

The molecular basis of chronic granulomatous disease

Christof Meischl, Dirk Roos

Central Laboratory of the Netherlands Red Cross Blood Transfusion Service
and Laboratory of Experimental and Clinical Immunology, Academic Medical Center,
University of Amsterdam, Plesmanlaan 125, 1066 CX Amsterdam, The Netherlands

Introduction

Chronic granulomatous disease (CGD) is a rare inherited immunodeficiency syndrome, caused by the inability of the patients' phagocytic leukocytes to produce (sufficient) superoxide [14]. Phagocytic cells (neutrophils, eosinophils, monocytes and macrophages) constitute a central part of the innate (nonspecific) immune system, forming as such a first line of defense against various invading microorganisms, principally bacteria and fungi. These leukocytes phagocytose the pathogens and then kill them intracellularly by means of reactive oxygen species and a number of oxygen-independent microbicidal agents. The highly reactive oxygen species (such as superoxide, hydrogen peroxide, hypochloric acid and others) not only attack the ingested microorganisms directly, they also optimize the intraphagosomal milieu for the cationic microbicidal peptides and proteins there present.

The enzyme responsible for the generation of those oxygen metabolites is the phagocyte-specific NADPH oxidase [13], and it are the defects of this multi-component redox-center that lead clinically to the severe immunodeficiency syndrome of CGD.

Clinical presentation

CGD is a rare disease, with an estimated incidence of 1 : 250,000, all ethnic groups being equally affected. While the most common form of the syndrome is X-linked, different modes of autosomal inheritance are also possible. The overwhelming majority of patients with X-linked disease is, obviously, male; in the autosomal forms no sex preference is discernible.

As an inherited and severe immune defect, CGD presents itself early in life in the form of acute or chronic infections, two-thirds of the patients showing the first symptoms already in their first year of life [39]. Nevertheless, one of the surprising features of the disease is its highly variable severity; thus, in some patients the diagnosis is established only in their adult years. As a general rule, the organs that represent the in-

dividual's border against the outside world, or the lymph stations downstream of those organs, are most frequently affected: lungs, skin and gastrointestinal tract. From here hematogenous spread to almost any other organ or organ system may take place, as demonstrated by studies in over 500 patients.

The isolated pathogens are usually catalase positive and/or relatively resistant to the other, non-oxidative killing mechanisms of the phagocytes. Catalase degrades hydrogen peroxide, which is also produced in small amounts by the microbes themselves, and thus deprives the phagocytes of the possibility to use this microbe-generated oxygen metabolite for killing. The microorganisms most frequently found in the above-mentioned studies are *Staphylococcus aureus*, various *Aspergillus* species, enteric gram-negative bacteria (including *Serratia marcescens* and various *Salmonella* species) and *Burkholderia cepacia*. When analyzing the culture and/or serological results, it should be kept in mind that pathogens that are harmless to a normal host may well be responsible for infections in a CGD patient.

Pneumonia is the most frequent serious infection in all age groups and is most commonly caused by *S. aureus*, *Aspergillus* species, *B. cepacia* and enteric gram-negative bacteria. Because sputum cultures are rarely informative, empiric treatment should be initiated the moment the clinical diagnosis of pneumonia has been established. In the case of severe pneumonia or of progression of disease under treatment, more aggressive diagnostic steps, such as bronchoscopy, needle biopsy or even open lung biopsy, may be warranted to determine rarer pathogens.

Burkholderia species (mainly *B. cepacia*, but also *B. gladioli*, *B. mallei*, *B. pseudomallei* and *B. pickettii*) are unusually virulent in the CGD patient and one of the main causes of fatal pneumonias [83]. These microorganisms, which are ubiquitously present in the environment and need free oxygen radicals to be effectively killed, grow slowly in cultures and may, therefore, be diagnosed (too) late.

The next most frequent sorts of infection are cutaneous abscesses and suppurative lymphadenitis, the later affecting often the cervical nodes. The most commonly found pathogens are *S. aureus* and – in the case of lymphadenitis – various gram-negative bacteria (including *B. cepacia* and *Serratia marcescens*). Perirectal abscesses occur frequently and may persist for years in spite of adequate antibiotic treatment and meticulous care.

Hepatic and perihepatic abscesses are unexpectedly common and typically caused by *S. aureus*. They are frequently painless, even on palpation, and present with such unspecific symptoms as fever, malaise, anorexia and weight loss. The laboratory findings are often normal. Osteomyelitis may be due to hematogenous spread of the pathogens (*S. aureus*, *Salmonella* species, *Serratia marcescens*) or to contiguous invasion of bone, as can be seen in *Aspergillus* pneumonia with consecutive destruction of the adjacent ribs or vertebral bodies.

