漢方薬学分野（10月31日まで） Division of Pharmacognosy
生薬資源科学分野（11月１日から）

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◇研究目的　Aims of the research projects

地球環境の変化により，薬用天然資源の減少が危惧される。そこで本分野では，生薬資源の現状の把握と代替生薬の開発，生薬の特徴を把握した効率的利用の促進並びに栽培薬用植物の選択と栽培拡充を目的にして，アジアにおける漢薬資源の調査と薬用生物の遺伝学的，生薬学的，成分化学的及び薬理学的多様性の解析を行う。また，生薬・漢方薬の品質管理と健康食品のレギュレーションを目的にして，遺伝子多型に基づく生薬同定法の開発並びに品質評価法の確立を行う。さらに，民族薬物データベースを拡充し，各国の生薬の標準化や適正使用に役立てる。

◇研究概要　Research projects

Ⅰ）薬用生物及び伝統薬物の調査研究

モンゴル国東部で *Ephedra* 属，*Glycyrrhiza* 属，*Astragalus* 属植物などの資源調査を行った。また，中国四川省及び甘粛省で野生及び栽培 *Rheum* 属植物の調査を行った。

Ⅱ）薬用植物・生薬の多様性の解析

モンゴル産 *Glycyrrhiza uralensis* の地下部の成分化学的多様性を薬理作用成分の含量から検討した。Glycyrrhizin含量は中国産甘草にほぼ匹敵したが，フラバノン類及びカルコン類が低含量であり，また産地間差が大きかった。

Curcuma 属７種に由来する鬱金類生薬の薬理学的多様性を，アジュバント関節炎に対する作用で検討した。莪朮の基源である３種の根茎に抗炎症作用が期待できた。とくに *C. phaeocaulis* メタノールエキスは，肢の腫脹と血清中の炎症マーカータンパク質の発現を有意に抑制し，また *in vitro* 実験においてCOX-2活性の抑制作用を有意に示した。

Ⅲ）生薬・健康食品の品質とレギュレーション

日本市場のガジュツについて，*trnK* 遺伝子の解析及び精油含量・エキス含量の定量を行った。四川省産ガジュツは *C. phaeocaulis* の根茎であったが，広西壮族自治区産は *C. kwangsiensis*（gl タイプ）が多かったものの，上記２種または *C. kwangsiensis*（pl タイプ）の１塩基または２塩基置換体が認められ，交雑が示唆された。

人参類及びウコン類健康食品の遺伝子解析を行い，同時に ginsenosides 6 成分または curcuminoids 3 成分を定量した。ウコン類には基源不明で curcuminoids 含量が4.5%の製品があり，成分組成も *C. longa* とは異なった。

Ⅳ）薬用植物の遺伝子多型に基づく生薬同定法の開発

Panax 属13分類群の 18S rRNA 遺伝子の塩基配列に基づいた合成オリゴを作成し，人参類同定用DNA マイクロアレイの試作品を開発した。

◇原著論文　Original papers

1）**Sasaki Y., Fushimi H., and Komatsu K.: Application of Single Nucleotide Polymorphisms Analysis of *trn*K Gene to the Identification of *Curcuma* Plants. *Biol. Pharm. Bull.*, 27: 144-146, 2004.**

Abstract: We previously found that *Curcuma* plants and drugs derived from *Curcuma longa, C. phaeocaulis, C. zedoaria,* and *C. aromatica* could be identified by the nucleotide differences at two sites and the existence of a 4-base indel on *trn*K gene. In this paper, based on species-specific nucleotide sequences, the application of a new method, single-nucleotide polymorphism (SNP) analysis was investigated to identify *Curcuma* plants more conveniently. First, three types of reverse primer were synthesized in different lengths, 34 mer, 26 mer, and 30 mer, to anneal the template DNAs from each species at sites immediately upstream from substitution positions 177 and 645, and at the site including the 4-base insertion from 728 to 731, respectively. After single-base extension reaction of these primers using fluorescent-labeled ddNTPs and PCR products of the *trn*K gene region as template, the resulting products were detected using an ABI PRISM 310 Genetic Analyzer. The electrophoretogram showed three or two peaks at different positions depending on the 27 mer, 31 mer, and 35 mer product lengths. Each peak was derived from the incorporated fluorescent-labeled ddNMPs complementary to template nucleotides at positions 645, 724, and 177, respectively. *C. phaeocaulis* showed three peaks of ddCMP, ddAMP, and ddAMP. The other three species showed two peaks derived from 27 mer and 35 mer products: peaks of ddCMP and ddAMP in *C. longa,* those of ddCMP and ddTMP in *C. zedoaria,* and those of ddTMP and ddAMP in *C. aromatica.* Thus SNP analysis to identify four *Curcuma* plants was newly developed.

