

Isoflavone Daidzein: Chemistry and Bacterial Metabolism

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Isoflavone daidzein is a phytoestrogen widely distributed in Leguminosae and is especially rich in the soybean. The C₆-C₃ (rings B and C) unit of isoflavones is derived from the phenylpropanoid pathway and the remaining C₆ (ring A) unit is from the polyketide pathway. This unique carbon skeleton is the result of isomerization of the flavone catalyzed by the isoflavone synthase, a cytochrome P450 enzyme. The isoflavones daidzein and genistein are present in the plant mostly in the glucosylated forms. However, in the human intestine, the glycosidic linkage is broken, and the free form is uptaken into blood stream. The free form is further metabolized into various reduction products to end up at the equol, which is known to have the most potent estrogenic effect among the metabolites. Several human intestinal bacteria that can convert daidzein into equol have been described, and the study into the chemistry and biochemistry of the daidzein reduction would be rewarding to the improvement of the human health.

Key words: daidzein, equol, genistein, intestinal microflora, isoflavonoids

Nomenclature and occurrences of isoflavone

The term "flavonoids" is generally used to describe a class of natural products that is comprised of a C₆-C₃-C₆ carbon framework, or phenylbenzopyran (or chroman) functionality [Marais *et al.*, 2006]. Depending on the position of the linkage of the aromatic ring to the benzopyrano moiety, they can be classified into three subclasses; flavonoids, isoflavonoids, and neoflavonoids (Fig. 1).

In this C₆-C₃-C₆ carbon framework, the two rings of chroman moiety are labeled as A and C rings, and the attached phenyl group as B ring. Isoflavonoid, a distinctive subclass of the flavonoids, differ from the flavonoids by the position of ring B on ring C. Whereas the B ring is located at C-2 in the flavonoids, in the isoflavonoids it is found at C-3. The numbering system of the isoflavone is shown in Fig. 2. Isoflavonoids are further classified into isoflavone, isoflavanone, and isoflavanol according to

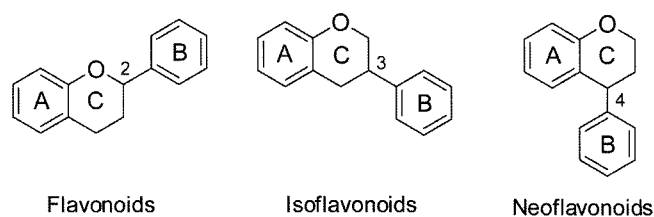


Fig. 1. Basic structures of flavonoids, isoflavonoids, and neoflavonoids.

their functionality on C1 through C3. Isoflavanone and isoflavanol have two and three chiral centers, respectively. Recently, the correlation between the absolute configuration and the chiroptical property, the Cotton effect, has been elucidated [Won *et al.*, 2008]. This finding will facilitate the determination of the absolute configuration of various isoflavanol metabolites in humans.

Plants are capable of accumulating large variety of low molecular-weight organic compounds, which are collectively termed as the secondary metabolites. These metabolites play important roles in the plant-environments interactions, as well as in the human nutrition and the medicine. Isoflavonoids are important secondary metabolites in Leguminosae that is capable of harboring symbiotic bacteria internalized within the root nodules, which play a

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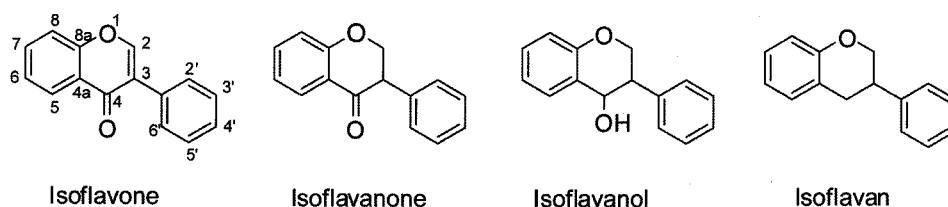


Fig. 2. Structures, names, and numbering system of the simple isoflavonoids.

