Process equipped with a sloped UV lamp for the fabrication of gradient-refractive-index lenses

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In this investigation, a method for the preparation of gradient-refractive-index (GRIN) lenses by UV energy-controlled polymerization has been developed. A glass reaction tube equipped with a sloped UV lamp was designed. Methyl methacrylate and diphenyl sulfide were used as the reactive monomer and nonreactive dopant, respectively. Ciba IRGACURE 184 (1-hydroxy-cyclohexyl-phenyl-ketone) was used as the initiator. The effects of initiator concentration, the addition of acrylic polymers, and the preparation conditions on the optical characteristics of the GRIN lenses produced by this method were also investigated. Refractive index distributions and image transmission properties were estimated for all GRIN lenses prepared.

Figure 1. Schematic representation of the equipment for UV-controlled polymerization of plastic rods. The UV lamp is equipped with a small slope angle. The highest energy exists at the bottom and decreases gradually from the bottom to the top, as indicated by the dotted lines. This is consistent with gel zone formed in the reaction tube between A and B.

Figure 2 shows the dependence of the initiator concentration on the $\Delta n$ distribution of the GRIN lens, where $n_p$ and $R_p$ denote the refractive index at the periphery and the radius of the plastic rod, respectively. The results of the refractive index distribution suggest that the concentration of high-refractive-index dopant decreases from the center axis to the periphery of the gel rod, resulting in a GRIN distribution. Higher initiator concentrations were found to increase the polymerization rate. By contrast, nonreactive DS was fixed more easily in the polymer matrix, leading to a decrease in refractive index at the central axis.
Figure 3 shows a color (online) image transmitted through a freshly fabricated GRIN lens with a 15 mm diameter and 80 mm length. An inverted virtual image was obtained through the plastic rod fabricated in this investigation. The distance between the image and the face of the GRIN lens was 60 mm in this trial. The quality of these results suggests that GRIN lenses can be successfully fabricated via UVcontrolled polymerization to produce GRIN lenses with excellent optical properties.

In conclusion, we have demonstrated that a UVcontrolled polymerization can be used to fabricate GRIN plastic rods. This method is a technique that is easy to perform and requires relatively inexpensive equipment and materials.
On-Resistance Degradation Induced by Hot-Carrier Injection in LDMOS Transistors with STI in the Drift Region

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High-voltage devices are integrated into CMOS technologies to fulfill the trend of lower cost and smaller chip size in recent specific high-voltage products. Lateral DMOS (LDMOS) transistors are the suitable devices to be integrated into smart-power applications because of their compatibility with CMOS process. Because LDMOS devices are usually operated under high drain voltage ($V_{ds}$) and high gate voltage ($V_{gs}$), hot-carrier-induced degradation is a major reliability concern in LDMOS transistors. In this work, the phenomenon and mechanisms of hot-carrier-induced on-resistance ($R_{on}$) degradation in n-type LDMOS transistors with shallow trench isolation (STI) in drift region are investigated. Based on experimental data and technology computer-aided-design (TCAD) simulation results, the mechanisms responsible for $R_{on}$ shift are discussed.

Fig. 1 shows the schematic cross section of the n-type LDMOS transistor used in this work. This device is integrated into a 0.25-$\mu$m CMOS process and features a STI in n$^-$ drift region near the drain. The channel length is about 0.3 $\mu$m. The gate oxide thickness and gate width of the device are 30 nm and 10 $\mu$m, respectively. The operational voltages are $V_{ds} = 40$ V and $V_{gs} = 12$ V. To investigate hot-carrier-induced degradation, stressing under $V_{gs} = 40$ V and various $V_{gs}$ is performed at room temperature with source and substrate connected to the ground. The stress tests are interrupted periodically to measure the degradation of device parameters including $R_{on}$. $R_{on}$ ($= \frac{V_{ds}}{I_d}$, where $I_d$ is drain current) is measured under $V_{ds} = 0.1$ V and $V_{gs} = 12$ V. Two-dimensional TCAD simulations are also performed to explain the experimental results.

