Pharmacogenetics of human ABC transporter ABCC11: new insights into apocrine gland growth and metabolite secretion

Toshihisa Ishikawa1,2*, Yu Toyoda1,3, Koh-ichiro Yoshiura4 and Norio Niikawa4,5

1 Graduate School of Bioscience and Biotechnology, Tokyo Institute of Technology, Yokohama, Japan
2 Omics Science Center, RIKEN Yokohama Institute, Yokohama, Japan
3 Department of Pharmacy, The University of Tokyo Hospital, Faculty of Medicine, The University of Tokyo, Tokyo, Japan
4 Department of Human Genetics, Nagasaki University Graduate School of Biomedical Sciences, Nagasaki, Japan
5 The Research Institute of Personalized Health Sciences, Health Sciences University of Hokkaido, Ishikari-Tobetsu, Japan

*Correspondence: toshi-i@gsc.riken.jp

INTRODUCTION

ATP-binding cassette (ABC) proteins form one of the largest protein families encoded in the human genome (Dean et al., 2001; Holland et al., 2003). Hitherto more than 48 human ABC protein genes have been identified and sequenced (Klein et al., 1999). Many of the human ABC proteins are involved in membrane transport of drugs, xenobiotics, endogenous substances, or ions, thereby exhibiting a wide spectrum of biological functions (Schinkel and Jonker, 2003). Based on the arrangement of molecular structure components, i.e., nucleotide binding domains and topologies of transmembrane domains, the hitherto reported human ABC proteins have been classified into seven different sub-families (A to G; Klein et al., 1999; Borst and Elferink, 2002; Ishikawa, 2003). When transfected exogenously, the ABCC11 wild-type (WT) protein was localized in the apical membrane of Madin–Darby canine kidney cells strain II (MDCK II cells; Bortfeld et al., 2006). The substrate specificity of ABCC11 WT was characterized in more detail by an in vitro transport assay with plasma membrane vesicles prepared from pig LLC-PK1 cells transfected with an ABCC11 WT expression vector (Chen et al., 2005). The predicted amino acid sequences of both gene products show a high similarity to those of ABC4 and ABC5, which suggests that they have the typical structure of “full” ABC transporters with 12 transmembrane helices and two ABCs. Interestingly, there is no putative mouse or rat orthologous gene corresponding to human ABCC11 (Shimizu et al., 2003), which indicates that ABCC11 is an orthologous gene but rather a paralogous gene generated by gene duplication in the human genome. In contrast, ABCC2 and its orthologous genes are found in several different species including humans, primates, and rodents (Shimizu et al., 2003; Ono et al., 2007). Transcript analyses suggest that human ABCC11 mRNA is ubiquitously expressed in human adult and fetal tissues (Tammur et al., 2001; Yabuchi et al., 2001). High levels of ABCC11 mRNA were observed in breast cancer tissues (Bera et al., 2001; Yabuchi et al., 2001). Table 1 summarizes major findings in the research of the ABCC11 gene.

Cell secretion is an important physiological process that ensures smooth metabolic activities and tissue repair as well as growth and immunological functions in the body. Apocrine secretion occurs when the secretory process is accomplished with a partial loss of cell cytoplasm. The secretory materials are contained within secretory vesicles and are released during secretion as cytoplasmic fragments into the glandular lumen or interstitial space. The recent finding that the non-synonymous single nucleotide polymorphisms (SNP) 538G > A (rs17822931; Gly180Arg) in the ABCC11 gene determines the type of earwax in humans has shed light on the novel function of this ABC (ATP-binding cassette) transporter in apocrine glands. The wild-type (Gly180) of ABCC11 is associated with wet-type earwax, axillary osmidrosis, and colostrum secretion from the mammary gland as well as the potential risk of mastopathy. Furthermore, the SNP (538G > A) in the ABCC11 gene is suggested to be a clinical biomarker for the prediction of chemotherapeutic efficacy. The aim of this review article is to provide an overview on the discovery and characterization of genetic polymorphisms in the human ABCC11 gene and to explain the impact of ABCC11 538G > A on the apocrine phenotype as well as the anthropological aspect of this SNP in the ABCC11 gene and patients’ response to nucleoside-based chemotherapy.

Keywords: apocrine gland, earwax, axillary osmidrosis, breast cancer, mastopathy, 5-fluorouracil, tamoxifen

doi: 10.3389/fgene.2012.00306

January 2013 | Volume 3 | Article 306 | 1

www.frontiernew.org
FIGURE 1 | Schematic illustration of the genomic structures of ABCC11 and ABCC12 genes on human chromosome 16q12.1. (A) The cytogenetic location of the ABCC11 gene as well as the structures of exons and introns were analyzed by BLAST searches on the human genome. A non-synonymous SNP: 538G > A (Gly180Arg), an earwax determinant, is located in exon 4. (B) Phylogenetic tree of the ABCC subfamily including CFTR, SUR1, SUR2, and MRPx. The phylogenetic tree was modified from Toyoda et al. (2008). The phylogenetic relationships among members of the "C" sub-family of human ABC transporters were calculated by using the distance-based neighbor-joining methods (Saitou and Nei, 1987).
Table 1 | Historical overview on identification of the ABCC11 gene and its function.