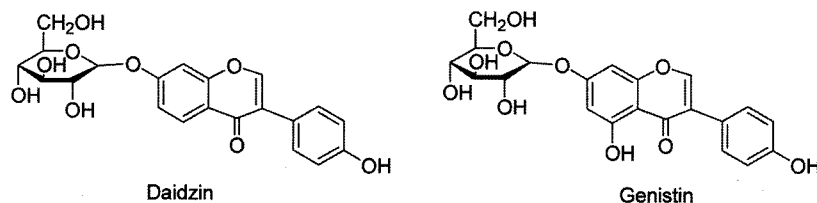


Fig. 3. Structures of daidzin and genistin.

protective role against microbial infection [Blount *et al.*, 1992].

The isoflavones are the largest group of isoflavonoids, and the legumes are the most important sources of isoflavones. The concentration of isoflavones in the soybeans is much higher than those in other legumes. Therefore, soy and soy-based foods are regarded as the main sources of isoflavones in the human diet [Mazur and Adlercruetz 1998; Liggins *et al.*, 2000]. The most abundant isoflavones are daidzein (7,4'-dihydroxyisoflavone) and genistein (5,7,4'-trihydroxyisoflavone), which together comprise 0.1-0.3 mg/g soybean [Wang and Murphy, 1994]. In plants the isoflavonoids mostly occur as sugar conjugates, frequently with glucose at the 7-*O*-position. The glucoside form of daidzein and genistein are called daidzin and genistin, respectively (Fig. 3). They are abundant in the soybean products, because they are heat stable [Setchell 1998].

Biosynthesis of isoflavone daidzein

Isoflavonoids are synthesized by a branch of the phenylpropanoid pathway in plants. The flavonoids, lignin, and anthocyanin pigments also share the phenylpropanoid pathway [Winkel-Shirley, 2001]. Ring B and part of the heterocyclic ring C are formed from 4-coumaric acid co-enzyme A (CoA) ester via shikimate pathway, starting from carbohydrate (Fig. 4). Ring A is formed via the polyketide pathway from three units of malonyl CoA, derived from acetyl CoA and carbon dioxide. Chalcones are synthesized via the addition of three malonyl groups into coumarate by chalcone synthase (CHS), which catalyzes the stepwise condensation of these precursors to a C15 intermediate. Chalcone isomerase (CHI) catalyzes the stereospecific cyclization of chalcone to form flavanone

(Fig. 4).

The committed step for the isoflavonoid biosynthesis is a unique aryl migration reaction catalyzed by a cytochrome P450 enzyme CYP93C, isoflavone synthase (IFS). The reaction is initiated by the abstraction of a hydrogen to form a radical at C-3 of the flavanone. The next step, the migration of ring B from C-2 to C-3 and subsequent hydroxylation of the resulting C-2 radical, completes the isomerization. Isoflavone synthase catalysis is regioselective, and only (2*S*)-flavanones are stereospecifically transformed into (2*R*,3*S*)-hydroxyisoflavanone. The product of the IFS reaction is the 2-hydroxyisoflavanone, which can be dehydrated into isoflavones either spontaneously or through the catalysis by 2-hydroxyisoflavanon dehydratase [Akashi *et al.*, 1995; 2005].

Genistein is the end product of the isoflavone synthase and 2-hydroxyisoflavanone dehydratase reactions when naringenin is used as the substrate (Fig. 4). Genistein biosynthesis shares the naringenin intermediate with the flavonoid/anthocyanin branch of the phenylpropanoid pathway, but is also the building block of many, structurally more complicated isoflavonoids compounds.

Because of the structural complexity of the secondary metabolites, their chemical synthesis is often difficult and expensive, partly due to the very low yields. Therefore, manipulation of the biosynthetic pathways to attain the accumulation of the isoflavonoid in plants through the expression of endogenous genes or by introducing foreign genes has been considered. Recent studies on tobacco, *Arabidopsis*, and maize demonstrated that isoflavonoids can be accumulated to a high level in the non-legume transgenic plants when soybean isoflavone synthase gene is incorporated through metabolic engineering [Yu *et al.*, 2001; Liu *et al.*, 2002; Yu *et al.*, 2003; Tian and Dixon 2006].

