results suggest that ML106 functions as an inhibitor of melanin synthesis in B16F10 cells. Furthermore, ML106-induced tyrosinase down-regulation is associated with p38 MAPK phosphorylation and subsequent tyrosinase degradation. These results suggest that ML106 is a new potential skin whitening agent that functions by decreasing tyrosinase.

4. Experimental

4.1. Materials

ML106 was synthesized at the Medicinal Chemistry Laboratory (Chung-Aug University, Seoul, Korea). The chemical name of ML106 is 2-(4-methylphenyl)-1-[2-(1-piperidiny)ethyl]-1*H*-Imidazo[1,2-*a*]benzimidazole. The structure of ML106 is shown in Fig. 1. ML106 was dissolved in DMSO and stored at -20°C as a stock solution (10 mM). Synthetic melanin, 3,4-dihydroxy-L-phenylalanine (L-DOPA), and mushroom tyrosinase were purchased from Sigma-Aldrich Co. (St. Louis, MO, USA). SB203580, MG132, and cycloheximide were purchased from Calbiochem (Darmstadt, Germany). Antibodies specific for phospho-p38 MAPK (#9211), phospho-Akt (ser473, #9271), phospho-GSK3β (#9336), and β-catenin (#9581) were purchased from Cell Signaling Technology (Beverly, MA, USA). Antibodies specific for tyrosinase (C-19) and actin (I-19) were purchased from Santa Cruz Biotechnology, Inc. (Santa Cruz, CA, USA), and microphthalmia Ab-1 (C5, MS-771-P0) was obtained from NeoMarkers (Fremont, CA, USA).

4.2. Cell culture

B16F10 murine melanoma cells were obtained from the Korean Cell Line Bank (Seoul, Korea). Cells were maintained in Dulbecco's modified Eagle's medium (DMEM) supplemented with 10% (v/v) fetal bovine serum (FBS; Hyclone, Logan, UT, USA) and 1% (v/v) penicillin-streptomycin in 5% CO₂ at 37°C.

4.3. Cell viability assay

Cell viabilities were determined using a crystal violet assay. After incubating cells with ML106 for 24 h, media was removed, and cells were stained with 0.1% crystal violet in 10% ethanol for 5 min at room temperature. Cells were then rinsed four times with distilled water, and the crystal violet retained by adherent cells was extracted with 95% ethanol. Absorbance was determined at 590 nm using an ELISA reader (VERSAMax; Molecular Devices, Sunnyvale, CA, USA).

4.4. Measurement of melanin content

B16F10 cells were incubated at a density of 1x10⁵ cells in 6-well plates overnight. α-MSH (1 μM) was then added and cells were treated with increasing concentrations of ML106 in phenol red-free DMEM for 3 days. Aliquots of media (200 μL) were then placed in 96-well plates and the optical density (OD) of each culture well was measured using an ELISA reader at 400 nm. Cell numbers were then counted using a hemocytometer. Melanin production was expressed as a percentage of the untreated control.

4.5. Tyrosinase activity

Tyrosinase activity was assayed as DOPA oxidase activity. B16F10 cells were incubated at a density of 1x10⁵ cells in 6-well plates, and incubated with ML106 in DMEM for 3 days. Cells were washed with PBS and lysed with lysis buffer (0.1 M phosphate buffer [pH 6.8] containing 1% Triton X-100). They were then disrupted by freeze-thawing, and lysates were clarified by centrifugation at 13,000 rpm for 30 min. After quantifying protein content using a protein assay kit (Bio-Rad, Hercules, CA, USA), cell lysates were adjusted to the same amount of protein with a lysis buffer, 90 μl of each lysate was placed in a well of a 96-well plate, and 10 μl of 10 mM L-DOPA was added. Control wells contained 90 μl lysis buffer and 10 μl 10 mM L-DOPA. After incubation at 37°C for 20 min, dopachrome formation was monitored by measuring absorbance at 475 nm using an ELISA reader. A cell-free assay system was used to investigate the direct effect of ML106 on tyrosinase activity. Seventy microliters of phosphate buffer containing ML106 was mixed with 20 μl of 10 μg/ml mushroom tyrosinase, and 10 μl of 10 mM L-DOPA was then added. Following incubation at 37°C, absorbance was measured at 475 nm.

4.6. Western blot analysis

Cells were lysed in cell lysis buffer (62.5 mM Tris-HCl [pH 6.8], 2% SDS, 5% β-mercaptoethanol, 2 mM phenylmethylsulfonyl fluoride, and protease inhibitors [Complete™; Roche, Mannheim, Germany], 1 mM Na₃VO₄, 50 mM NaF, and 10 mM EDTA). Twenty microgram of protein per lane was separated by SDS-polyacrylamide gel electrophoresis and blotted onto PVDF membranes, which were then saturated with 5% dried milk in Tris-buffered saline containing 0.5% Tween 20. Blots were then incubated with the appropriate primary antibodies at a dilution of 1:1000, and further incubated with horseradish peroxidase-conjugated secondary antibodies. Bound antibodies were detected using an enhanced chemiluminescence plus kit (Amersham International, Little Chalfont, UK).

4.7. Statistics

Significance of differences between treatment groups was assessed by Student's t-test. *P* values < 0.01 were considered significant.

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