| Year | Scientific progress | Reference |
|------|--------------------|-----------|
| 2001 | Discovery of human ABCC11 (MRP8) gene | Bera et al. (2001), Tammur et al. (2001), Yabuchi et al. (2001) |
| 2003 | Characterization of ABCC11 as a cyclic nucleotide efflux pump | Guo et al. (2003) |
| 2005 | In vitro characterization of substrate selectivity of ABCC11 | Chen et al. (2005) |
| 2006 | Characterization as an apical efflux pump for steroid sulfates in CNS | Bortfeld et al. (2006) |
| 2006 | Identification of ABCC11 SNP c.538G > A as the determinant of human earwax type | Yoshura et al. (2006) |
| 2007 | Association between the degrees of apocrine colostium secretion and ABCC11 genotype | Muria et al. (2007) |
| 2008 | Involvement of ABCC11 in 5-fluorouracil resistance in lung cancer cell line | Ogi et al. (2007) |
| 2008 | Regulation of ABCC11 expression by estrogen in MCF7 cells | Honos et al. (2008) |
| 2009 | Discovery of ubiquitination and proteosomal degradation of SNP c.538G > A variant | Toyota et al. (2009) |
| 2009 | Association between ankyr必需osmotics and ABCC11 wild-type | Nakano et al. (2009), Toyota et al. (2009), Inoue et al. (2010) |
| 2009 | Japanese map of the earwax gene frequency: a nationwide collaborative study | Super Science High School Consortium (2009) |
| 2010 | Association between breast cancer risk and ABCC11 wild-type in Japanese women | Ota et al. (2010), Toyoda and Ishikawa (2010) |
| 2010 | Involvement of ABCC11 in pemetrexed resistance in lung cancer | Uemura et al. (2010) |
| 2011 | No association between breast cancer risk and ABCC11 wild-type in European women | Beasley et al. (2011), Lang et al. (2011) |
| 2011 | Down-regulation of ABCC11 protein in human breast cancer | Sosonkina et al. (2011) |

as estrone-3-sulfate (E13S) and dhydroepiandrosterone-3-sulfate (DHEAS), glucuronides such as estradiol-17β-D-glucuronide (E217βG), the monoanionic bile acids glycocholate and taurocholate, as well as folic acid and its analog methotrexate (MTX; Chen et al., 2005; Bortfeld et al., 2006). Chemical structures of these compounds are presented in Figure A1 in Appendix. While ABCC11 transports a variety of organic anions, endogenous natural substrates for this transporter have not yet been identified.

GENETIC POLYMORPHISMS AND PHYSIOLOGICAL FUNCTION OF ABCC11

To date, more than 10 non-synonymous single-nucleotide polymorphisms (SNPs) have been reported in the human ABCC11 gene (Figure 2). Among those SNPs, one SNP (rs17822931; 538G > A, Gly180Arg) determines the human earwax type (Yoshura et al., 2006). Interestingly, this SNP (538G > A) exhibits wide ethnic differences in allelic frequency (Table 2). In Mongoloid populations in Asia, the frequency of the 538A allele is predominantly high, whereas the frequency of this allele is low among Caucasians and Africans (Yoshura et al., 2006; Toyota et al., 2008; Figure 3A). The frequency of the 538A allele exhibits a north-south and east-west downward geographical gradient with the highest peak in Korea. It is suggested that the 538A allele arose in northeast Asia and thereafter spread throughout the world (Yoshura et al., 2006), apparently reflecting the inter-continental migration of Homo sapiens (Figure 3B). A similar geographical gradient was also observed in the frequency of the 2677G (Ala893) allele of the ABCB1 (P-glycoprotein/MDR1) gene (Sakurai et al., 2007). In this regard, anthropological aspects of SNP 538G > A in the ABCC11 gene are described in the following section.

Earwax (cerumen) is a secretory product of the ceruminous apocrine glands, which can be classified into two phenotypes in humans, wet (sticky) and dry. The dry-type is most commonly found within the Asian population, especially among Koreans, Japanese, and Chinese; whereas the wet-type is the dominant phenotype for many Africans and Caucasians. The 538A/A genotype gives the dry phenotype, whereas both the 538G/A and G/G genotypes give the wet phenotype. This relationship is consistent with observations that earwax type is a Mendelian trait and that the wet phenotype is dominant to the dry one.
Table 2 | Frequencies of ABCC11 genotypes and allele c.538A among different ethnic groups.