Two substrate current ($I_{sub}$) peaks are observed in $I_{sub}$-$V_{gs}$ characteristics in our LDMOS devices. The first $I_{sub}$ peak occurs at $V_{gs} = 4$ V that is similar to the behavior in conventional MOSFETs. As $V_{gs} > 8$ V, $I_{sub}$ rises again because of Kirk effect and the second $I_{sub}$ peak occurs at $V_{gs} = 12$ V. When our LDMOS devices are stressed under...
V_{ds} = 40 \text{ V} with various V_{gs} (2.5, 4, 8, and 12 \text{ V}), the device stressed under V_{gs} = 12 \text{ V} degrades the most. As a result, the following analysis is focused on the device stressed under V_{gs} = 12 \text{ V}. Fig. 2 shows $R_{on}$ shift as a function of stress time for the device stressed under $V_{ds} = 40 \text{ V and } V_{gs} = 12 \text{ V}. An unexpected reduction in $R_{on}$ is observed at the beginning of stress. When the stress time is shorter than 10 s, $R_{on}$ is smaller than its fresh value ($I_d$ increases). As the stress time is longer than 10 s, $R_{on}$ is greater than its fresh value ($I_d$ decreases).

To investigate the mechanism of $R_{on}$ degradation, TCAD simulation results are analyzed. Fig. 3(a) shows simulated impact ionization (ii) rate along Si/SiO$_2$ interface when the device is biased at $V_{ds} = 40 \text{ V and } V_{gs} = 12 \text{ V}. Results show that an ii peak exists at the STI corner closest to the channel. Another severe ii generation caused by Kirk effect occurs at the STI edge closest to the drain. Fig. 3(b) shows simulated vertical electric field ($E_y$) along the Si/SiO$_2$ interface under the same bias condition. Positive $E_y$ indicates that the direction of $E_y$ is pointing downward and is favorable for electron injection. Negative $E_y$, on the contrary, is favorable for hole injection. From Fig. 3(a) and Fig. 3(b), the mechanisms of $R_{on}$ degradation are suggested as follows. At the STI corner closest to the channel, energetic electron-hole pairs are generated because of severe ii generation. Holes are injected into STI because of negative $E_y$. Such a hot-hole injection may create hole trapping. Trapping of holes in STI induces negative mirror charges at Si/SiO$_2$ interface in drift region, resulting in an effective increase in drift region concentration. As a result, $I_d$ increases and $R_{on}$ decreases. This inference explains why $R_{on}$ is reduced at the beginning of stress. On the other hand, the severe ii generation at the STI edge closest to the drain results in hot-electron injection because of positive $E_y$. Such an electron injection may create electron trapping and interface trap (N_{it}), leading to $R_{on}$ increase. The damage created at the STI edge closest to the drain is expected to dominate $R_{on}$ degradation as the stress time is longer. This explains why $R_{on}$ is greater than its fresh value after 10 s as in Fig. 2.

To verify the existence of hole trapping, Fig. 4 shows $I_d$ shift measured at different $V_{gs}$ as a function of stress time for
the device in Fig. 2. When $I_d$ is measured at low $V_{gs}$ (= 3.5 V), the current path under STI is deeper. This argument can be confirmed in Fig. 5, where the simulated accumulated current as a function of the depth from Si/SiO$_2$ interface at the location of the STI corner closest to the channel is shown. The current is accumulated from the bottom of n'-region to Si/SiO$_2$ interface. Results show that the accumulated current near Si/SiO$_2$ interface under $V_{gs}$ = 3.5 V rises less rapidly than that under $V_{gs}$ = 12 V, indicating that current path is away from Si/SiO$_2$ interface at low $V_{gs}$. As current flows deeper, the effect of negative mirror charges on $I_d$ increase is less apparent. Thus, $I_d$ decreases monotonously during stress when $I_d$ is measured at $V_{gs}$ = 3.5 V as in Fig. 4. The results in Fig. 4 reveal that hole trapping is responsible for the unexpected $R_{on}$ reduction in the early stage of stress.

