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**Commentary**

Paroxysmal nocturnal hemoglobinuria (PNH) is a disorder of hematopoietic stem cells that has largely been considered a monogenic disorder due to acquisition of mutations in the gene encoding PIGA, which is required for glycosylphosphatidylinositol (GPI) anchor biosynthesis. In this issue of the *JCI*, Shen et al. discovered that PNH is in fact a complex genetic disorder orchestrated by many genetic alterations in addition to *PIGA* mutations. Some of these mutations predate the acquisition of *PIGA* mutations, while others occur later. Surprisingly, this work indicates that PNH has a clonal evolution and architecture strikingly similar to that of other myeloid neoplasms, highlighting a potentially broader mechanism of disease pathogenesis in this disorder.

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The mutational landscape of paroxysmal nocturnal hemoglobinuria revealed: new insights into clonal dominance

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Paroxysmal nocturnal hemoglobinuria (PNH) is a disorder of hematopoietic stem cells that has largely been considered a monogenic disorder due to acquisition of mutations in the gene encoding PIGA, which is required for glycosylphosphatidylinositol (GPI) anchor biosynthesis. In this issue of the JCI, Shen et al. discovered that PNH is in fact a complex genetic disorder orchestrated by many genetic alterations in addition to PIGA mutations. Some of these mutations predate the acquisition of PIGA mutations, while others occur later. Surprisingly, this work indicates that PNH has a clonal evolution and architecture strikingly similar to that of other myeloid neoplasms, highlighting a potentially broader mechanism of disease pathogenesis in this disorder.

Deep sequencing reveals collective mutations in PNH
In this issue, Shen et al. present a comprehensive description of the constellation of somatic mutations present in PNH clones (5). Shen and colleagues performed whole-exome sequencing (WES) in 12 PNH patients and targeted deep sequencing in 36 additional patients on 61 genes that are commonly mutated in myeloid malignancies. Sequencing was performed on DNA extracted from CD59+ hematopoietic cells (indicative of PNH), with CD59+ cells serving as a premutation reference. Shen et al. have provided an extensive report using unbiased sequencing on a large patient cohort to examine the genomic landscape of PNH. They revealed that many mutations, most of which have not been previously associated with PNH, occur in tandem with PIGA mutations. Moreover, Shen et al. found that these additional mutations arise either as a sub-clone within the PIGA-mutant cell population or as an initial genetic event prior to the acquisition of the PIGA mutation (Figure 1).

One of the key findings by Shen et al. is the revelation that PNH clones with multiple mutations were present at substantially higher frequencies than those of clones with only mutations in PIGA (5). This finding implies that the presence of additional mutations confers an intrinsic growth advantage for PIGA-mutant cells. The clonal dominance in PNH has previously been speculated to occur due to either an intrinsic growth advantage of PIGA-mu-
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OMOS aspect of PNH clonal dominance came from the observation that PNH frequently co-occurs with immune-mediated aplastic anemia (AA), in which hemopoiesis is compromised due to suppression of a proportion of HSCs. In addition to the absence of CD55 and CD59, the lack of GPI-APs also renders PNH immune cells deficient in a number of cell-surface proteins that normally mediate immune responses and activate T cell receptor signaling. The “immune escape hypothesis” of PNH posits that the lack of immune-mediated recognition provides PIGA-deficient HSCs an extrinsic survival advantage, allowing escape from effector immune cell attack. Gene expression profiling of GPI-normal CD34+ cells from PNH patients showed upregulation of genes involved in immune responses, while expression patterns of GPI-deficient CD34+ cells were remarkably similar to those found in healthy donors. More interestingly, expression of

Figure 1. Clonal architecture and evolution of PNH. PNH arises from an initial mutation in PIGA (orange) or in a different founder gene (green) in HSCs. Over time, the acquisition of additional cooperating lesions, which can include additional mutations in PIGA (yellow) or other genes (blue) (e.g., TET2, SUZ12, JAK2, and U2AF1), in addition to the founder mutation, adds complexity to the clonal architecture and confers a growth advantage and subsequent progression into overt PNH. On rare occasions, PNH clones can transform into myeloid malignancies such as MDS and acute AML, or into AA. Future work to identify the complement of events responsible for the transformation of PNH into MDS or AML will be enlightening. Moreover, it will be important to determine whether AA harbors a genetic complexity and clonal architecture similar to that of PNH.
The observations by Shen and colleagues raise immediate questions regarding the functional consequences of these genetic lesions in hematopoiesis and their impact on the pathophysiology of PNH (5). For instance, what are the roles of these co-occurring mutations in PNH and how do they influence HSC function and differentiation? While it is unsatisfactory to hypothesize that these mutations that otherwise drive MDS play a passenger role in the presence of PIGA mutation, one can only infer that mutations occurring in clones with existing PIGA mutations possess the ability to alter the MDS disease phenotype. Indeed, most PNH patients with PIGA mutations and additional mutations in TET2, SUZ12, ASXL1, JAK2, or U2AF1 had no signs of progressing to MDS or AML. Development of multiple murine models that harbor the mutations found to coexist with PIGA mutations will provide precious reagents to formally demonstrate the genetic interactions between PIGA deficiency and the mutations identified by Shen and colleagues.

Despite the extensive work performed on PNH, there are still many interesting questions that remain unanswered. One key clinical feature in PNH patients is the defective hematopoietic function of HSCs without PIGA mutations, a phenomenon thought to be primarily driven by autoimmunity, as observed in AA patients. While it is apparent that extrinsic factors are predominantly involved in the destruction of HSCs and the bone marrow microenvironment, one cannot exclude the possibility that there are cell-intrinsic abnormalities in HSCs with WT PIGA from PNH patients. Characterizing the genetic differences between CD59+ and CD59– HSCs from PNH patients will be a fascinating next step.

Now that we have gained a glimpse and new insight into the complex genomic landscape of PNH, a benign disease that shares a clonal architecture and disease evolution similar to that seen in malignant neoplasms, it will be important to determine whether a similar mutation acquisition occurs in related hematological disorders. For example, ongoing genome-wide mutation discovery efforts in AA, an autoimmune disease of the bone marrow in which patients harbor PNH, will be very informative in this regard (18). Moreover, a better understanding of the genetic events responsible for the transformation of PNH into malignant neoplasms, including MDS and AML, will hopefully continue the legacy of molecular discovery and therapeutic advances in PNH.

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