| Ethnic groups | Tribes or inhabitants | No. of individuals with genotypes | Number of individuals genotyped | Frequency of allele “A” |
|---------------|-----------------------|-----------------------------------|---------------------------------|-------------------------|
| Korean§        | Daegu city inhabitants | 100 (1.000) 0 0 100 | 1.000 | |
| Chinese§       | Northern and southern Han Chinese | 42 (0.888) 10 0 52 | 0.904 | |
| Mongolian      | Khalkha tribe§ | 126 (0.703) 36 4 166 | 0.687 | |
| Japanese       | Nagasaki people (West-end prefecture of Japan mainland§) | 87 (0.690) 35* 4 126 | 0.829 | |
| Vietnamese     | People from multiple regions | 62 (0.536) 60 11 153 | 0.732 | |
| Thai           | Northern Thai (Luai, Shan, Liu, Hmong, Akha, Miaburi, and Karen (Mae-sot Thai) tribes combined) | 215 (0.505) 163 48 426 | 0.696 | |
| Korean§        | Daegu city inhabitants | 100 (1.000) 0 0 100 | 1.000 | |
| Chinese§       | Northern and southern Han Chinese | 42 (0.888) 10 0 52 | 0.904 | |
| Mongolian      | Khalkha tribe§ | 126 (0.703) 36 4 166 | 0.687 | |
| Japanese       | Nagasaki people (West-end prefecture of Japan mainland§) | 87 (0.690) 35* 4 126 | 0.829 | |
| Vietnamese     | People from multiple regions | 62 (0.536) 60 11 153 | 0.732 | |
| Thai           | Northern Thai (Luai, Shan, Liu, Hmong, Akha, Miaburi, and Karen (Mae-sot Thai) tribes combined) | 215 (0.505) 163 48 426 | 0.696 | |
| Korean§        | Daegu city inhabitants | 100 (1.000) 0 0 100 | 1.000 | |
| Chinese§       | Northern and southern Han Chinese | 42 (0.888) 10 0 52 | 0.904 | |
| Mongolian      | Khalkha tribe§ | 126 (0.703) 36 4 166 | 0.687 | |
| Japanese       | Nagasaki people (West-end prefecture of Japan mainland§) | 87 (0.690) 35* 4 126 | 0.829 | |
| Vietnamese     | People from multiple regions | 62 (0.536) 60 11 153 | 0.732 | |
| Thai           | Northern Thai (Luai, Shan, Liu, Hmong, Akha, Miaburi, and Karen (Mae-sot Thai) tribes combined) | 215 (0.505) 163 48 426 | 0.696 | |
| Korean§        | Daegu city inhabitants | 100 (1.000) 0 0 100 | 1.000 | |
| Chinese§       | Northern and southern Han Chinese | 42 (0.888) 10 0 52 | 0.904 | |
| Mongolian      | Khalkha tribe§ | 126 (0.703) 36 4 166 | 0.687 | |
| Japanese       | Nagasaki people (West-end prefecture of Japan mainland§) | 87 (0.690) 35* 4 126 | 0.829 | |
| Vietnamese     | People from multiple regions | 62 (0.536) 60 11 153 | 0.732 | |
| Thai           | Northern Thai (Luai, Shan, Liu, Hmong, Akha, Miaburi, and Karen (Mae-sot Thai) tribes combined) | 215 (0.505) 163 48 426 | 0.696 | |

Data are from Yosihara et al. (2006). § Examined for a 27-bp deletion (A27) in ABCC11; *One exceptional case of dry cerumen who has the deletion; † One each case of the deletion; ‡ Nine cases of the deletion.

Frontiers in Genetics | Pharmacogenetics and Pharmacogenomics January 2013 | Volume 3 | Article 306 | 4
It is generally accepted that, since they migrated out-of-Africa, humans spread all over the world with great diversity (Cavalli-Sforza, 2005). The last wave of land and Sahuland, and finally reached the Australian continent migrated more south-eastwardly through the so-called Sunda bridge (Beringia) to the American continent during the past 15,000 years (Horai et al., 1993; Bonatto and Salzano, 1997; Tokuoka et al., 2001; Dillehay, 2003). Based on recent craniometric studies of skeletons from archeological remains in the Baja California peninsula, however, it has also been postulated that an earlier migration wave from that via the northern route might have occurred from islands of south-eastern Asia by an ancestor common to both Palaeoamericans and Australians around 40,000–12,000 years ago (González-José et al., 2003). Furthermore, the allelic data for South Americans revealing the 538A allele frequency of 0.400 in Bolivia, 0.200 in the Andes region, 0.093–0.380 in Paraguay, 0.053 in Colombia, and 0.000 in Venezuela rather favors a hypothesis of an ancient migration through a “pacific coast road” along the Andes mountain range.

### ROUTES OF THE JAPANESE POPULATION

The Japanese population is considered to have a dual structure comprising descendants of mixtures between the ancient “Jomon” and “Yayoi” populations. The term “Jomon” is derived...
from characteristic twisted cord situations or marks on earthenware used during a prehistoric time (13,000–3,000 years ago) in Japan. As it has been reported that the Jomon had occupied various areas of Japan prior to the Yayoi’s appearance, they apparently were either assimilated or rather moved away from the Yayoi (Iizuka and Nakahashi, 2002; Temple, 2008; Temple, 2010). It is hypothesized that the dry earwax type was introduced by the Yayoi people to the Jomon population, where the wet-type had been predominant.