In conclusion, the phenomenon and mechanisms of hot-carrier-induced $R_{on}$ degradation in n-type LDMOS transistors with STI in drift region are discussed. $R_{on}$ decreases at the beginning of stress but $R_{on}$ increases afterwards. Experimental data and TCAD simulation results suggest that $R_{on}$ reduction is attributed to hot-hole injection and trapping at the STI corner closest to the channel. According to results presented in this study, the unexpected $R_{on}$ decrease should be paid special attention in evaluating LDMOS transistors’ reliability.

Fig. 4. $I_d$ shift measured at different $V_{gs}$ as a function of stress time for the device in Fig. 2.

Fig. 5. Simulated accumulated current as a function of the depth from Si/SiO$_2$ interface at the location of bottom-left corner of STI.
Paxillin is a 68-kDa adapter protein with five LD motifs at the N-terminus and four tandem LIM domains towards the C-terminus. Paxillin is phosphorylated on specific tyrosine and serine residues mostly located in the N-terminal half in response to growth factors.\textsuperscript{1} Phosphorylation of these residues results in the generation of specific SH2 interaction sites. Several studies clearly demonstrate a role for paxillin in cell motility and metastasis. Our lab has previously shown significantly elevated levels of paxillin in various lung cancer tissue samples as compared to adjacent normal lung tissue.\textsuperscript{2} It is likely that paxillin could contribute both to the lung cancer cell transformation and its metastasis.

In order to understand the role of paxillin in lung tumorigenesis we have systematically examined paxillin expression in lung tumor samples and also determined their relationship to tumor type, stages, cancer progression and metastasis. Paxillin levels increased from normal to dysplasia and to tumor (Fig. 1A). The level of expression of paxillin increased with increasing stage (Fig. 1B), thus clearly implicating paxillin in higher stage tumors—that reflect metastatic setting.

![Image of protein expression](image_url)
To further study the role of paxillin in lung cancer, we determined the mutations of its gene in 191 primary lung and 151 other non-lung tumor samples and 71 cell lines. Bi-directional DNA sequence analysis was carried out and the observed genetic alterations in paxillin are summarized (Fig. 2). We identified a total of 21 somatic paxillin mutations among the lung cancer tissues and cell lines tested. Interestingly, identified paxillin mutations (19/21) were located as two clusters in the region between LD1 and LD2 domains (amino acid residues Pro30 to Gly139) and the region spanning the LIM domains (Fig. 2A). All sequence alterations in this group were heterozygous in the tumor DNA except two cell lines (SK-LU-1 and H820) and four tumor tissues; in each case, paired adjacent normal lung tissue from the same patient showed wild-type sequence, confirming that the mutations are somatic in origin (Fig. 2B-C). The mutational spectra of paxillin were characterized by a high proportion (94% or 32/34) of C:G > T:A transitions, compatible with the mutagenic effects of tobacco carc inogens. It appears that Caucasians, African-Americans, and Taiwanese each show their unique mutational spectrum (Fig. 2B). In addition, we have identified single nucleotide polymorphism for paxillin and differences noticed in the various ethnic groups.

The cytoskeletal protein paxillin was originally identified in focal adhesions and is a natural substrate for several
oxygenic tyrosine kinases, thereby raising the possibility that it itself could contribute to carcinogenesis. Using H522 cells that lack paxillin expression, we also tested the effect of ectopically expressed wild type and paxillinA127T on cell viability after serum starvation. The viability of cells expressing wild type paxillin was comparable to that of vector control cells. Proliferation and colony formation of cells expressing paxillinA127T was at a significantly higher rate (Fig. 3).  