2）**Zhao J., Nakamura N., Hattori M., Yang X. W., Komatsu K., and Qio M. H.: New Triterpenoid Saponins from the Roots of *Sinocrassula asclepiadea. Chem. Pharm. Bull.*, 52: 230-237, 2004.**

3）**Tohda C., Matsumoto N., Zou K., Meselhy M. R., and Komatsu K.: Aβ (25-35)-induced memory impairment, axonal atrophy and synaptic loss are ameliorated by M1, a metabolite of protopanaxadiol-type saponins. *Neuropsychopharmacology,* 29: 860-868, 2004.**

Abstract: We previously screened neurite outgrowth activities of several Ginseng drugs in human neuroblastoma, and demonstrated that protopanaxadiol (ppd)-type saponins were active constituents. Since ppd-type saponins are known to be completely metabolized to 20-*O*-β-D-glucopyranosyl-20(*S*)-protopanaxadiol (M1) by intestinal bacteria when taken orally, M1 and ginsenoside Rb1, as a representative of ppd-type saponins, were examined for cognitive disorder. In a mouse model of Alzheimer's disease (AD) by Aβ (25-35) i.c.v. injection, impaired spatial memory was recovered by p.o. administration of ginsenoside Rb_1 or M1. Although the expression levels of phosphorylated NF-H and synaptophysin were reduced in the cerebral cortex and the hippocampus of Aβ (25-35)-injected mice, their levels in ginsenoside Rb_1- and M1-treated mice were almost completely recovered up to control levels. Potencies of the effects were not different between ginsenoside Rb_1 and M1 when given orally, suggesting that most of the ginsenoside Rb_1 may be metabolized to M1, and M1 is an active principal of ppd-type saponins for the memory improvement. In cultured rat cortical neurons, M1 showed extension activity of axons, but not dendrites. The axon-specific outgrowth was seen even when neuritic atrophy had already progressed in response to administration of Aβ (25-35) as well as in the normal condition. These results suggest that M1 has axonal extension activity in degenerated neurons, and improve memory disorder and synaptic loss induced by Aβ (25-35). M1 was shown to be effective in vitro and in vivo, indicating that Ginseng drugs containing ppd-type saponins may reactivate neuronal function in AD by p.o. administration.

4） **Zhu S., Fushimi H., Cai S. Q., and Komatsu K.: Species Identification from Ginseng Drugs by Multiplex Amplification Refractory Mutation System (MARMS). *Planta Med.*, 70: 189-192, 2004.**

Abstract: The multiplex amplification refractory mutation system (MARMS) was applied to the identification of 5 *Panax* species (*P. ginseng, P. japonicus, P. quinquefolius, P. notoginseng* and *P. vietnamensis*). A set of specific primers, including 2-pair primers on chloroplast *trn*K gene and nuclear 18S rRNA gene regions, respectively, was designed and synthesized for each species on the basis of species-specific sequences of the 2 genes. By using 5 sets of specific primers, in turn, PCR amplifications were performed with total DNA extracted from 5 *Panax* species as template under appropriate condition, and each resulting product was detected by agarose gel electrophoresis. The results showed that two expected fragments, one from *trn*K gene and another from 18S rRNA gene regions, were observed simultaneously only when the set of species-specific primers encountered template DNA of the corresponding species. This assay could give more reliable results for identification of not only 5 *Panax* species but also corresponding Ginseng drugs by simultaneous detection of 4-site nucleotide differences on 2 completely different genes.