Since the admixture of the two Jomon and Yayoi populations is still not complete in Japan even now, the 538G allele frequency is higher in the rather remote areas where the Jomon moved away from the Yayoi’s peopling route within the Japanese islands. The Ainu-Japanese people living in a Japanese northern island “Hokkaido” are aboriginal inhabitants of Japan. Based on morphological and mitochondrial DNA polymorphism studies, it has been hypothesized that both the Ainu- and the Okinawa-Japanese living in a Japanese southern island “Okinawa” are descendants of the ancient native Japanese, “Jomon” people (Horai et al., 1991). Molecular studies demonstrated that Ainu-Japanese still retain a certain degree of their own genetic uniqueness among surrounding populations, and exhibit considerable genetic distance from other East Asian populations (Tokunaga et al., 2001; Tajima et al., 2004). As far as wet-type of earwax and the 538G allele frequency are concerned, the Ainu- and Okinawa-Japanese people are not the direct descendants “Yayoi” from the Ancient Northern Mongoloids of Siberian origin.

To analyze the nationwide allele frequency, the Super Science High School (SSH) consortium collected a total of 1963 fingernail samples of pupils/students from at least one high school/university in every prefecture in Japan (Super Science High School Consortium, 2009). Although the 538G allele frequency varied among the 47 prefectures, the G/G/Kyoto and Okinawa prefectures showed the lowest and highest values for the 538G allele, respectively. Other areas with low frequencies of the 538G allele included Northeastern Kyushu, Northern Shikoku, and Kinki districts, showing a belt-like zone, whereas those with high frequencies of the 538G allele next to Okinawa were the Southwestern Kyushu, Hiroshima prefecture, and Tohoku districts. Those observations strongly suggest that the admixture of “Jomon” and “Yayoi” populations is still not complete in Japan.

**STRONG ASSOCIATION BETWEEN AXILLARY OSMIDROSIS AND THE GENOTYPE OF ABCB11 538G > A**

Today in Japan, axillary osmidrosis is recognized as a disease that is covered by the national health insurance system. Axillary osmidrosis, which is exemplified by unpleasant odors, sweating and staining of clothes, is often perceived, especially by young women, as a distressing and troublesome problem (Wu et al., 1994). Axillary osmidrosis is a chronic skin condition characterized by an excessive, axillary malodor resulting from apocrine gland dysfunction (Hess et al., 2010). Certain people display an excessive fear, aversion or psychological hypersensitivity to unpleasant smells or odors. They tend to opt for aggressive surgical treatments and are sometimes categorized as having osmophobia. Interestingly, an association between wet-type earwax and axillary osmidrosis had already been recognized more than half a century ago (Matsunaga, 1962). Hence, the wet-type of earwax has frequently been used as one of diagnostic criteria and characteristics in the clinic. This relationship, however, had only been based on the observations of those two respective phenotypes. Therefore, there has been a need for objective evidence for diagnosis of axillary osmidrosis to prevent unnecessary treatments for such patients.

Recently, it has been reported that the ABCB11 WT allele is intimately associated with axillary osmidrosis as well as the wet-type of earwax (Table 3). Several studies have already concluded that the genotypes at ABCB11 538G > A would be useful biomarkers for the diagnosis of axillary osmidrosis (Nakano et al., 2009; Toyoda et al., 2009; Inoue et al., 2010; Martin et al., 2010). Indeed, it is suggested that genotyping of the ABCB11 gene would provide an accurate and practical criterion for guidance of appropriate treatment and psychological management of patients (Toyoda et al., 2009; Inoue et al., 2010; Ishikawa and Hayashizaki, 2012). Rapid genotyping of the ABCB11 gene is briefly described in Appendix.

Sweat produced by the axillary apocrine glands is odorless. Secretions from the apocrine glands, however, can be converted to odoriferous compounds by bacteria (Corynebacteria), which results in the formation of the unique “human axillary odor” (Shehadeh and Kilgman, 1963). Axillary osmidrosis patients (538G/G homozygote or G/A heterozygote) were observed to have significantly more numerous and larger-sized axillary apocrine glands as compared with those in subjects carrying the A/A homozygote. Indeed, the 538G allele in the ABCB11 gene is associated with axillary osmidrosis (Nakano et al., 2009; Toyoda et al., 2009; Inoue et al., 2010; Martin et al., 2010), and ABCB11 WT (Gly180) would be responsible for the secretion of proustiforous compounds from the axillary apocrine gland. In primates, axillary odors may play a role in olfactory communication, although no documented behavioral or endocrine changes resulting from volatiles produced in the axillae have been reported to occur in humans. Previous studies have described the presence of androgen steroids in the axillary area. Androsterone sulfate (AS) and DHEAS were detected in an extract of axillary hairs in addition to high levels of cholesterol (Julez, 1968). It was also demonstrated, following injection of radioactive pregnenolone or progesterone, that steroid secretion was concentrated in the axillary area (Brooksbank, 1970). In those studies, however, the axillary sweat collected from the skin surface contained a mixture of materials from apocrine, eccrine, and sebaceous glands, in addition to desquamating epidermal cells. In this respect, Luborsky et al. (1979) demonstrated that pure apocrine secretions contained at least two androgen steroids, AS and DHEAS, in addition to cholesterol. It is strongly suggested that
Why does one SNP (c.538G > A) in the human ABCC11 gene affect the function of apocrine glands? To address this question, we have recently provided evidence that proteasomal degradation of the SNP variant (Arg180) of ABCC11 is the underlying molecular mechanism (Tiroda et al., 2009). ABCC11 WT with Gly180 is an N-linked glycosylated protein, which is localized within intracellular granules and large vacuoles as well as at the luminal membrane of secretory cells in the cerumen apocrine gland (Tiroda et al., 2009). N-linked glycosylation occurs at both Asn88 and Asn844 in the extracellular loop between transmembrane domains 7 (TM7) and 8 (TM8) of the ABCC11 WT protein. In contrast, the SNP variant (Arg180) lacks N-linked glycosylation and readily undergoes proteasomal degradation, most probably via ubiquitination. As a consequence, no granular or vacuolar localization was detected in the cerumen apocrine glands of people homozygous for the SNP variant.

Morphological differences were previously reported between the secretory cells of wet and dry types of human ceruminous glands (Shagyo et al., 1988). In the wet-type glands, the Golgi apparatus was reportedly well developed, whereas it was generally small in the corresponding cells of the dry-type. Furthermore, numerous intracellular granules were observed in the wet-type gland in close relationship to their well-developed Golgi apparatus, whereas intracellular granules were rare in the dry-type gland.

The endoplasmic reticulum (ER) and Golgi apparatus are the synthesis and maturation sites of proteins destined for the plasma membrane, the secretary and endocytic organelles, and secretion (Ellgaard et al., 1999; Helenius and Aebi, 2004). Efficient quality control systems have evolved to prevent incompletely folded proteins from moving along the secretory pathway. Accumulation of misfolded proteins in the ER would detrimentally affect cellular functions. Therefore, misfolded proteins may be removed from the ER by retrotranslocation to the cytosol compartment where they are degraded by the ubiquitin-proteasome system. This process is known as ER-associated degradation (ERAD; Moro, 2005; Ellgaard and Helenius, 2001; Hampton, 2002; Kleiner and Braakman, 2004). It is likely that the product of the SNP variant (Arg180) is recognized as a misfolded protein in the ER and readily undergoes proteasomal degradation. An electrostatic charge (either positive or negative) at amino acid 180 in the transmembrane domain 1 (TM1) might interfere with correct folding of the de novo synthesized ABCC11 protein in the ER (Tiroda et al., 2009). This ERAD processing of the SNP variant (Arg180) of ABCC11 may greatly influence the activity of ceruminous apocrine glands and determine the type of human earwax.

Similar ERAD processing is considered to take place for the SNP variant (Arg180) of ABCC11 in eccrine and mammary apocrine glands. Figure 4 schematically illustrates the impact of this SNP on the cellular localization and function of ABCC11 in secretory cells of the apocrine gland. Asn88 and Asn844 are glycosylation target sites in the human ABCC11. The N-linked glycans are thought to be subjected to extensive modification as glycoproteins mature and move through the ER via the Golgi apparatus to their final destinations as, for example, intracellular granules and large vacuoles of secretory cells in the apocrine gland.

**ABCC11 WILD-TYPE ALLELE AND BREAST CANCER RISK**

In 1971, Petrakis (1971) first reported that international mortality and frequency rates for breast cancer seemed to be associated with the frequency of the allele for wet-type earwax. Caucasians and African-Americans in the USA as well as Germans exhibited approximately fourfold higher rates of breast cancer mortality as compared with Japanese and Taiwanese women (Petrakis, 1971). Nevertheless, the phenotypic association of the wet-type of earwax with breast cancer remained controversial (Petrakis, 1971; Ing et al., 1973).

At the present time, it is not well understood whether ABCC11 WT really contributes to breast cancer risk. Therefore, we have most recently carried out a genotyping study of the SNP 538G > A (Gly180Arg) for a total of 543 Japanese women to examine the association between the frequency rate of breast cancer and the allelic frequency of the G allele (WT). We obtained blood samples from patients with invasive breast cancer (n = 270) and control volunteers (n = 273) and genotyped the SNP c.538G > A in the ABCC11 gene. The frequency of the 538G allele in the breast cancer patients was higher than that in the control volunteers. The odds ratio for the women with genotypes (G/G + G/A) to develop breast cancer was estimated as 1.63 (p-value = 0.026), suggesting that the 538G allele in the ABCC11 gene is moderately associated with the risk of breast cancer (Ota et al., 2010). The relative ratio of breast cancer patients carrying the homozygous 538GG allele was 1.77-fold greater than that of the corresponding healthy volunteers (Ota et al., 2010). This relative ratio was even greater than that (1.41-fold) for breast cancer patients carrying heterozygous alleles 538G/A. The G allele appears to be positively related to breast cancer frequency in the groups of Japanese women studied. In contrast, no significant association with breast cancer risk was observed in Europeans (Belsey et al., 2011; Laing et al., 2011).

We initially thought that some genetically determined variation(s) in the apocrine system might influence susceptibility to breast cancer, although the genetic determinant (538G > A SNP in ABCC11) was not known at that time. It is hypothesized that the function of ABCC11 per se, or metabolites transported by ABCC11, may stimulate the proliferation of apocrine gland cells to enhance the risk of mastopathy (Figure 5). This hypothesis is supported by evidence that apocrine glands are large in individuals carrying the WT allele of the ABCC11 gene. So far as the cell cycle machinery is operating normally, proliferation of apocrine gland cells should be controlled to a certain extent. When a somatic mutation has occurred in BRCA1, BRCA2, p53, or p21, however, it can lead to deleterious and unregulated proliferation of these cells (Figure 5).

**REGULATION OF ABCC11 GENE EXPRESSION**

In 2004, Bieche et al. (2004) reported that ABCC11 was up-regulated in estrogen receptor positive breast tumors, as compared with normal breast tissue. In contrast, Sosonkina et al. (2011) reported down-regulation of ABCC11 protein in human breast cancer, although the genetic determinant (538G > A SNP in ABCC11) was not known at that time. It is hypothesized that the function of ABCC11 per se, or metabolites transported by ABCC11, may stimulate the proliferation of apocrine gland cells to enhance the risk of mastopathy (Figure 5). This hypothesis is supported by evidence that apocrine glands are large in individuals carrying the WT allele of the ABCC11 gene. So far as the cell cycle machinery is operating normally, proliferation of apocrine gland cells should be controlled to a certain extent. When a somatic mutation has occurred in BRCA1, BRCA2, p53, or p21, however, it can lead to deleterious and unregulated proliferation of these cells (Figure 5).
FIGURE 4 | Schematic illustration of intracellular sorting of ABCC11 WT and proteasomal degradation of the R180 (Arg180) variant in secretory cells of the apocrine gland. De novo synthesized ABCC11 WT is N-linked glycosylated at Asn838 and Asn844 in the ER, further processed in the Golgi apparatus, and destined for the membranes of intracellular granules and vacuoles. Ceruminous components are thought to be transported by ABCC11 WT and sequestered in intracellular granules and vacuoles. SNP variant R180 lacking N-linked glycosylation is recognized as a misfolded protein in the ER and readily undergoes ubiquitination and proteasomal degradation (ERAD pathway). ER, endoplasmic reticulum; ERAD, ER-associated degradation. This scheme is modified from Toyoda et al. (2009).

FIGURE 5 | The potential impact of ABCC11 WT (538G) on the apocrine phenotype, patients’ response to nucleoside-based chemotherapy, and the potential risk of mastopathy and breast cancer. BRCA-1, breast cancer-1; BRCA-2, breast cancer-2; PI3K, phosphatidylinositol 3-kinase; ERα(+), estrogen receptor α-positive; 5-FU, 5-fluorouracil; AraC, cytarabine. This scheme is modified from Toyoda and Ishikawa (2010).

breast cancer. Park et al. (2006) investigated the mRNA levels of ABC transporter genes in breast cancer patients who underwent sequential weekly paclitaxel/FEC (5-fluorouracil, epirubicin, and cyclophosphamide) neoadjuvant chemotherapy. Their analysis showed that the expression of ABCC11 was increased (fold ratio = 2.71) in those patients with residual disease as compared with the patients having no pathologic evidence of any residual invasive cancer cells in the breast.

Honorat et al. (2008) have demonstrated that endogenous ABCC11 mRNA levels in breast cell lines are correlated with their estrogen receptor α-status. Interestingly, they found that ABCC11 expression was reduced in vitro by E2 treatments. Furthermore, this E2-dependent down-regulation of ABCC11 expression was blocked by co-treatment with tamoxifen, an E2 antagonist. These findings suggest that ABCC11 expression is regulated directly or indirectly by estrogen receptor α and that the prolonged exposure of breast cancer cells to tamoxifen can lead to up-regulation of ABCC11.