![Image of transfected H522 cells with empty EGFP vector, wild-type paxillin construct or A127T mutant paxillin construct.](image)

Fig. 3. Transfected H522 cells with empty EGFP vector, wild-type paxillin construct or A127T mutant paxillin construct were plated and anchorage independent cell growth of paxillin mutant was assayed. The colonies were then stained and counted. The left panel depicts a representative experiment. The results presented in the right panel are expressed as the number of colonies obtained in control, Wt Paxillin and A127T paxillin respectively (average ± S.D. of three independent experiments).

These findings are particularly interesting in light of recent evidence implicating paxillin in cancer aggressiveness and it will be important to assess the relevance of this alteration for metastasis. These findings have important implications for developing biomarkers and new molecular targeted therapeutic approaches for cancer showing such alteration.

References

A novel homodimeric geranyl diphosphate synthase from the orchid *Phalaenopsis bellina* lacking a DD(X)2–4D motif

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The flowers of many plants emit volatile compounds as a means of attracting pollinators or defense of herbivore attack. Orchidaceae is one of the largest monocotyledon families and various species-specific pollinators often are attracted to spread the pollen by different floral scents (van der Pijl and Dodson, 1969). *Phalaenopsis* spp. has been developed as an important cash plant in Taiwan ornamental industry. Many cultivators would like to breed new scented *Phalaenopsis* spp. species and then promote competition of orchid business. However, cross incompatibility between scented and scentless species usually is a main problem that restricts the traditional breeding techniques for the production of scented offsprings. In some successful cases of cross-breeding, the progenies may either contain a fainted scent or are no longer able to produce scent. Therefore, it would be extremely beneficial if molecular breeding of scent species is the resolution. The scentless orchid plants will be transformed into scented species by introducing the genes encoding for key enzymes involved in scent biosynthesis into the scentless species or cultivars.

Previously, we have identified that floral scents are mainly composed of geraniol and linalool, and their derivatives of monoterpenes in *Phalaenopsis bellina* (Orchidaceae, monocot) by using gas chromatography-mass spectrometry (GC-MS). Combining chemical analysis, genomics, and bioinformatics, we were able to uncover the scent biosynthesis pathway and the relevant genes (Hsiao *et al*., 2006). Terpenoids are one of the largest families in the plant secondary metabolites and play important roles for plant growth and development. All terpenoids are derived from five carbons isoprene as a constructed unit and are produced by a group of the short-chain trans-prenyltransferase family catalyzing including geranyl diphosphate synthase (GDPS), farnesyl diphosphate synthase (FDPS) and geranylgeranyl diphosphate synthase (GGDPS), which synthesize farnesyl diphosphate (FDP, C₁₅) and geranylgeranyl diphosphate (GGDP, C₂₀), respectively (Ogura and Koyama, 1998; Reiling *et al*., 2004).

In this article, the amino acid sequence of *P. bellina* GDPS is analyzed. The alignment of different GDPS
sequences has revealed several conserved regions. These include two prominent aspartate-rich (Asp-rich) motifs, designated as the first Asp-rich motif (FARM) and the second Asp-rich motif (SARM), that share the consensus sequence DD(X)\textsubscript{2–4}D (where X represents any amino acid), and are critical for catalytic function and substrate binding in the trans-prenyltransferase family (Koyama et al., 1996; Wang and Ohnuma, 2000). However, PbGDPS does not contain the FARM and SARM. In the functional assay using radio-TLC, we identified that PbGDPS reveal dual prenyltransferase activities, producing both GDP and FDP. Furthermore, yeast two-hybrid assay and gel filtration indicate that PbGDPS is able to form a homodimer. Molecular modeling was performed to understand how PbGDPS can act as a prenyltransferase without Asp-rich motifs. *Sinapis alba* (mustard) GGDPS (SaGGDPS; PDB ID: 2J1O and 2J1P) was recruited as the best template. We found that the Glu-rich motif in PbGDPS occupied the equivalent positions within these structures of the SARM in SaGGDPS. The Glu-rich motif probably provides a chelating site for Mg\textsuperscript{2+} ions, which are required for the enzyme activity, as is found in the more common SARM (Figure 1). We also performed site-directed mutagenesis of the Glu-rich motif. We replaced the third and fifth glutamate residues (EAEVE) with either two non-polar alanine residues (Ala, A) or two polar aspartate residues (Asp, D), and named the mutants PbGDPS-Ala (EAAVA) and PbGDPS-Asp (EADVD), respectively, and performed prenyltransferase activity assay. The result showed that the PbGDPS-Asp contains about half activity of the wild type PbGDPS (EAEVE), yet the mutant PbGDPS-Ala abolishes the enzyme activity. These results suggest that the glutamate residues in the corresponding SARM motif are crucial for PbGDPS catalytic efficiency.