While the above affections normally represent acute disease states, CGD – as the name implies – is typically characterized by a chronic struggle of the immune system with the pathogens. Thus the granulomas, which can be found in a large variety of organs and to which CGD owes its name, are the result of chronic inflammatory cell reactions, involving mainly lymphocytes and histiocytes. The cytoplasm of the histiocytes is typically foamy and brown. These characteristic granulomas, while not pathognomic, should at least make CGD part of the differential diagnosis [44].

Clinically, the granulomas can become symptomatic by pain or signs of obstruction. When narrowing the upper gastrointestinal tract, they may present as dysphagia, stomach pain or recurrent vomiting, which, in the first months of life, can be misdiag-

nosed as pyloric stenosis. When affecting the urinary tract, the granulomas may cause dysuria, penile pain, a decreased urine volume or hydronephrosis [2].

Another chronic affection is the inflammatory bowel disease of CGD, which closely resembles Crohn's disease. Found in ten percent of the CGD patients, it typically involves the colon, but involvement of other parts of the gastrointestinal tract has also been described. The severity of this complication can vary widely, with symptoms ranging from mild diarrhea to a debilitating state of bloody diarrhea and malabsorption, necessitating colectomy [3].

Other manifestations of chronic inflammation are an eczematoid dermatitis, which may be present already at birth and mainly affects infants and children, gingivitis, chorioretinitis, glomerulonephritis and destructive white matter lesions of the brain. Very rarely, discoid or, even more rarely, systemic lupus erythematosus (SLE) is observed.

The children are often underweight and of short stature. Especially the X-linked patients tend to grow beneath the 5th percentile, which may be partially corrected in adolescence, when some catch-up growth can occur. The end of the first decade of life represents anyhow a milestone, since thereafter the infections are often less severe and occur less frequently, and the anemia typically found in those patients tends to resolve spontaneously. This anemia, with Hb values of 8–10 g/100 ml and with microcytosis, is an expression of the chronic disease state and does not respond therefore to therapies of iron deficiency, a common misdiagnosis.

Lymphadenopathy, hepatosplenomegaly and hypergammaglobulinemia can all be found in CGD independently of any acute disease process. Very rarely, other clinical syndromes, such as Duchenne muscular dystrophy, retinitis pigmentosa or McLeod's syndrome, may be associated with the X-linked form of CGD. As a rule, carriers of CGD are symptomfree. The proverbial exception to this rule are the carriers of X-linked CGD, who may present with a few syndrome-related conditions. Roughly half of them are troubled by recurrent stomatitis and/or moderately severe gingivitis and about one-fourth of these women will develop discoid lupus erythematosus. The latter condition manifests itself typically in the second decade of life, with (sun)light-sensitive, discoid lesions on face, arms and upper torso, is usually mild, rarely severe, and does not progress to SLE [7, 80].

Finally, extremely lyonized carriers of X-CGD can have a – usually mildly – increased risk of infection [56]. This is, however, exceptionally rare since as little as ten percent, or sometimes even less, of the phagocytes expressing a normally functional NADPH oxidase are sufficient to keep those individuals asymptomatic.

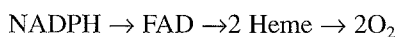
Molecular basis of the disease

The NADPH oxidase is a multi-component enzyme with a redox center that transfers electrons from intracellular NADPH onto extracellular (or intraphagosomal) molecular oxygen, thereby generating superoxide (Fig. 1):



The weakly microbicidal superoxide is then – spontaneously or enzymatically catalyzed – converted into hydrogen peroxide and other, more potent metabolites.

The electron transfer itself is a multistep process, during which the electrons are transported sequentially along several moieties of the oxidase:



Although FAD and the two heme groups are part of the redox center of the enzyme, cytochrome b_{558} , NADPH cannot bind to it unless the complete enzyme has been assembled during activation, and only then can electron transfer actually take place.

Cytochrome b_{558} , a flavo-hemoprotein, is composed of two of the enzyme's subunits, gp91^{phox} and p22^{phox}, in a 1 : 1 stoichiometry [36, 63, 77, 88]. Incorporated in the membranes of specific granules and secretory vesicles in resting cells, cytochrome b_{558} becomes expressed on the phagolysosome and on the cell surface when the granules/vesicles fuse with those larger membrane systems during cell activation (Fig. 1). The stimulus for this activation is the binding of opsonized microorganisms or high concentrations of chemoattractants to phagocyte surface receptors.

As part of this activation, the enzyme's three cytosolic components, p47^{phox}, p67^{phox} and p40^{phox}, as well as several low-molecular weight GTP-binding proteins, translocate to the cytochrome b_{558} in the membrane to form there the complete and active form of the NADPH oxidase (Fig. 1).