Hauswald et al. (2009) have shown that some of the histone deacetylase inhibitors induced the expression of several ABC
ABCC11 is directly involved in 5-FU resistance by means of the transport of the ABCC11 WT may affect the efficacy of nucleoside-based chemotherapy. Since histone deacetylase inhibitors can be utilized in combination with conventional anti-cancer drugs in clinical trials, such induction of the ABC11 WT may affect the efficacy of nucleoside-based chemotherapy. The potential involvement of ABCC11 in drug resistance of breast cancer has recently been reported. For example, ABCC11 mRNA is found to be highly expressed in breast tumors (Berta et al., 2001; Yabuuchi et al., 2001; Bieche et al., 2004), and particularly in invasive ductal adenocarcinomas (available at: https://www.oncomine.org/resource/login.html, accessed October 01, 2012). This expression is reportedly regulated by estrogen receptor-β (Honchar et al., 2008) and induced by 5-fluorouracil (5-FU; Oguri et al., 2007). Furthermore, it has been shown that ABC11 is directly involved in 5-FU resistance by means of the efflux transport of the active metabolite 5-fluoro-2′-deoxyuridine 5′-monophosphate (FdUMP; Gao et al., 2003; Kruh et al., 2007; Oguri et al., 2007). It remains to be elucidated whether the expression of ABC11 WT (538G) is related to drug resistance of breast cancer and high rates of mortality. Further clinical studies, including protein expression studies in tumors, will be needed to clarify the potential contribution of ABC11 to breast cancer risk and prognosis, including drug resistance and chemosensitivity. Because of their structural similarities, it could be anticipated that substrate specificity of ABC11 would be related to those of ABC4 and ABC5. This indeed has been the case. Ecotropic expression of ABC11 in mammalian cells enhances the cellular efflux of cyclic nucleotides and confers resistance to certain anticancer and antiviral nucleotide analogs (Guo et al., 2003). In fact, it has been reported that ABC11 WT has an ability to efflux cyclic nucleotides (e.g., cGMP and cAMP) and confers resistance to several antiviral and anticancer nucleotide analogs, such as 5′-FdUMP and 9′-(2′-phosphonylmethoxy)adenine (PMEA; Gao et al., 2003; Kruh et al., 2007; Oguri et al., 2007).

Therapy with nucleoside-derived drugs is characterized by inter-individual variability (Heinemann et al., 1988; Aubezzeze et al., 1991). Genetic variants that affect protein products involved in all steps leading to a drug’s action may be major contributors to this heterogeneity of responses to nucleoside-based treatments. In particular, variants of drug metabolizing enzymes and transporters might affect the amount of drug needed for an efficient therapeutic response (Irati-Murugarren and Pantet-Angladé, 2010).

Successful treatment of cancer remains a therapeutic challenge, with a high percentage of patients suffering from drug resistance or relapsed disease. One of such examples involves anti-leukemia treatment with nucleoside analogs, such as cytarabine (AraC). Gao et al. (2009) have recently presented evidence that expression of ABC11 WT is an important factor affecting acute myeloid leukemia patient survival. It is very likely that the cause of treatment failure in those patients with high expression of ABC11 WT is an increased extrusion of AraC from blast cells mediated by the transporter. Uemura et al. (2010) have recently found that both gene and protein expression of ABC11 were higher in pemetrexed (MTA)-resistant cells than in the parental cells. The MTA-resistant cells showed cross-resistance to MTX, which is a substrate for ABC11, and intracellular MTX accumulation in MTA-resistant cells was lower than that in the parental cells. They then tested the effect of decreasing the expression of ABC11 by siRNA and found that decreased expression of ABC11 enhanced MTA cytotoxicity and increased intracellular MTX accumulation in MTA-resistant cells. These findings suggest that ABC11 confers resistance to MTA by enhancing the efflux of the intracellular anti-cancer drug. They further analyzed the relationship between the ABC11 gene expression and MTA sensitivity of 13 adenocarcinoma cell lines. In contrast to their expectation, there was no correlation. Instead, the 13 lung adenocarcinoma cell lines could be classified into three groups based on the genotypes of the ABC11 SNP (538G > A); G/G, G/A, and A/A. The A/A group showed a significant reduction in the IC50 value of MTA compared with those values for the combined G/G and G/A groups, indicating that ABC11 538G > A is an important determinant of MTA sensitivity. These results suggest that ABC11 538G > A may be one of the biomarkers for selection of MTA treatment in adenocarcinomas. This finding, however, should be carefully evaluated by clinical studies to determine whether ABC11 538G > A is truly a clinically important biomarker for the prediction of chemotherapeutic efficacy.

CONCLUSION
Apocrine secretion occurs when the secretory process is accomplished with a partial loss of cell cytoplasm. The secretory materials may be contained within the secretory vesicles or dissolved in the cytoplasm and then released during excretion as cytoplasmic fragments into the glandular lumen or interstitial space (Geseas and Satoh, 2003). Hitherto, apocrine secretory mechanisms have not been well characterized (Geseas and Satoh, 2003). Although the biochemical and physiological pathways that regulate the apocrine secretory process are not clearly known, our recent findings (Yoshiura et al., 2006; Toyoda et al., 2009; Inoue et al., 2010) that the SNP (538G > A, Gly180Arg) in the ABC11 gene determines both earwax type and axillary osmidrosis have shed light on the novel function of this ABC transporter in apocrine glands. Further studies are needed to explore the clinical significance of ABC11 so as to elucidate whether there are any other diseases that involve apocrine secretion.