5） **Yang D. Y., Fushimi H., Cai S. Q., and Komatsu K.: Molecular Analysis of *Rheum* Species Used as Rhei Rhizoma Based on Chloroplast *mat*K Gene Sequence and Its Application for Identification. *Biol. Pharm. Bull.*, 27: 375-383, 2004.**

Abstract: Rhei Rhizoma (Dahuang in Chinese) is widely known as a purgative and antiinflammatory agent. In the Japanese Pharmacopoeia, Rhei Rhizoma is prescribed for four *Rheum* species, *Rheum palmatum, R. tanguticum, R. officinale,* and *R. coreanum,* while the first three species are prescribed for Dahuang in the Chinese Pharmacopoeia. Due to the morphologic similarity of the aerial parts and frequent occurrence of intermediate forms, the taxonomy of this genus and the correct identification of *Rheum* species and their derivative drugs are very difficult. To resolve taxonomic problems of the genus Rheum and develop an ultimate identification method for plants and drugs, molecular analysis of the chloroplast *mat*K gene and nuclear 18S ribosomal RNA gene were performed on nine species. The sequence comparison of the *mat*K gene revealed that most species had variable sequences not only inter- but also intraspecies. However, the specimens of the same species belonged to the same subclade in the phylogenetic tree constructed based on *mat*K gene sequences, except for *R. palmatum,* in which specimens belonged to three subclades related to their production areas. The nucleotide differences at positions 587, 707, and 838 distinguished official species from others, while specific nucleotides at positions 367 and 937 became identification markers for *R. palmatum, R. tanguticum,* and *R. officinale* (or *R. coreanum*). Moreover, three groups of *R. palmatum,* each belonging to three subclades, were characterized by the nucleotides at positions 619, 769, 883, and 1061. By detecting marker nucleotides, the botanical origins of Rhei Rhizoma were determined.

6） **Teerawatanasuk N., Nakamura E. S., Wangma-neerat A., Komatsu K., Saiki I: Anti-invasive and anti-angiogenic activities of *Curcuma* sp. extracts. *J. Trad. Med.*, 21: 27-33, 2004.**

7） **Yang D. Y., Fushimi H., Cai S. Q., and Komatsu K.: Polymerase Chain Reaction - Restriction Fragment Length Polymorphism (PCR-RFLP) and Amplification Refractory Mutation System (ARMS) Analyses of Medicinally Used *Rheum* Species and Their Application for Identification of Rhei Rhizoma. *Biol. Pharm. Bull.*, 27: 661-669, 2004.**

Abstract: Previously, we have determined marker nucleotides on the chloroplast *mat*K gene to identify *Rheum palmatum, R. tanguticum* and *R. officinale* used as Rhei Rhizoma officially. In the present study, we further developed a convenient and efficient identification method on the basis of marker nucleotides with Amplification Refractory Mutation System analysis. On the basis of the nucleotide substitutions at positions 367 and 937 among

the three species on the *mat*K gene, at each position two kinds of reverse primers with complementary 3'-terminal nucleotides were designed. Upon PCR amplification using three sets of primers and template DNA from each species, one or two fragments (202 bp or/and 770 bp) were detected. As the resultant three fragment profiles were species-specific, the procedure enabled us to classify the botanic origins of 22 drug samples of Rhei Rhizoma.

8) **Zhu S., Zou K., Fushimi H., Cai S. Q., and Komatsu K.: Comparative Study on Triterpene Saponins of Ginseng Drugs. *Planta Med.*, 70: 666-677, 2004.**