**Figure 1.** Comparison of 3D Phalaenopsis bellina geranyl diphosphate synthase (PbGDPS) modelling structure and *Sinapis alba* geranylgeranyl diphosphate synthase (SaGGDPS) crystal structure (2J1P_A). (A) The SaGGDPS crystal structure showed residues contacting with diphosphates in the two substrate-binding aspartate-rich motifs directly or via Mg\textsuperscript{2+}. The first and second aspartate-rich motifs are highlighted in purple and green, respectively. (B) Modeling structure of PbGDPS. The positions corresponding to two common substrate-binding aspartate-rich motifs in SaGGDPS are highlighted in purple and green. The residue (E192) in the glutamate-rich region corresponding to D237 of SaGGDPS, and the residue E194 corresponding to D98 of SaGGDPS, which was far away from the binding site in the modelling structure, are labelled in red.

Spatial and temporal expression analyses showed that the expression of PbGDPS was flower specific, and that maximal PbGDPS expression was concomitant with maximal emission of monoterpenes on day 5 post-anthesis. We suggest that PbGDPS play a vital role in the emission of floral scents controlling. Therefore, we further analyzed PbGDPS expression in various orchid species with different scent-producing abilities. The major volatiles of *P. bellina* are linalool and geraniol (Hsiao et al., 2006). The flowers of *Doritaenopsis* Kenneth Schubert ‘five’, the progeny of a cross between *Doritaenopsis pulcherrima* × *P. bellina*, emitted only linalool, and the level of linalool was much lower than that emitted from the parental scented species *P. bellina*. In contrast, the progeny of another cross between *D. pulcherrima* × *P. bellina*, *D. Kenneth Schubert*, does not produce any scent that can be detected by humans. We also analyzed two varieties of *Phalaenopsis* equestris. The scented flowers of *P. equestris* ‘W-72’ emit volatiles that are not monoterpenes (Hsiao *et al*., 2006), as do those of the scentless.
species *P. equestris*. The results show that analysis of PbGDPS in these plants with contents of linalool and geraniol revealed similar expressed tendency (Figure 2). Therefore, we suggest that PbGDPS play a key role in the regulation of scent production in *P. bellina* flowers.

![Figure 2](image)

Figure 2. Scented species of *Phalaenopsis bellina*, *Phalaenopsis equestris* ‘W9-72’ and *Doritaenopsis* Kenneth Schubert ‘five’, and scentless species of *P. equestris* and *D. Kenneth Schubert*. (A) Scented and scentless *Phalaenopsis* species. (B) Detection of PbGDPS transcripts by RT-PCR with PbGDPS gene-specific primers and RNA isolated from various flowers on day 5 post-anthesis. (C) The flowers volatile components were collected from three flowers during each sampling period for 9 h (from 09:00 h to 18:00 h) from day 5 post-anthesis and were analyzed by GC-MS. The resulting products were separated by gas chromatography and identified by comparison of mass spectra and retention times with those of authentic standards (bottom panel). The black circle indicates linalool and the white circle indicates geraniol.

References:
