ABCG2 polymorphisms in gout: insights into disease susceptibility and treatment approaches

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Abstract: As a result of the association of a common polymorphism (rs2231142, Q141K) in the ATP-binding cassette G2 (ABCG2) transporter with serum urate concentration in a genome-wide association study, it was revealed that ABCG2 is an important uric acid transporter. This review discusses the relevance of ABCG2 polymorphisms in gout, possible etiological mechanisms, and treatment approaches. The 141K ABCG2 urate-increasing variant causes instability in the nucleotide-binding domain, leading to decreased surface expression and function. Trafficking of the protein to the cell membrane is altered, and instead, there is an increased ubiquitin-mediated proteosomal degradation of the variant protein as well as sequestration into aggresomes. In humans, this leads to decreased uric acid excretion through both the kidney and the gut with the potential for a subsequent compensatory increase in renal urinary excretion. Not only does the 141K polymorphism in ABCG2 lead to hyperuricemia through renal overload and renal underexcretion, but emerging evidence indicates that it also increases the risk of acute gout in the presence of hyperuricemia, early onset of gout, tophi formation, and a poor response to allopurinol. In addition, there is some evidence that ABCG2 dysfunction may promote renal dysfunction in chronic kidney disease patients, increase systemic inflammatory responses, and decrease cellular autophagic responses to stress. These results suggest multiple benefits in restoring ABCG2 function. It has been shown that decreased ABCG2 141K surface expression and function can be restored with colchicine and other small molecule correctors. However, caution should be exercised in any application of these approaches given the role of surface ABCG2 in drug resistance.

Keywords: ABCG2, BCRP, gout, urate, uric acid, polymorphism, allopurinol

Introduction

Gout is an inflammatory arthritis caused by an extremely painful but self-limiting innate immune response to monosodium urate (MSU) crystals deposited in synovial fluid.1 Without effective management, in some individuals, gout can become chronic with the development of tophi (organized lumps of urate and immune cells)2 and permanent bony erosion and disability. Gout is also comorbid with other metabolic-based conditions such as heart and kidney disease and type 2 diabetes.3 An elevated concentration of urate (hyperuricemia) is necessary, but not sufficient, for the development of gout. Host-specific and environmental factors are required for the progression from hyperuricemia to gout. Approximately 30 genetic loci, including ABCG2, influence serum urate concentrations,4 but less is understood about the genetic control of the formation of MSU crystals and the subsequent inflammatory response.5 Urate-lowering therapy is a cornerstone of gout management; however, for various reasons, it is often not...
effective.\textsuperscript{1} Despite the availability of a range of cost-effective urate-lowering drugs, there is a need for the development of better therapies for acute gout.

The ATP-binding cassette G2 (ABCG2) protein first came to biomedical attention through its contribution to an ATP-dependent multidrug resistance phenotype in a breast cancer cell line.\textsuperscript{6} It is one of a superfamily of 48 human ABC transporters that, in general, transport a wide array of substrates and are dependent on ATP binding to activate transport. The ABCG2 transporter is one of three well-studied multidrug transporters (others are multidrug resistance protein 1 and P-glycoprotein encoded by the \textit{ABCC1} and \textit{ABCB1} genes, respectively). These transporters export a wide range of compounds, including in the case of ABCG2, uric acid from cells. ABCG2 is a “half transporter” ABC protein, containing one membrane-spanning domain of six transmembrane helices, a N-terminal single intracellular portion containing a nucleotide-binding domain (NBD), and a short intracellular C-terminal tail (Figure 1). “Half transporters” like ABCG2 need to homodimerize to function in vitro but more likely exist in higher-order tetrameric or greater assemblages.\textsuperscript{7,8}

ABCG2, also known as breast cancer resistance protein, is overexpressed in human and animal cell lines resistant to chemotherapeutic drugs\textsuperscript{9,10} and transports anticancer drugs such as mitoxantrone and doxorubicin\textsuperscript{6} (reviewed in reference 11). ABCG2 is important in stem cell biology.\textsuperscript{12,13} Also, the wide expression pattern in normal tissues (Figure 2) suggests that ABCG2 may fill an important physiological role as an excretor of environmental and endogenous toxins, for example, heme.\textsuperscript{14} This assertion is supported by the susceptibility of ABCG2 knockout mice to diet-induced phototoxicity and protoporphyria.\textsuperscript{15} It is expressed in the small intestine (excretion and limiting absorption), blood–brain and blood–placental barriers (mediating distribution), liver and kidney (elimination and excretion), and mammary gland (transporting into milk).\textsuperscript{16} The pattern of ABCG2 expression is consistent with its role as a uric acid efflux transporter (reviewed in reference 17).