Abstract: A comparative study on the triterpene saponins of 47 samples of Ginseng drugs derived from 12 *Panax* taxa was conducted using a reverse-phase high-performance liquid chromatography (HPLC) method. Eleven ginsenosides, which represent 4 types of typical sapogenins, were chosen as standards for quantitative determination in order to characterize the chemical constituent pattern of each Ginseng drug and investigate the relationship between genetic varieties and chemical constituent pattern. The results showed that the ginsenoside compositions in Ginseng drugs of different origins were of considerable variability. Total saponin contents varied by 10-fold from the highest drug to the lowest one. Chikusetsu-ninjin derived from *P. japonicus* (Japan) was found to have the highest content (192.80 - 296.18 mg/g) and Ginseng from *P. ginseng* to be the lowest (5.78 - 15.63 mg/g).Two main groups (I and II) suggested by phytochemical data were clearly observed; group I mainly containing dammarane saponins consisted of *P. ginseng, P. quinquefolius, P. notoginseng, P. vietnamensis* and *P. vietnamensis* var. *fuscidiscus*; and group II containing a large amount of oleanolic acid saponins was composed of *P. japonicus* (Japan), *P. zingiberensis, P. japonicus* (China), *P. japonicus* var. *angustifolius, P. japonicus* var. *major, P. japonicus* var. *bipinnatifidus* and *P. stipuleanatus.* The ratios of the subtotal of dammarane saponins to that of oleanolic acid saponins (D/O) were found to be > 1.9 and < 0.25 for groups I and II, respectively. The drug samples derived from the same botanical origin revealed similar constituent patterns, in other words, each *Panax* taxon showed its own characteristic chromatographic profile,which appeared in the specific shape of an 11-direction radar graph constructed on the basis of the result of quantitative analysis. Similarities of chemical constitution were seen among the closely phylogenetically-related taxa, including *P. ginseng* and *P. quinquefolius, P. vietnamensis* and *P. vietnamensis* var. *fuscidiscus, P. japonicus* (China) and its varieties were demonstrated, except *P. japonicus* (Japan) and *P. zingiberensis.*

9) **Zhu S., Zou K., Cai S. Q., Meselhy M. R., and Komatsu K.: Simultaneous Determination of Triterpene Saponins in Ginseng Drugs by High Performance Liquid Chromatography. *Chem. Pharm. Bull.*, 52: 995-998, 2004.**

Abstract: A HPLC method for the simultaneous determination of 11 triterpene saponins with four-type aglycones (protopanaxadiol, protopanaxatriol, ocotillol and oleanolic acid types) in Ginseng drugs was developed and validated. Using a gradient of acetonitrile and 10 mM K-phosphate buffer (pH 5.80) as the mobile phase and UV detection at 196 nm, more than 18 ginsenosides with different aglycones were separated satisfactorily within 60 min. The detection limits (signal/noise> or =3) were 0.1 μg for ginsenosides Rb_1, Rc, Rd, Re and Rg_1, chikusetsusaponin III, and notoginsenoside R_2, 0.2 microg for gisenoside Ro and chikusetsusaponin IVa, 0.3 μg for chikusetsusaponin IV, and 3 μg for majonoside R_2. The calibration curve of each saponin had a correlation coefficient close to 1. Intra- and interday precisions were less than 2.1% (n = 5) and 3.3% (n = 15), respectively. The recovery rates of extraction were in the range of 96.4-102.7% for all ginsenosides. By adopting this method, the determinations of 11 ginsenosides in three Ginseng drugs derived from *Panax ginseng, Panax vietnamensis* var. *fuscidiscus* and *Panax japonicus* (Japan) were achieved.

10) **Ahn E. M., Akao T., Nakamura N., Komatsu K., Nishihara T., and Hattori M.: Screening of Medicinal Plant Extracts for Estrogenic Activity in Combination with a Glycosidase**

Treatment. *J. Trad. Med.*, 21: 81-86, 2004.

11) **Long C. F., Kakiuchi N., Takahashi A., Komatsu K., Cai S. Q., and Mikage M.: Phylogenetic Analysis of the DNA Sequence of the Non-Coding Region of Nuclear Ribosomal DNA and Chloroplast of *Ephedra* Plants in China. *Planta Med.*, 70: 1080-1084, 2004.**

Abstract: Twenty-four *Ephedra* plants belonging to 8 species grown in the northern and western parts of China were phylogenetically analyzed for their non-coding DNA sequences, internal transcribed spacers (ITSs) of nuclear ribosomal DNA as well as *trn*L intron and intergenic spacers between *trn*L and *trn*F (*trn*L/ *trn*F) of the chloroplast. Based on the ITS sequences, the 8 species could be divided into 3 groups: Group 1 (*Ephedra intermedia, E. sinica, E. przewalskii*), Group 2 (*E. equisetina, E. monosperma, E. gerardiana*), and Group 3 (*E. likiangensis, E. minuta*). The species classified into Group 1 grow mainly in the north, Group 3 in the south and Group 2 in the center, suggesting their genetic and geographic relationships. A specific primer set was designed to classify the 3 groups by routine PCR. Combined analysis of ITS and *trn*L/ *trn*F differentiated the 8 *Ephedra* species.