ACKNOWLEDGMENTS
The authors’ studies were supported in part by CREST from the Japan Science and Technology Agency (JST) and Grants-in-Aid for Scientific Research (Category S, No. 13085024; and Priority Area “Applied Genomics” No. 17190055) from the Ministry of Education, Culture, Sports, Science and Technology of Japan (to Norio Nikawa) as well as by the JST research project “Development of the world’s fastest SNP detection system” (to Yoshihisa Ishikawa). Yu Toyoda is a research fellow of the Japanese Society for Promotion of Science (JSPS).
Ohashi, J., Naka, I., and Tsujiya, N. (2011). The impact of natural selection on the ABCC11 SNP determining earwax type. Mol. Biol. Evol. 28, 849–857.

Otto, N., van der Heiden, I., Schiffer, G. E., van de Wetering, K., van Doorn, E., de Haas, M., et al. (2007). Multifrugal resistance-associated protein 9 (ABCG2) is present in sperm. Biochem. J. 406, 53–60.

Ota, I., Sakurai, A., Toyoda, Y., Morita, A., Sasaki, T., Chishima, T., et al. (2009). Down-regulation of ABCC11 protein expression in prehistoric Japan. J. Invest. Dermatol. 130, 5189–5194.

Ota, I., Sakurai, A., Shimizu, C., Shimoyama, S., Ota, I., Sakurai, A., Toyoda, Y., Morita, A., Sasaki, T., Chishima, T., et al. (2010). The impact of natural selection on the ABCC11 SNP determining earwax type. Mol. Biol. Evol. 28, 849–857.

Pathak, S., Shinmu, C., Shimonoura, T., Takino, M., Ando, M., Kohno, Y. W., Fang, R. H., and Yeh, F. L. (2010). Pharmacogenomics of human ABC transporter ABCC11. Pharmazie 65, 853–862.

Toyoda, Y., Sakurai, A., Miyan, T., Nakahima, M., Yoshida, K., Nakagawa, H., et al. (2009). Earwax, odors, and breast cancer: why does one SNP (359 G→A) in the human ABC transporter ABCC11 gene determine earwax types? FASEB J. 23, 2001–2013.

Toyoda, Y., and Ishikawa, T. (2010). Pharmacogenetics of human ABC transporter ABCC11 (MRP8): potential role of breast cancer and chemotherapy failure. Anticancer Agents Med Chem. 10, 617–624.

Uemura, T., Oguri, T., Ohashi, H., Takahama, O., Miyahara, M., Maeno, K., et al. (2010). ABCC11/MRP8 confers resistance to pemetrexed in vivo. Anticancer Res. 30, 579–585.

Uemura, T., Oguri, T., Ohashi, H., Takahama, O., Miyahara, M., Maeno, K., et al. (2010). ABCC11/MRP8 confers resistance to pemetrexed in vivo. Anticancer Res. 30, 579–585.

Conflict of Interest Statement: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.
APPENDIX

CLINICAL GENOTYPING OF SNP 538G > A (Gly180Arg) IN THE ABCC11 GENE

The rapid growth of personalized medicine is being supported by emerging new technologies together with accumulating knowledge of pharmacogenomics. We tried to create a clinical method, the SmartAmp, to genotype the SNP 538G > A in the human ABCC11 gene. The SmartAmp-based method enables us to detect genetic polymorphisms or mutations in about 30 min under isothermal conditions without requiring DNA isolation and PCR processes for sample preparation (Ishikawa and Hayashizaki, 2012). Figure A2A schematically illustrates the strategy of SNP detection by this clinical method. To determine the SNP 538G > A (Gly180Arg) in the ABCC11 gene, we prepared one set of primers designated TP, FP, BP, OP, and CP (Figure A2A). The TPS discriminate the polymorphism 538G or 538A in the ABCC11 gene, and the CPS inhibit the background amplification from mismatch sequence pairs (Toyoda et al., 2009; Ishikawa and Hayashizaki, 2012). These primers selectively recognized the SNP 538G > A of the ABCC11 gene to discriminate homozygous 538G/G, heterozygous 538G/A, and homozygous 538A/A (Figure A2A). Thus, this genotyping method would provide a practical tool to support clinical diagnosis (Ishikawa and Hayashizaki, 2012).

![Chemical structures of ABCC11 substrates](image)

**FIGURE A1** | Chemical structures of ABCC11 substrates. Cyclic adenosine monophosphate (cAMP), cyclic guanosine monophosphate (cGMP), leukotriene C4 (LTC4), S-(2,4-dinitrophenyl)-glutathione (DNP-SG), estrone 3-sulfate (E13S), dehydroepiandrosterone 3-sulfate (DHEAS), and estradiol 17β-D-glucuronide (E217βG).
FIGURE A2 | Detection of SNP 538G > A in ABCC11 gene. (A) Strategy and primers for the SmartAmp-based detection of SNP 538G > A residing in exon 4 of the ABCC11 gene on chromosome 16q12 (upper panel) and the sequences of ABCC11 allele-specific primers needed for the SNP detection (lower panel). Arrows indicated the sequence difference between the WT and SNP alleles. (B) Time-courses of the SNP detection reaction with ABCC11 allele-specific primers. Data are from Toyoda et al. (2009).