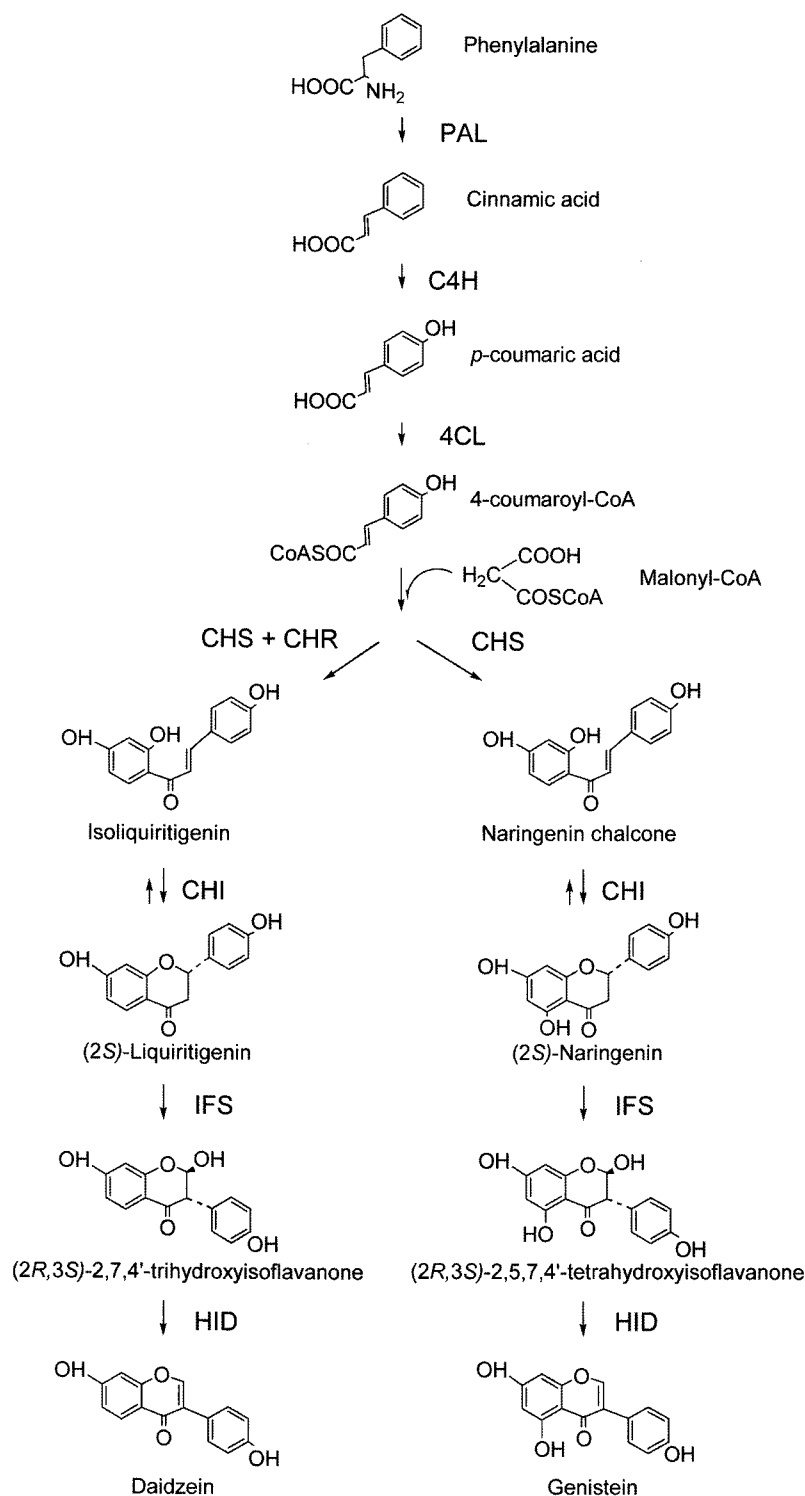


Fig. 4. Modified pathway of isoflavone biosynthesis in legumes [Tian and Dixon, 2006]. PAL, L-phenylalanine ammonia-lyase; C4H, cinnamate-4-hydroxylase; 4CL, 4-coumarate CoA ligase; CHS, chalcone synthase; CHR, chalcone reductase; CHI, chalcone isomerase; IFS, isoflavone synthase; HID, 2-hydroxyisoflavanone dehydratase.