12) **Ahn E. M., Nakamura N., Fushimi H., Komatsu K., Batkhuu J., and Hattori M.: Constituents of the seeds of *Glycyrrhiza uralensis*. *Nat. Med.*, 58: 311, 2004.**

13) **Li J., Wang X., Ma F. Y., Jia X. H., Cai S. Q., Liang X. M., and Komatsu K.: Several Factors Affecting the HPLC-Fingerprinting of *Panax notoginseng*. *Chi. J. Nat. Med.*, 2 (1): 33-41, 2004.**

Abstract: **Aim**: To study how can the way and the degree of dryness and the period of storage of crude drug samples affect the HPLC-fingerprinting of *Panax notoginseng*. **Methods**: The HPLC-fingerprinting method: Luna C_{18} analytical column (250 x 4.6 mm, 5 μm); acetonitrile-water as gradient eluent with flow rate at 1.0 ml/min, detective wavelength at 200 nm. Notoginseng samples made in different ways of dryness and samples in different degrees of dryness and different moments of storage were analyzed to discover how they can affect the HPLC-fingerprinting of Notoginseng. Two shapes of Notoginseng, Notoginseng in integrity and pieces, were dried in shade and by baking (35℃) respectively. Notoginseng in integrity, in pieces and in powder which had been stored for 0 days, 10 days, 20 days, 30 days(1 month), 2 months, 4 months, and 6 months were analyzed individually. **Results**: ① Different drying ways work on the components of Notoginseng in different ways: some components were affected more by the temperature and period of dryness, which had higher area values of peaks under drying in heat (or in shade); some were affected more by the shape of drug, which had higher peak area value in the shape of pieces (or integrity); some were affected by the both factors mentioned above. ② In the experiment, peak No. 15, whose relative peak area is 12.7% - 28.1% in fresh and drying drugs, was discovered to be characteristic. Its relative peak area was keeping on declining during drying and dropped to 0.2% when the drug was dried completely. However the value rose to 0.7% - 1.4% when the dried drug was hydrated, so the reaction was concluded to be reversible. ③ The discipline of changes during storage was found: two peaks (No. 10 and No. 12), areas kept on going up during storage, while most others' went down; drug of different shapes changed differently, e. g. drug in powder changed more rapidly than that in pieces and integrity. **Conclusion**: The way and the degree of dryness and the period of storage all can affect the HPLC-FPS of Notoginseng in a certain extent.

14) **Liu J. H., Wang X., Cai S. Q., Komatsu K., and Namba T.: Analysis of the Constituents in the Chinese Drug Notoginseng by Liquid Chromatography-Electrospray Mass Spectrometry. *J. Chin. Pharm. Sci.*, 13 (4): 225-237, 2004.**

Abstract: **Aim**: To develop a HPLC-UV-MS method for identifying the constituents in the Chinese drug Notoginseng (the root of *Panax notoginseng*). **Methods**: A Phenomenex Luna C_{18} column (250 mm x 4.6 mm ID,

5 μm) was utilized. Water containing 0.005% formic acid (A) and acetonitrile containing 0.005% formic acid (B) were used as gradient eluents. UV spectra were recorded in range 195 - 400 nm. Both positive and negative ion ESI modes were used. **Results**: The constituents in Notoginseng were well separated and detected. Fourteen compounds were identified by comparing their retention time and ESI-MS data with those obtained from the reference compounds. Forty-one compounds were deduced by data analysis of MS and literature; among them, yesanchinosides-H and -E, chikusetsusaponin-L_5, malonyl-ginsenoside-Rg_1, the isomers of notoginsenosides-J, -A, -R_1, -G, -R_2, and ginsenoside-Rh_3 were discovered in Notoginseng for the first time. **Conclusion**: This method gives high sensitivity and good separation, and is suitable for identifying the constituents in Notoginseng. This result is helpful for further phytochemical research on Notoginseng. Based on this result, further quality control can be studied.