A defect in any one of the four components gp91^{phox}, p22^{phox}, p47^{phox} or p67^{phox} abolishes (or reduces) the activity of the oxidase and leads thus to CGD. Defects in the other enzyme components are not known. While p40^{phox} might not be essential for the function of the enzyme (and mutations, therefore, would not become symptomatic), a defect in one of the GTP-binding proteins (rac1/2, rap1A), which are in-

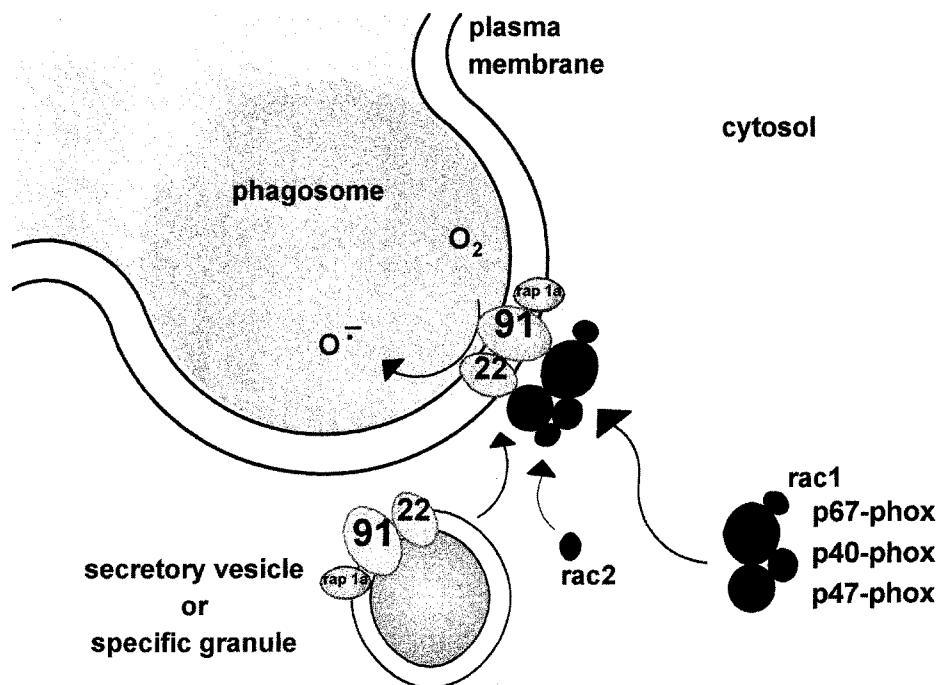


Fig. 1. Activation of the NADPH oxidase. Assembly of the activated enzyme and phagosome formation are concomitant processes. Translocation of cytosolic proteins is initiated by serine phosphorylation in p47^{phox} and controlled by small GTP-binding proteins (rac1, rac2, rap1A). This translocation leads to a conformational change in gp91^{phox} that permits NADPH binding, thus activating the NADPH oxidase enzyme

volved in the regulation of a great number of cellular functions, might be incompatible with life.

gp91^{phox}

The CYBB gene, which codes for gp91^{phox}, is located on the X-chromosome (Xp21.1), has a length of 30 kb and comprises 13 exons [20, 75, 86]. The translation product, a protein of 570 amino acids, needs for its further maturation and stabilization the presence of p22^{phox} – in such a way, that abolished expression of one protein automatically leads to simultaneous absence of the other [67]. Post-translational modifications are the glycosylation of three of its five potential N-linked glycosylation sites [89]. The N-terminal half of the mature protein contains four or five hydrophobic, probably membrane-spanning domains, while the hydrophilic C-terminal part is thought to represent the cytosolic side of the protein. The hydrophobic part contains the heme moieties (one shared with p22^{phox}) [68] and is probably also involved in the interaction with p22^{phox}. For the C-terminal part a three-dimensional model has been deduced from sequence homology with the ferridoxin NADP⁺ reductase flavoenzyme family [79]. Putatively, therefore, this part of the protein contains one binding site for NADPH and the FAD-binding site. In the inactive state of the enzyme, the NADPH-binding site is probably covered by a loop of 20 amino acids [85].

p22^{phox}

p22^{phox} is encoded by the gene CYBA, which is located on chromosome 16q24 and spans 8.5 kb and six exons [21, 64]. The resulting protein of 195 amino acids is thought to share one heme moiety with gp91^{phox}, and has one proline-rich region involved in interaction with SH3 (src homology region 3) domains.

p47^{phox}

NCF1, the gene on chromosome 7q11.23 coding for p47^{phox}, has a length of 15 kb, encompassing 11 exons [29]. Its product, a protein of 390 amino acids, contains nine serine phosphorylation sites, two SH3 domains and one proline-rich region.

p67^{phox}

NCF2 on chromosome 1q25 codes for p67^{phox}, is 40 kb long and comprises 16 exons [46]. p67^{phox} itself, with its 526 amino acids possesses a (higher affinity) binding-site for NADPH [81], two SH3 domains and one proline-rich region.

p40^{phox}

Very little is known yet about p40^{phox}, a protein of 339 amino acids. Its gene, NCF4, spans 18 kb and 10 exons and is located on chromosome 22q13.1 [96]. The protein contains one SH3 domain [94].