Bioactivities of daidzein and its derivatives

Isoflavonoids were initially recognized for their roles in plant disease resistance and induction of nodulation [Lee *et al.* 1991]. However, in recent years they received much

attention due to their estrogenic, antioxidant, and anticancer activities on humans [Cornwell *et al.*, 2004; Dixon, 2004].

The incidences of the hormone-related disease, such as breast and prostate cancers, in the Asians with a high

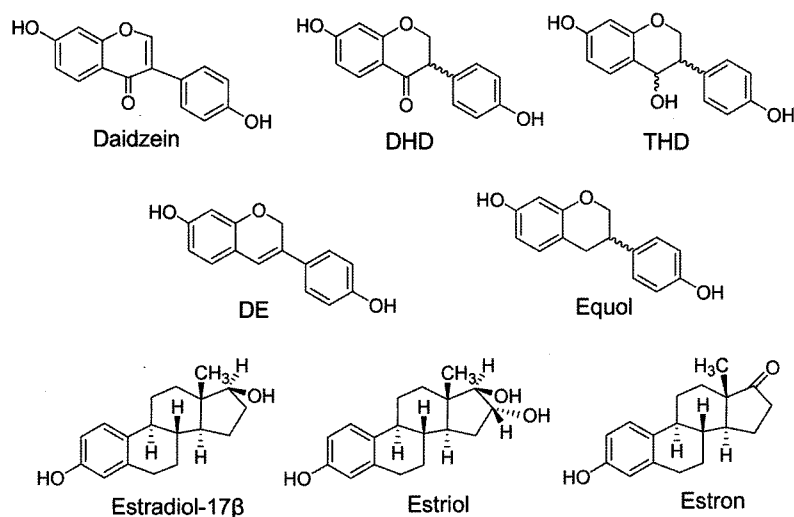


Fig. 5 . Chemical structures of daidzein, its metabolites, and three human estrogens.

isoflavone intake are significantly lower than those of the Western counterparts. For examples, the average intake of isoflavones among the Japanese adults was estimated as 30-50 mg/day in the forms of miso, tofu, and soy sauce [Wakai *et al.*, 1999], and the Chinese adults also consume similar amounts of isoflavones (~40 mg/day) [Chen *et al.*, 1999]. The Korean population was estimated to take up 15 mg/day of isoflavonoids [Kim and Kwon, 2001]. In contrast, the intake of isoflavones is very low in the Western population, typically less than 5 mg/day isoflavones. Urinary excretion of isoflavones and their metabolites were shown to be 13-30 times lower in USA and England than in Japan [Herman *et al.*, 1995; Mazur and Adlercreutz, 2000].

Estrogens are strongly bound to the serum proteins, albumin, and sex hormone-binding globulin, whereas phytoestrogens are weakly bound to these serum proteins. For example, equol shows 10-fold less affinity than estradiol, thus enabling a greater proportion of equol to occupy the estrogen receptor. This could explain the effectiveness of isoflavones [Setchell and Cassidy, 1999; Dixon and Sumner, 2003]. The molecular structures of daidzein, its metabolites, and three human estrogens are given in Fig. 5.

Daidzein has been shown to be less active than genistein in the estrogenic activity [Verma and Goldin, 1998]. However, daidzein, through the reductive metabolism, is converted into its metabolites, including DHD (dihydrodaidzein), *cis*- and *trans*-THDs (tetrahydrodaidzeins), *O*-desmethylangolensin, DE (dehydroequol), and equol, by the intestinal microflora after ingestion [Kelly *et al.*, 1995]. Lehmann *et al.* [2005] reported the estrogenic and genotoxic potentials of equol. Interestingly, among the metabolites of daidzein, (3*S*)-equol has about 100 times

higher estrogenic activity than the daidzein itself [Hwang *et al.*, 2006].

Daidzein was shown to inhibit the growth of human prostate and the estrogen-sensitive breast cancer cells MCF-7 [Adlercreutz, 2003; Cross *et al.* 2004; Holzbereierlein *et al.* 2005; Matsumura *et al.*, 2005]. Choi and Kim [2008] also reported that daidzein significantly inhibited the cell proliferation dose- and time-dependently via the cell cycle arrest in G1 and G2/M phases. Wähälä *et al.* [1997] showed that THD was more active than daidzein, and the activity was comparable to that of genistein against the prostate cancer cells. On the other hand, 3'-OH-daidzein and 6-OH-daidzein, the oxidized forms of the daidzein metabolite, showed markedly lower activities.

Dietary daidzein may lower the cholesterol level by increasing the receptor activity of low-density lipoprotein, and this reduction in the cholesterol level may offer some protection against atherosclerosis [Kirk *et al.*, 1998]. Jiang *et al.* [2003] showed that DHD could decrease both the total cholesterol and the proatherogenic non-HDL cholesterol levels. The cardiovascular protective activities of *cis*-THD, *trans*-THD, DE, and DHD have been elucidated [Chin-Dusting *et al.* 2001; Chin-Dusting *et al.* 2004; Kanellakis *et al.* 2004; Ling *et al.* 2004; Nestel *et al.* 2007].

Daidzein metabolism in human

Intestinal microflora plays a key role in the metabolism and the bioavailability of daidzein [Setchell *et al.* 1984]. Daidzein metabolites occur in blood plasma, urine, and feces of humans as a result of the biotransformation by the intestinal microorganisms. The absorption of daidzein appears to be dependent on the specific enzyme that is

capable of hydrolyzing the sugar moiety. This enzyme is found in the small intestinal brush border and enterocytes. Daidzein may be directly absorbed or further metabolized by the microflora into its metabolites, including dihydrodaidzein (DHD) and equol before absorption. The presence of this reductive metabolism, however, appears to vary among individuals.

Like endogenous estrogen, daidzein undergoes an enterohepatic circulation to be secreted in bile. But, the main route of excretion is via the kidney: urinary excretion of daidzein has been found to account for approximately 30-61% of administered doses [Setchell *et al.*, 2003], the remaining ingested compounds being converted into the metabolites, such as 6,7,4'-trihydroxyisoflavone, 7,3,4'-trihydroxyisoflavone, 7,8,4'-trihydroxyisoflavone, 7,8,3',4'-tetrahydroxyisoflavone, 6,7,8,4'-tetrahydroxyisoflavone, 6,7,3',4'-tetrahydroxyisoflavone, through oxidative pathway [Kulling *et al.*, 2001]. These oxidative seems to have lower bioactivity compared to the microbially reduced products of daidzein [Chang, 2007].

In urine, daidzein exists mainly (~90%) as glucuronides, 7-*O*-monoglucuronides being the most abundant metabolites; free daidzein accounts for 1-10% and the sulfated daidzein about 10% [Shelnutt *et al.*, 2000; Shelnutt *et al.*, 2002]. the level of glucuronides of daidzein is significantly lower in the plasma than in the urine. The sulfate level of daidzeins in the plasma is about two times higher (26%) than that in the urine, while the occurrence of free daidzein is much higher in the plasma than in the urine [Shelnutt *et al.*, 2002; Zhang *et al.*, 2003].

The fecal excretion of daidzein has only recently been investigated. From the data of the few available studies, it is suggested that only about 1% of the ingested daidzein is excreted through the feces. Isoflavones occur mainly in the free aglycone form, with the conjugated isoflavones accounting for less than 10% of the total isoflavones [Adlercreutz *et al.*, 1995; Watanabe *et al.*, 1998; Xu *et al.*, 1995].