15) 牧野利明，山路誠一：薬用植物・生薬に関する副作用と薬害．薬用植物研究，26 (1) : 30-37，2004.

◇総説 Review papers

1) Komatsu K., Zhu S., and Sasaki Y.: Systematic Pharmacognostical Study on *Panax* Drugs and *Curcuma* Drugs - Phylogenetic Analysis, Molecular Authentication and Quality Evaluation -. *J. Trad. Med.*, 21: 251-270, 2004.

◇学会報告 Scientific presentation (*: 招待講演)

1) 田村隆幸，東田千尋，鄒 坤，小松かつ子：黄耆によるAβ25-35誘発性の神経突起萎縮に対する抑制作用—基源植物の差異および修治が及ぼす影響—．日本薬学会第124年会，2004, 3.29-31, 大阪.
2) 小松かつ子：フィールドワークの2つの視点—比較民族薬物学と生薬資源学，ミニシンポジウム「天然薬物のフィールドワークを考える」．日本薬学会第124年会，2004, 3.29-31, 大阪.
3) Rauchensteiner F., Matsumura Y., Yamamoto Y., Yamaji S., and Tani T.: Development of environmental friendly analysis of *Glycyrrhiza* species from Europe and China by capillary zone electrophoresis (CZE). The 124th Annual Meeting of Pharmaceutical Society of Japan. 2004, 3.29-31, Osaka.
4) Zhu S., Fushimi H., Cai S. Q., and Komatsu K.: Phylogenetic Relationship in the Genus *Panax*: inferred from Chloroplast *trn*K Gene and Nuclear 18S rRNA Gene Sequences. International Symposium on Asian Plant Diversity and Systematics, The Japanese Society for Plant Systematics, International Association of Plant Taxonomists, 2004, 7.29-8.1, Chiba, Japan.
5) Cai S. Q., Wang X., Ma F. Y., Li J., and Komatsu K.: Studies on HPLC-Fingerprinting of Notoginseng. JSP-KSP-CCTNM Joint Seminar 2004 -International Symposium on Natural Medicines-, The Japanese Society of Pharmacognosy, 2004, 8.9-11, Kaga, Japan.
6) 橋本斎，東田千尋，小松かつ子：Aβ25-35誘発性の神経突起萎縮に対するprotopanaxadiol系サポニンの腸内細菌代謝物M1による軸索伸展作用とそのメカニズム．第21回和漢医薬学会大会，2004，8.21-22，富山.
7) 東田千尋，畠中史幸，中山なつき，小松かつ子：NO産生系を指標とした鬱金類生薬の駆瘀血作用．第21回和漢医薬学会大会，2004，8.21-22，富山.
8) 高橋京子，松田秀康，松永和憲，隅田昭彦，木下香葉子，小松かつ子，服部征雄，高橋幸一，東純一：動物性生薬由来成分の肝薬物代謝酵素に及ぼす影響．第21回和漢医薬学会大会，2004，8.21-22，富山.
9) 西田裕子，高橋京子，上島悦子，小松かつ子，佐々木陽平，畠中史幸，高橋幸一，荒川行生，黒川信夫，東純一：ウコン属生薬の基源と品質：ヒト肝CYP代謝活性への影響．第21回和漢医薬学会大会，2004，8.21-22，富山.
10) 久保山友晴，東田千尋，小松かつ子：Withanolide A, withanoside IV, withanoside VIによる神

経突起再伸展とシナプス再形成作用．日本生薬学会第51年会，2004，9.9-10，神戸．

11）Zhu S., Zou K., Fushimi H., Cai S. Q., and Komatsu K.: Comparative study on triterpene saponins of Ginseng drugs. 日本生薬学会第51年会，2004，9.9-10，神戸．

12）佐々木聡子，佐々木陽平，伏見裕利，南雲清二，合田幸広，小松かつ子：日本市場に流通するガジュツの基原—*trn*K 遺伝子の塩基配列—．日本生薬学会第51年会，2004，9.9-10，神戸．

13）佐々木陽平，佐々木聡子，伏見裕利，南雲清二，合田幸広，小松かつ子：ガジュツ及びウコンの試験法に関する研究．日本生薬学会第51年会，2004，9.9-10，神戸．

14）久保山友晴，東田千尋，小松かつ子：神経突起伸展及びシナプス形成を機序とする withanolide 類の空間記憶障害改善作用．第27回日本神経科学大会・第47回日本神経化学大会合同大会 Neuro 2004，2004，9.21-23，大阪．

＊15）Komatsu K.: Recent Research on Genus *Curcuma*: Molecular Analysis, Identification and Quality Evaluation on Vasomotion Effect. The First International Conference presented by Western Pacific Regional Forum for the Harmoni- zation of Herbal Medicines, WHO/WPRO, 2004, 9.21-22, Shanghai, China.

◇その他　Others

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1）小松かつ子，佐々木陽平，佐々木聡子，伏見裕利，南雲清二：平成15年度「日本薬局方の試験法に関する研究」研究報告—ガジュツ及びウコンの試験法に関する研究（第1報）—．医薬品研究，35：416-424，2004.

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◇共同研究　Co-operative researches

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1）合田幸広：国立医薬品食品衛生研究所，「生薬及び漢方処方の科学的品質保証に関する研究」，2004～

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2）Vajrgupta Opa : Mahidol University,「DNA fingerprint of Thai Medicinal Plants」, 2004

◇非常勤講師　Part-time lecturer

1）小松かつ子：九州大学大学院薬学府・大学院担当科目「薬用植物育種学特論」，2004, 6.7，福岡.

2）小松かつ子：金沢大学教養的科目・総合科目「ヒマラヤ風土記」第11回「中国ヒマラヤの自然と文化」，2004, 12.16，第12回「チベット医学と仏教」，2005, 1.13，金沢.

◇研究費取得状況　Acquisition of research funds

1）21世紀 COE プログラム「東洋の知に立脚した個の医療の創生」（事業推進担当者：小松かつ子）「漢方薬資源の開発と基原や規格に関する基盤研究」

2）文部省科学研究費，基盤研究(B)(2)（第３年度）（代表：小松かつ子）「漢薬の資源をアジアに探る：モンゴル及びタイ産薬用植物の調査研究」，220万

3）（財）ヒューマンサイエンス振興財団（分担：小松かつ子）「生薬及び漢方処方の科学的品質保証に関する研究」：「生薬の科学的品質保証に関する研究」，100万

4）（財）田村科学技術振興財団（代表：小松かつ子）「各種ウコン属生薬の生活習慣病予防・治療薬としての有効性評価」，30万

5）富山医科薬科大学特別経費「戦略的経費」（分担：小松かつ子）「東洋の知に立脚した個の医療の創生」，70万

6）富山県受託研究「和漢薬・バイオテクノロジー研究」（分担：小松かつ子）「富山県で栽培可能な生薬に関する総合的研究：優良種選抜を志向した和漢薬の品質の多様性に関する研究」，50万

7）富山県受託研究（代表：小松かつ子）「富山産ヤマブシタケの抗痴呆作用の検討」，40万

◇研究室在籍者　Research members（11月から）

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大学院前期２年：佐々木聡子，杉山玲子

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技術補佐員：林　和子

◇学位（修士，博士）取得者　Academic degrees and theses

卒業論文：

中山なつき：病態モデルマウスを用いた鬱金類生薬の薬理作用の比較

松山修二：痴呆を治療する新しい漢方処方の開発およびその作用機序の解析

修士論文：

佐々木聡子：アジア産ウコン類を原料とする生薬及び健康食品の基源と品質に関する研究－遺伝子解析と Curcuminoids 含量－

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久保山友晴：インド生薬 Ashwagandha（*Withania somnifera* Dunal）成分による神経回路網再構築を機序とした抗痴呆作用の研究