**Figure 1** Schematic representation of gout- and hyperuricemia-related polymorphisms in ABCG2. The ABCG2 protein consists of 655 amino acids and can be divided into an intracellular N-terminal domain, a nucleotide binding domain, six transmembrane domains, and a C-terminal end. The nucleotide-binding domain (amino acids 44-288) contains several signature sequences, named Walker A (A), Walker B (B), and the ABC signature sequence (C). The beginning and end amino acid position numbers are given for the signature sequences and the transmembrane domains. The third extracellular loop contains two cysteine residues connected by a disulfide bridge, and a glycosylated asparagine residue, both of which influence stability of the receptor. The cysteine residue at position 603 is important for homodimer formation. The V12M polymorphism is located in the N-terminal domain. The Q126X and Q141K polymorphisms are both located in the nucleotide-binding domain between the Walker A and the ABC signature sequences.

**Abbreviation:** ABCG2, ATP-binding cassette G2.
ABCG2 polymorphisms in gout

The ABCG2 transporter was identified as a uric acid efflux transporter only after it was associated with serum urate concentrations in a large genome-wide association study.18,19 This review explores the effects of several polymorphisms in the ABCG2 gene on susceptibility to hyperuricemia, gout, and chronic kidney disease. Furthermore, the role of ABCG2 in inflammatory responses and the possibility of ABCG2 as a treatment target are discussed.

**Major ABCG2 genetic variants**

The ABCG2 transporter, expressed on erythrocytes, is the basis of a recently explained blood group system, Junior (Jr).20,21 Individuals null for ABCG2 produce an ABCG2 alloantibody upon blood transfusion that can cause transfusion reactions, in extreme cases leading to fatal hemolytic disease of the fetus and newborn. The Jr(a-) phenotype is most prevalent in Japan with the most common Jr(a-) mutations being Q126X (Japanese) and R246K (Europeans).19,20

There are only two common (≥1%) missense genetic variants in the ABCG2 gene (V12M; rs2231137 and Q141K; rs2231142) and one common nonsense variant (Q126X; rs72552713) that is specific to South East Asian populations (Figure 1). The Q141K and Q126X variants influence expression levels of ABCG2 and contribute risk to phenotypes such as serum urate levels, gout, and response to the urate-lowering drug allopurinol (Table 1). Numerous other rare (<1%) variants are identified (http://www.ensembl.org), some of which have been phenotyped.22–28 The most widely studied variant is Q141K, a variant that is clinically relevant and has significant impact on ABCG2 characteristics. It is prevalent in most major population groups with the 141K allele frequency varying between 1% in African and 29% in South East Asian populations. There is consistent evidence for the 141K variant reducing the amount of ABCG2 protein expressed both in vitro19,22–25,28,29 and, in vivo, from human liver samples.30

Residue 141 is located in the E-helix31 of the NBD of ABCG2, an area critical for the packing of the soluble portion of the protein. The 141K variant reduces ATPase activity,26,27 uric acid transport activity, and total and surface abundance (Table 1 and Figure 3A). These defects are believed to be caused by reduced NBD stability.32 Although proteolysis and thermo-stability as assessed by melting point curves of the isolated 141K NBD showed only small differences from the wild type,33 work done on the whole protein shows evidence of increased NBD instability in mammalian expression
Table 1 Major genetic variation in ABCG2 and impact on protein expression and phenotype

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</thead>
<tbody>
<tr>
<td>V12M: 0.06/0.00/0.15/0.00</td>
<td>Unchanged22,24,28</td>
<td>Same15,17,130</td>
<td>Same26,27</td>
<td>Same26,27</td>
<td>Same26,27</td>
<td>Same26,27</td>
<td>Same26,27</td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>Q126X: 0.00/0.00/0.10/0.00</td>
<td>Null24</td>
<td>Same25,26,32,36</td>
<td>Same26</td>
<td>Reduced26,27</td>
<td>Reduced26,27</td>
<td>Increased26,27</td>
<td>Same26,27</td>
<td></td>
<td></td>
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<td></td>
</tr>
<tr>
<td>Q141K (rs2231142)</td>
<td>0.09/0.09/0.10/0.01</td>
<td>Same25,26,32,36</td>
<td>None25</td>
<td>Reduced26,27</td>
<td>Reduced26,27</td>
<td>Increased26,27</td>
<td>Same25,26,36</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>rs10011796 T: 0.39/0.63/0.48/0.27</td>
<td>0.39/0.63/0.48/0.27</td>
<td>Same25,26,32,36</td>
<td>None25</td>
<td>Reduced26,27</td>
<td>Reduced26,27</td>
<td>Increased26,27</td>
<td>Same25,26,36</td>
<td></td>
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</table>

Notes: Phenotype and prevalence information is given to the minor (alternative) allele. All phenotypes are compared to wild-type. Study systems: naturally occurring humans4,30,58,67,69,70,73,82,86,87,117,130–132; HEK293 (human embryonic kidney) and derivative cells22,25,27–29,36; LLC-PK1 (porcine epithelial kidney cells)25,26; Sf-9 insect cells26,27,33; Xenopus oocytes.32 The Sf-9 cells were used for ATPase activity assays. *Meta-analyses.

Regulation of ABCG2 expression

The expression of ABCG2 is regulated by several transcription factors and hormones. A large number of cis-regulatory regions of ABCG2 (reviewed in30). Hypoxia-inducible factor 1 (HIF-1α) stabilizes under hypoxic conditions and has been found to bind to a hypoxia-responsive element in the ABCG2 promoter and increase expression.40,41 Upstream of HIF-1α, a regulator, ABC2-38 and ABC2-39 promoter, nuclear factor E2-related factor 2 (Nrf2), a nuclear transcription factor involved in activating oxidative stress responses, can induce ABCG2 transcription.6 In addition to transcription factors, the expression of ABCG2 is also influenced by miRNAs.37 Interestingly, the ABCG2 F142 residue is in an analogous position to the cystic fibrosis transmembrane receptor (encoded by ABCC7).2 In vitro deletion of F142 from ABCG2 leads to major processing and folding defects with no surface expression,24 thereby abolishing the NBD directly induces production of the ABCG2 protein. With either suppressor mutations or small molecules that may bind as evidenced by rescued protein abundance. Q141K substitution occurs to shift outward caused by the putative pocket created by the residue.41 Furthermore, recent modeling of the 14K NBD suggested that a loop adjacent to the loop. This potential packing of the 14K NBD may move the NBD into the transmembrane region of ABCG2, preventing it from folding properly. The NBD stability of the 14K variant increases the interaction of the protein with the endoplasmic reticulum-associated degradation pathway and subsequent ubiquitin-mediated degradation.25 The ABCG2 F142 residue is in an analogous position to the cystic fibrosis transmembrane receptor (encoded by ABCC7).2 In vitro deletion of F142 from ABCG2 leads to major processing and folding defects with no surface expression,24 thereby abolishing the NBD directly induces production of the ABCG2 protein. With either suppressor mutations or small molecules that may bind as evidenced by rescued protein abundance. Q141K substitution occurs to shift outward caused by the putative pocket created by the residue.41 Furthermore, recent modeling of the 14K NBD suggested that a loop adjacent to the loop. This potential packing of the 14K NBD may move the NBD into the transmembrane region of ABCG2, preventing it from folding properly. The NBD stability of the 14K variant increases the interaction of the protein with the endoplasmic reticulum-associated degradation pathway and subsequent ubiquitin-mediated degradation.25...
associated molecules (including perhaps ABCG2) are factors β and possible that systematically linked changes in PGC1 association with gout has not yet been replicated and it is unknown if PP ARGC1B levels or gout. However a variant in PPARGC1B (rs45520937) has been associated with gout in Han Chinese.52 PPARGC1B encodes the PGC1β transcriptional repressor, a coactivator for PPARγ that is involved in estrogen signaling53,54 in addition to a key role in maintaining mitochondrial biogenesis.55 However the association of PPARGC1B with gout has not yet been replicated and it is unknown if rs45520937 is itself associated with ABCG2 expression. Since reduced mitochondrial DNA copy number is associated with gout56 it is possible that systematically linked changes in PGC1β and associated molecules (including perhaps ABCG2) are factors connecting mitochondrial dysfunction and gout.57

**ABCG2, urate control, and risk of gout**

An individual’s serum urate level, like other complex traits, is a function of a suite of inherited genetic variants and environmental exposures.5 A genome-wide association study identified the Q141K variant in the ABCG2 gene as associated with serum urate concentration in people of European ancestry, with the 141K allele associated with increased urate concentration.18 This genome-wide significant level of association has been consistently replicated in other genome-wide association studies in people of European and east Asian ancestry4,59,60 but not in people of African–American ancestry.59,60 Lack of association in African–Americans in GWAS is likely because of the reduced power because of lower allele frequency in African–Americans (≤3%) – there is nominal evidence for the association of the 141K variant with increased serum urate levels in African–Americans19 and the increased risk of gout.19 The Q141K variant (and other variants) has been associated with serum urate levels or hyperuricemia in other populations, for example, Tibetan41 and Korean.62 Uric acid transport assays in Xenopus oocytes showed that ABCG2 transports uric acid with the 141K variant causing ~50% reduced ability to secrete uric acid.19 The regulation of ABCG2 protein in epithelial cells is largely unknown. However, similar to other uric acid renal influx transporters, ABCG2 co-immunoprecipitates with the scaffold protein PDZK1,63 suggesting a possible common regulatory pathway.

The magnitude of association of Q141K with serum urate levels is the second strongest genome-wide behind SLC2A9, which is consistently the strongest in Europeans and East
Asians. Each copy of the 141K allele associates with a 0.22 mg/dL increase in serum urate in Europeans\(^4\) and an 0.14 mg/dL increase in east Asians.\(^5\) The magnitude is stronger in men than women and is modulated by body mass index (BMI), with the magnitude being stronger in lean people than those who are overweight and obese. The sex difference is most marked in lean people.\(^6\) The sex difference in association with serum urate levels is an interesting observation given the regulation of ABCG2 expression by estrogen.\(^49-51\) Compared to other typical genetic variants controlling complex phenotypes, Q141K has a very large magnitude of association, explaining \(-1\%\) of variance in serum urate levels. This compares with \(-0.3\%\) for the strongest genetic association with BMI at the FTO/IRX3 locus.\(^65\)

When associations of other SNPs within the ABCG2 locus with serum urate levels are tested conditionally on Q141K genotype, there is evidence for a second independent association at the ABCG2 locus, marked by intronic SNP rs2622629.\(^66\) This second association is of clinical relevance, explaining \(0.1\%\) of variance in serum urate levels. This compares with \(1.24\%\) for the strongest genetic association in Europeans within the UK Biobank (odds ratio [OR] \(= 1.24\) [T Merriman, unpublished data, October 2016]).

Aside from Q141K, the only other common (>1%) missense variant in ABCG2 is V12M situated in a short N-terminal section of ABCG2 prior to the structurally well-defined NBD (Figure 3). This variant is genetically independent of both Q141K \((r^2 = 0.002\) in Europeans) and rs2622629 \((r^2 = 0.009\) in Europeans). However, the impact on ABCG2 characteristics are, compared to Q141K, very moderate and inconsistent (Table 1). There are some data on association with serum urate and gout, suggesting an independent role for V12M in urate control and risk of gout (given the genetic independence from Q141K and rs2622629). Hence, V12M can be considered a third independent effect on gout in ABCG2, after Q141K and rs10011796/rs2622629. The largest genome-wide association study in serum urate in Europeans reported an increase in serum urate of \(0.077\) mg/dL\(^4\) and in East Asians an increase of \(0.108\) mg/dL\(^5\) per copy of the 12V allele. In gout, the common 12V allele consistently confers risk in five separate samples drawn from four ancestral groups: Europeans within the UK Biobank (odds ratio [OR] \(= 1.24\) [T Merriman, unpublished data, October 2016]), Taiwanese Aborigines (OR \(= 1.36\)),\(^69\) Han Chinese in Taiwan (OR \(= 1.33\)),\(^69\) Han Chinese in Shanghai (OR \(= 1.82\)),\(^70\) and New Zealand Māori and Pacific (Polynesian) (OR \(= 1.31\) [T Merriman, unpublished data, October 2016]). Any impact of this variant on the uric acid transport activity of ABCG2 is currently unknown. A combined meta-analysis is shown in Figure 4. Based on the impact of the V12M variant on ABCG2 characteristics (Table 1), it is not obvious how the 12V allele increases serum urate levels and risk of gout. It is possible that

### Table 1: Meta-analysis of association of ABCG2 V12M (rs2231137) with gout

<table>
<thead>
<tr>
<th>Population</th>
<th>Coefficient</th>
<th>Std error</th>
<th>OR</th>
<th>95% CI</th>
<th>W(fixed)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Taiwan Han (Tu et al(^69))</td>
<td>-0.288</td>
<td>0.1208</td>
<td>0.750</td>
<td>[0.592; 0.950]</td>
<td>13.9%</td>
</tr>
<tr>
<td>Taiwan Aboriginal (Tu et al(^69))</td>
<td>-0.304</td>
<td>0.0837</td>
<td>0.738</td>
<td>[0.626; 0.870]</td>
<td>29.0%</td>
</tr>
<tr>
<td>Chinese Han (Zhou et al(^70))</td>
<td>-0.599</td>
<td>0.1282</td>
<td>0.549</td>
<td>[0.427; 0.706]</td>
<td>12.4%</td>
</tr>
<tr>
<td>Polynesian (rs4148153)</td>
<td>-0.274</td>
<td>0.0977</td>
<td>0.761</td>
<td>[0.628; 0.921]</td>
<td>21.3%</td>
</tr>
<tr>
<td>UK Biobank</td>
<td>-0.217</td>
<td>0.0933</td>
<td>0.805</td>
<td>[0.670; 0.968]</td>
<td>23.4%</td>
</tr>
<tr>
<td>Overall (95% CI)</td>
<td></td>
<td></td>
<td>0.732</td>
<td>[0.670; 0.800]</td>
<td>100%</td>
</tr>
</tbody>
</table>

**Heterogeneity:** \(Q=6.3, df=4, P=0.181\)

**Test for overall effect:** \(P<0.0001\)

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**Figure 4** Meta-analysis of association of ABCG2 V12M (rs2231137) with gout: Han Chinese (China),\(^70\) Han Chinese (Taiwan),\(^69\) Taiwanese Aboriginal,\(^69\) New Zealand Polynesian (982 cases and 941 controls), and the UK Biobank (2,422 cases and 152,249 controls). Effect is shown to the minor allele (12M). Variant rs4148153 is a surrogate marker for rs2231137 in people of Polynesian ancestry.

**Abbreviations:** ABCG2, ATP-binding cassette G2; OR, odds ratio; CI, confidence interval; Std, standard.
the V12M variant is itself not causal and in genetic correlation (linkage disequilibrium) with a separate causal variant (which is not Q141K or rs10011796/rs2622629).

The kidney is the major regulator of serum urate levels, which are determined by the balance of secretion and reabsorption. This is controlled by reuptake transporters such as GLUT9 (SLC2A9) and URAT1 (SLC22A12) and secretory transporters ABCG271 and NPT1/NPT4 (SLC17A1, SLC17A3),72 all of which are genetically associated with serum urate concentration.4 Expression of most of these transporters is relatively high in the kidney or, for URAT1, restricted to the kidney. However, expression of ABCG2 is also relatively high in the gut (Figure 2).71 Recent work in a restricted to the kidney. However, expression of ABCG2 is also relatively high in the gut (Figure 2).71 Recent work in a Japanese gout cohort has demonstrated the role of ABCG2 in uric acid excretion in both the gut and kidney. In this well-defined Japanese population sample, it was possible to create grades of ABCG2 dysfunction based on Q141K and Q126X genotype combinations. Individuals positive for the dysfunctional variants 126X and 141K had the highest serum urate levels and highest risk for gout, and those homozygous for 141Q and 126Q had the lowest serum urate levels and lowest risk for gout.73 ABCG2 dysfunction has been shown to influence extra-renal excretion by correlating with an increase in total urinary uric acid excretion. This results in a renal overload (ROL) type of hyperuricemia.74 The presence of 141K (and 126X) alleles reduces excretion through the gut and adds to the circulating urate, overloading the kidney excretion system, resulting in increased urinary uric acid levels. Further study also revealed that ABCG2 dysfunction resulted in a renal under-excretion (RUE) type of hyperuricemia consistent with a critical role in ABCG2-mediated uric acid secretion in the kidney.75 Other studies support a primary role for ABCG2 in excretion of uric acid by the gut. A Spanish study demonstrated considerably stronger association of the 141K allele with gout in patients classified as normo-excretors than in those classified as under-excretors,76 and two New Zealand studies demonstrated 141K-positive individuals not to be renal under-excretors of uric acid.77,78

Predictably, therefore, ABCG2 Q141K associates with gout in most, but not all, ancestral groups analyzed – European, Han Chinese, Japanese, Korean, African American, Taiwanese Aborigine, and Pacific Islanders but not New Zealand Māori.69,79-84 The 126X variant, specific to East Asian populations, confers a higher risk to gout than 141K in Han Chinese and Japanese sample sets.73 In the context that the magnitude of association of ABCG2 on serum urate concentration is less than that of SLC2A9,4 it is interesting that the magnitude of association of ABCG2 Q141K on the risk of gout is consistently larger than that of SLC2A9.4,5,85 This does not equate with the hypothesis that ABCG2 influences gout solely through contributing to hyperuricemia. Emerging evidence (described in the ‘ABCG2: a regulator of gouty inflammation?’ section) indicates that ABCG2 has pleiotropic effects in gout, contributing to the etiology of gout in the presence of hyperuricemia.

ABCG2: a regulator of acute gouty inflammation?

The key initial checkpoint in gout is hyperuricemia.7 Further checkpoints are formation of MSU crystals, the acute inflammatory response to these crystals (gout flare), and tophus formation. A gout flare typically presents as an acutely inflamed and extremely painful lower limb joint. The symptoms peak over the first 24 h and then gradually resolve over the next 10–14 days. Flares are usually recurrent, and the patient is well in between flares. In some patients with prolonged hyperuricemia, tophi can develop both in the joint and non-articular tissues; these are collections of MSU crystals surrounded by a chronic inflammatory granulomatous response.2

As described earlier, it is well established from genome-wide association studies that ABCG2 variants are associated with elevated serum urate concentrations. However, as pointed out above, these studies show that the influence of ABCG2 variants on serum urate is lower than SLC2A9 variants. In contrast, ABCG2 variants are more strongly associated with risk of gout than SLC2A9; Köttingen et al reported ORs for gout of 1.73, P=1.7×10^{-5} for ABCG2 and 1.56, P=1.9×10^{-5} for SLC2A9. In a more recent analysis,86 ABCG2 was associated with an increased risk of gout; compared with asymptomatic hyperuricemia controls, the OR for gout was 1.83, P=2.6×10^{-14}, in European people, and was 2.35, P=3.9×10^{-3}, in Polynesian people. In contrast, SLC2A9 variants were not associated with increased risk of gout when compared with asymptomatic hyperuricemia controls.86 These are intriguing findings that suggest a role for ABCG2 in developing gout once hyperuricemia is established. They do, however, require replication in other sample sets.

ABCG2 variants have also been associated with tophaceous disease in people with gout. In a Taiwanese study of people with gout, 141K was associated with tophi in both Han and Aborignal Taiwanese populations (OR 1.51 and 1.50, respectively, for the 141K allele, pooled OR 1.55, P=7.8×10^{-5}).69 Recently, a New Zealand study of people with gout has reported that risk alleles for two ABCG2 SNPs, Q141K and rs10011796, were associated with tophi (compared with gout patients without tophi), with effects
observed in participants of Western Polynesian (Samoan, Tongan, Niuean, and Tokelaun) ancestry (OR for rs2331142 1.71, \(P=0.017\) and for rs10011796, 3.76, \(P=0.002\)) but not in people of other ancestries (European and Eastern Polynesian [NZ Māori, Cook Island Māori]). The ABCG2 associations persisted in Western Polynesian people even after accounting for serum urate and disease duration in the regression models. Given that only two studies have thus far associated ABCG2 with tophus in gout, further studies are required to substantiate this relationship.

These genetic data suggest a role of ABCG2 in the presentation of gout that is, at least in part, independent of hyperuricemia. Supporting this, cyclosporine inhibits ABCG2 in vitro,\(^8^8\) hyperuricemia and gout can be induced by cyclosporine,\(^8^9\) and there is an interaction between cyclosporine and colchicine\(^9^0\) (colchicine is commonly used to treat gout attacks and is able to correct the dysfunctional internalization of ABCG2 141K\(^1^4^6\)). Collectively, these observations suggest that ABCG2 may be influenced by off-target effects of cyclosporine. It is possible that ABCG2 influences other checkpoints, such as MSU crystal formation or the inflammatory response to these crystals. Although the mechanisms of MSU crystal formation are incompletely understood, it is conceivable that ABCG2 variants lead to preferential transport of urate into the joint (or reduced efflux out of the joint), resulting in higher saturating urate concentrations and MSU crystal formation.

**Mechanistic aspects of ABCG2 in inflammation**

A schematic diagram of the role of ABCG2 in inflammation is shown in Figure 3B. NLRP3 (NBD, leucine-rich family [NLR], pyrin containing 3) inflammasome activation leading to mature interleukin (IL)-1\(β\) release through caspase-1 is a key step in the initiation of the acute gout flare.\(^9^1\) An initial signal (signal 1) is required to stimulate the expression of pro-IL-1\(β\) and inflammasome components.\(^9^2\) Signal 1 includes Toll-like receptor-4 (TLR4) and TLR2 ligands, as well as unsaturated long-chain free fatty acids,\(^9^3,^9^4\) and can be inhibited by omega-3 fatty acids and HDL-cholesterol.\(^9^5,^9^6\) MSU crystals act as signal 2, inducing NLRP3 inflammasome complex oligomerization and activation of caspase-1.\(^9^1\) Genes in this system have been associated with gout. A variant in TLR4, that likely influences TLR4 expression, has been associated with gout in two studies.\(^9^7,^9^8\) Two SNPs in NLRP3-related genes have been associated with gout.\(^9^9–^1^0^0\) The first one is a nonsense variation in the caspase recruitment domain-containing protein 8 (CARD8, rs2043211), a negative regulator of the NLRP3 inflammasome. One of the studies also found a multiplicative interaction between this SNP and an IL-1\(β\) polymorphism (rs1143623)\(^1^0^1\) consistent with a pathogenic model whereby greater inflammasome activity from reduced CARD8 expression, combined with higher levels of pre-IL-1\(β\) expression, leads to increased production of mature IL-1\(β\) and an amplified immune response. Furthermore, the PPARGC1B SNP associated with gout (rs45529037) upregulates the expression of NLRP3 and IL-1\(β\).\(^5^2\)

The role of ABCG2 in regulating inflammation has been described in nonarticular cells. In HEK293 cells cultured with \(\text{H}_2\text{O}_2\), ABCG2 inhibited reactive oxygen species generation, enhanced anti-oxidant capacity of the cells, and protected cells from reactive oxygen species-induced toxicity.\(^1^0^2\) This may be mediated by the role of ABCG2 in exporting urate, an established pro-oxidant in the intracellular setting\(^1^0^3\) by mechanisms that include promotion of mitochondrial dysfunction.\(^1^0^4\) In animals, ABCG2 also inhibited NF-κB and the expression of the inflammatory gene IL-8 induced by reactive oxygen species.\(^1^0^5\) In rheumatoid arthritis, a chronic autoimmune inflammatory arthritis, ABCG2 is highly expressed in the intimal lining layer and on macrophages and endothelial cells in the synovial sub-lining layer.\(^1^0^6\) The synovium is also a very important tissue in gouty arthritis. In several cell culture systems, the expression and function of ABCG2 is reduced when stimulated with pro-inflammatory cytokines.\(^1^0^6–^1^0^8\) Collectively, these results suggest both a suppressive effect of ABCG2 on pro-inflammatory signaling pathways and that ABCG2 is itself a target of pro-inflammatory cytokines, where its expression and activity is suppressed. To date, the influence of ABCG2 variants on the inflammatory response to MSU crystals has not been reported, although genetic and other data suggest a role for the 141K variant in promoting gout once hyperuricemia is established (see the ‘ABCG2: a regulator of gouty inflammation?’ section).

**ABCG2 and autophagy**

In addition to its effects through increased serum urate concentration and the inflammatory responses described earlier, ABCG2 has been reported to play a role in autophagy. In a study by Ding et al,\(^1^0^9\) ABCG2 overexpressing cell lines were more resistant to stressors such as nutrient deprivation due to increased autophagy. The authors observed more degradation of autophagy receptor p62 and increased accumulation of LC3-II, a protein essential for autophagosome formation and function. Knockdown of ABCG2 in these cells subsequently abolished these effects.\(^1^0^9\) It was shown previously that effective autophagy is essential in acute gouty arthritis.
to clear mitochondria that have been damaged by MSU crystals. This prevents the release of mitochondrial DNA and the production of reactive oxygen species, which can activate the NLRP3 inflammasome. When autophagy is not effective, p62 accumulates, causing nuclear factor E2-related factor 2 (Nrf2), a transcription factor involved in oxidative stress responses, to be released from its repressor, kelch-like ECH-associated protein 1 (keap-1), and translocate to the nucleus. Previously, Nrf2 has been shown to induce transcription of heme oxygenase-1 and superoxide dismutase, which can in turn also activate the NLRP3 inflammasome. Finally, ABCG2 expression has been shown to be upregulated by Nrf2, which promotes cancer stem cell survival. Taken together, ABCG2 plays a role in autophagy and its expression is induced through Nrf2. Decreased or a lack of ABCG2 function could therefore induce or prolong NLRP3 inflammasome activation in acute gout through defective autophagy of damaged mitochondria in response to MSU crystals.

**ABCG2 as a drug target**

Restoring the expression and function of ABCG2 molecules that harbor detrimental genetic polymorphisms may be an important next step to limit urate levels and inflammatory responses. Recently, several papers have shown that histone deacetylase (HDAC) inhibitors can restore the function of the 141K ABCG2 variant. Woodward et al demonstrated that the HDAC inhibitor 4-phenylbutyrate restores trafficking and dimer expression of 141K ABCG2. Basseville et al showed that several different HDAC inhibitors, as well as colchicine, inhibit targeting of 141K ABCG2 to the aggresome and promote relocation on the cell surface. Colchicine is an anti-inflammatory agent that acts by inhibiting microtubule polymerization through binding to tubulin. This suggests that HDAC inhibitors, as does colchicine, inhibit trafficking of ABCG2 to the aggresome along microtubules. Finally, in addition to restoring surface localization of 141K ABCG2, the HDAC inhibitor romidepsin was shown to increase gene transcription of ABCG2 by activating the aryl hydrocarbon pathway. Recently, small molecules that are effective at rescuing the trafficking, abundance, and function of the 141K variant protein have been found. The compounds VRT-325 and 4a, both from the corrector class of molecules found in efforts to rescue mutant CFTR protein, are effective rescue agents for mutant ABCG2 as well. These results should encourage further research into the use of less toxic small molecules than HDAC inhibitors to restore defective ABCG2 function in patients with the 141K polymorphism.

**ABCG2 and allopurinol response**

Allopurinol is the most commonly used urate-lowering therapy for people with gout. It is rapidly metabolized to oxypurinol which is responsible for the majority of the urate-lowering effect through the inhibition of xanthine oxidase. Despite widespread use of allopurinol, many people fail to achieve the recommended target serum urate of <0.36 mmol/L. For example, in the Febuxostat versus Allopurinol Controlled Trial, only 21% of those receiving allopurinol 300 mg daily achieved the primary endpoint of the last three serum urates being ≤0.36 mmol/L. Although poor adherence and restricted dosing based on kidney function are frequently associated with failure to reach target serum urate, genes encoding the enzymes involved in the metabolism, mechanism of action, and excretion of allopurinol may also have a role.

Most studies related to the pharmacogenetics of allopurinol have focused on adverse events rather than predicting efficacy. However, two recent studies have highlighted a potential role for ABCG2 in allopurinol response. A significant association between ABCG2 Q141K and reduced allopurinol response was initially identified in a genome-wide association study. However, the definition of response used in this study was allopurinol-related change in serum urate, and there was only assessment of adherence with allopurinol using administrative data. A subsequent study, in which poor response was defined as serum urate ≥0.36 mmol/L despite allopurinol >300 mg daily, and with adherence confirmed by plasma oxypurinol concentrations, replicated the finding with 141K conferring a significantly increased risk of poor response to allopurinol (OR 2.71 (1.70–4.48), P=6.0x10^-5). This effect remained significant after adjustment for various variables that influence serum urate and allopurinol response including age, sex, BMI, ethnicity, eGFR, diuretic use, and serum urate off urate-lowering therapy. The association between ABCG2 Q141K and allopurinol response is a very interesting observation that should be further replicated in further studies.

The mechanism by which ABCG2 modulates allopurinol response is not clear. Wen et al reported ABCG2 to be an efficient allopurinol and oxypurinol efflux pump. HEK 293 cells transfected with 141K had significantly impaired ABCG2 function leading to intracellular accumulation of allopurinol and oxypurinol. These authors suggested that the ABCG2 141K variant might impair allopurinol response by increasing allopurinol and oxypurinol concentrations in renal tubular cells and decreasing concentration in the tubule fluid, thereby reducing the inhibition of uric acid influx pumps within the kidney. However, this theory is unproven, and modeling the complexity of the relative contribution
of reabsorbed allopurinol\textsuperscript{118} versus nonsecreted allopurinol is extremely difficult; therefore, in vivo experiments are required to further explore this possible mechanism.

**ABCG2 and chronic kidney disease**

It is clinically established that chronic kidney disease is a cause of hyperuricemia and gout. However, the physiological response to disrupted renal uric acid handling in kidney disease is a question of clinical interest. Bhatnagar et al\textsuperscript{119} addressed this question by evaluating the strength of genetic association with urate of variants in a suite of genes encoding uric acid transporters (including \textit{SLC2A9}, \textit{ABCG2}, \textit{SLC17A1-A3}, and \textit{SLC22A11-A12}) in 3,598 individuals with chronic kidney disease. In contrast to the situation in healthy individuals where \textit{SLC2A9} has the strongest magnitude of association on serum urate levels (0.37 mg/dL increase in urate per risk allele compared with 0.22 mg/dL for \textit{ABCG2} in sex-adjusted analysis),\textsuperscript{4} each \textit{ABCG2} risk allele increased serum urate by 0.68 mg/dL in people of European ancestry, compared with 0.30 mg/dL for \textit{SLC2A9} in sex-adjusted analysis.\textsuperscript{119} Although this finding requires replication, it does suggest that the extra-renal (gut) urate handling of \textit{ABCG2} necessarily compensates in renal injury.\textsuperscript{119} This is consistent with the observation, in nephrectomized rats, of increased gut expression of \textit{ABCG2} and maintenance of normal serum urate concentration.\textsuperscript{120} Bhatnagar et al\textsuperscript{119} evoke the “remote sensing and signaling” hypothesis whereby the action of multi-specific SLC and ABC transporters is critical in disrupted homeostasis resulting from organ injury.\textsuperscript{121} The hypothesis posits that the transporters cooperate in sensing and controlling fluctuations in important substances, with the ABC (and SLC) transporters facilitating interorgan communication through small molecules,\textsuperscript{121} including those important in oxidant status such as urate.\textsuperscript{122} One specific example of this is the ability of \textit{ABCG2} to transport and transfer heme, through an extracellular loop, to albumin.\textsuperscript{123}

In a study of fructose-induced hyperuricemia in humans, the urate-increasing 141K allele was associated with a lower increase in serum urate but greater increase in fractional excretion of uric acid when compared with the 141Q allele,\textsuperscript{78} consistent with the previously reported ROL type of hyperuricemia. Supporting \textit{ABCG2} as a “remote sensor and signaler,” the 141K allele was associated with a lower glucose response to the fructose load.\textsuperscript{78} Whether or not the urate and glucose effects are related is unclear; however, the remote sensing hypothesis could relate to differential ATP utilization by the 141Q and 141K alleles given that the 141K variant has significantly reduced ATPase activity.\textsuperscript{122}

Hyperuricemia predicts reduced renal function and chronic kidney disease, independent of measured confounders, in observational studies.\textsuperscript{124} However, whether or not urate is causal of reduced renal function is unresolved. Mendelian randomization studies, in which urate-associated genetic variants inherited at conception are used as an un-confounded proxy for exposure to urate,\textsuperscript{125} suggest that urate is not causal of reduced renal function in healthy people\textsuperscript{126} but could promote progression of declining renal function in chronic kidney disease.\textsuperscript{127} Based on the observation in mice that uric acid may compete with toxins as an efflux substrate of \textit{ABCG2}, Dankers et al postulate that, in the kidney, hyperuricemia promotes reduced renal \textit{ABCG2}-mediated secretion of toxic molecules.\textsuperscript{128}

**Conclusion**

The \textit{ABCG2} transporter is an important molecule in urate excretion. Decreased \textit{ABCG2} expression and function due to genetic polymorphisms leads to both ROL hyperuricemia and RUE hyperuricemia. The most extensively studied genetic variant is Q141K. Besides significantly increasing serum urate concentration, the 141K \textit{ABCG2} variant has also been associated with acute gout, tophaceous gout, and poor allopurinol response. In addition, 141K-induced hyperuricemia may lead to excessive inflammatory responses and decreased \textit{ABCG2} function may cause defective autophagy. All of these effects warrant further research to the restoration of 141K \textit{ABCG2} function and surface expression, for example, by small molecules.

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**Disclosure**

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