Since the discovery of equol in human urine for the first time in 1982 by Axelson *et al.*, daidzein metabolites including DHD, THD, DE, and *O*-desmethylangolensin have been successively detected in the human urine (Table 1). On the basis of these detected metabolites, Joannou *et al.* [1995] suggested the metabolic pathway of daidzein by human intestinal microflora?. Based on the presence of various reduced metabolites of daidzein, the metabolic sequence prosecuted by the human intestinal bacteria has been proposed; daidzein is reduced to DHD, to THD and dehydroequol, and finally to (3*S*)-equol in a sequential manner (Fig. 6). However, the pathway and the individual reaction in the pathway are yet to be fully elucidated.

Table 1. Identification of daidzein and its metabolites in human urine

Compound	Year	Reference
Daidzein	1984	Bannwart <i>et al.</i>
	1987	Bannwart <i>et al.</i>
DHD (Dihydrodaidzein)	1987	Adlercreutz <i>et al.</i>
	1993	Kelly <i>et al.</i>
	1995	Joannou <i>et al.</i>
THD (Tetrahydrodaidzein)	1993	Kelly <i>et al.</i>
	1995	Joannou <i>et al.</i>
2,3-Dehydroequol	1987	Adlercreutz <i>et al.</i>
Equol	1982	Axelson <i>et al.</i>
		Adlercreutz <i>et al.</i>

Bacterial strains capable of metabolizing daidzein and its derivatives

Although equol has been known to have the highest estrogenic activity among the metabolites of daidzein, only 30 to 40% of humans can produce the equol from daidzein [Kelly *et al.*, 1993; Rafii *et al.*, 2003]. In addition, a high correlation was found between the beneficial effects of the soy food intake and the presence of equol in the urines of the females [Atkinson *et al.*, 2008]. Therefore, the ability to metabolize daidzein into equol conferred by the intestinal microflora in human is regarded as a hallmark of daidzein responsiveness.

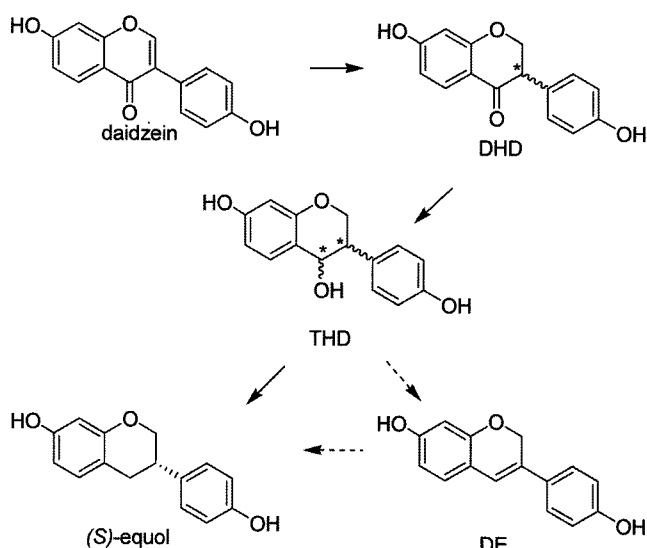
In vitro fermentation of daidzein with the human faces samples under anaerobic conditions results in the production of dihydrodaidzein or equol. Setchell *et al.* [1984] demonstrated that incubation of the textured vegetable protein made from soy protein with the cultured human fecal bacteria resulted in the formation of equol. Chang and Nair [1995] also reported the metabolism of daidzein into dihydrodaidzein and equol when incubated with the human faces. Atkinson *et al.* [2004] investigated the metabolism of daidzein by the feces sampled from the equol producer and assessed the effect of antibiotics on the metabolism. The results showed that some antibiotics inhibited the production of equol, but had no effect on the DHD production, suggesting the involvement of many different bacteria in the daidzein metabolism.

Although there have been attempts to isolate the bacterial strains capable of metabolizing daidzein into equol, very little is known about the bacteria responsible for daidzein metabolism in humans. So far, only a few bacterial species have been isolated, characterized, and studied for their activity to metabolize daidzein.

Recent study reported the hydrolysis of the 7-*O*-glycosides daidzein by *Eubacterium ramulus* [Hur *et al.*, 2000a]. The human intestinal bacterium, *Clostridium sp.*

Table 2. Isolated human origin bacterial stains capable of daidzein metabolism

Strains	Activity	Year	Reference
<i>Clostrium</i> Sp. HGH6	Daidzein to DHD	2000	Hur <i>et al.</i>
<i>Eubacterium ramulus</i>	Daidzein to <i>O</i> -desmethylangolensin	2002	Schoefer <i>et al.</i>
<i>Eubacterium ramulus</i> Julong 601	Daidzein to <i>O</i> -desmethylangolensin	2004	Wang <i>et al.</i>
<i>Eggerthella</i> sp. Julong732	DHD to equol	2005	Wang <i>et al.</i>
<i>Clostridium</i> -like strain TM-40	Daidzein to DHD	2007	Tamura <i>et al.</i>
<i>Slackia</i> sp. DZE	Daidzein to equol	2008	Jin <i>et al.</i>
<i>Eggerthella</i> sp. YY7918	Daidzein to DHD and equol	2008	Yokoyama <i>et al.</i>

**Fig. 6. Proposed pathway for daidzein reduction by intestinal microflora leading to equol formation.**

HGH136 [Hur *et al.*, 2002] and *Eubacterium ramulus* Julong 601 [Wang *et al.*, 2004] catalyze the C-ring cleavage of daidzein into nonestrogenic *O*-desmethylangolensin. Two additional strains of the bacteria capable of metabolizing glycoside of daidzein have been isolated from the human faces: *E. Coli* HGH21 (Hur *et al.*, 2000b) and *Clostrium* sp. HGH6 (Hur *et al.*, 2002). However, in spite of their isoflavone daidzein or genistein-specific activity, these strains could not metabolize flavones.

Clostridium-like bacterium strain TM-40 (Tamura *et al.*, 2007) and an anaerobic bacterium *Clostrium* sp. HGH6 (Hur *et al.*, 2000b) reduce the double bond of the isoflavone ring C to yield dihydrodaidzein from daidzein. Recently, an *Eggerthella* strain Julong 732 was found to further reduce DHD into equol [Wang *et al.*, 2005], thus establishing the aforementioned reduction sequence leading to equol from daidzein via DHD in the human intestine [Joannou *et al.*, 1995; Heinonen *et al.*, 1999]. In addition, the human microbial phenotypes that can reduce daidzein all the way to equol were reported [Jin *et al.*, 2008; Yokoyama and Suzuki, 2008]. Nevertheless, the enzymology

of the reduction, such as nature of the responsible enzyme and the reaction mechanism, has yet to be established.

The studies on these intestinal microorganisms and the enzymology have been hampered by the strict anaerobic nature of the microorganisms, which calls for the use of special techniques, equipments, and gases. However, the recent availability of the commercial anaerobic chamber would facilitate the investigation on the anaerobes.

Conclusion

The metabolites of daidzein, (3*S*)-equol in particular, play an important role in the human health due to their estrogenic, antioxidative, and anti-cancer activities. It is now recognized that the estrogenic effect, notably alleviation of the post-menopausal syndromes and the prevention of prostate cancer, is due to the (3*S*)-equol that possesses about 100 times higher activity than daidzein. However, the microbiology and biochemistry of the daidzein-metabolizing intestinal bacteria is still in infancy. In light of the importance of equol in the phytoestrogenic effect of the dietary phytoestrogen, the chemistry and enzymology of the DHD reduction to yield (3*S*)-equol should receive extensive attention. For example, the responsiveness toward the dietary daidzein intake is directly correlated with the presence of the equol-producing microbe in the intestinal microflora. The evaluation of the intestinal microbes that could convert daidzein into equol would be important in the development of probiotics.

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