Activation of the enzyme

Responding to as yet only partially unravelled upstream events that transmit the signals originating from the cell surface receptors, the activation of the NADPH oxidase itself seems to be initiated by a change in the phosphorylation of p47^{phox} [78]. The different protein kinases implicated in this process apparently phosphorylate different groups of serines [25], with each different state of phosphorylation corresponding to a different three-dimensional conformation of the protein. This process would disrupt the cytosolic complex of p47^{phox}/p67^{phox}/p40^{phox} in the resting cell, exposing until then inaccessible SH3 and/or proline-rich domains [32, 45]. This change results in translocation of these three proteins to the membrane, where they associate themselves with cytochrome *b*₅₅₈ (Fig. 1). The interactions of the cytosolic components with each other and with the cytochrome are mediated by SH3 domains binding specifically to certain proline-rich regions [18, 26, 31, 45, 47, 84], but other types of protein-protein interaction seem to play a role as well [17, 66].

In the membrane-associated complex, p47^{phox} appears to stabilize the interaction of p67^{phox} – and possibly rac1 – with the cytochrome [10, 11]. P67^{phox} with its high-affinity binding site for NADPH, on the other hand, could bind to gp91^{phox}, which contains a lower-affinity NADPH-binding site, to form the catalytically efficient binding site of the active enzyme [81]. The loop of 20 amino acids that covers the NADPH-binding site in gp91^{phox} in the resting state, is thought to move out of the way, as a result of either the complex formation or of an independent control mechanism. NADPH then

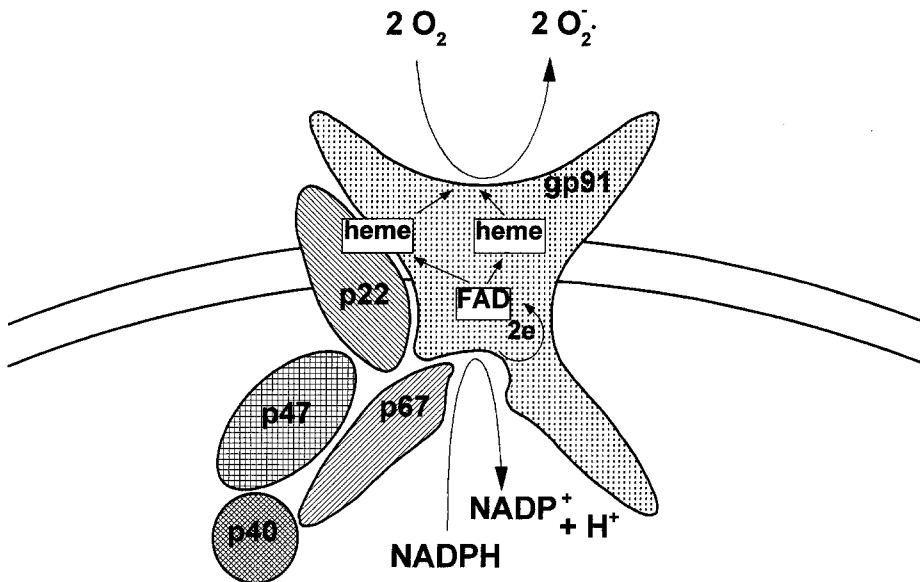


Fig. 2. Schematic illustration of the electron transfer mechanism of the NADPH oxidase (see text). After assembly of the NADPH oxidase complex, NADPH from the cytosol can bind to the enzyme and donate its electrons. These electrons are then transmitted via FAD and heme groups to molecular oxygen on the other side of the plasma membrane, thus generating superoxide in either the phagosome or in the extracellular environment

binds to the completely assembled oxidase, electron transfer will start and superoxide generation starts (Fig. 2).

Both the assembly of the enzyme and the electron flow itself are subject to a complex network of regulating and modifying influences. P40^{phox}, for instance, besides stabilizing the cytosolic complex in resting cells, seems to down-regulate NADPH oxidase activity through competition of its SH3 domain with that of other, essential oxidase components [76].

Furthermore, three low-molecular weight GTP-binding proteins, rac1, rac2 and rap1A, are known to play an important role in the activation and function of the enzyme [1, 41]. Functioning as molecular switches in signalling cascades, with an inactive GDP-bound and an active GTP-bound state, they themselves are again under the control of GDP-dissociation inhibitor (GDI) and GDP-dissociation stimulator (GDS) proteins [1, 57]. The activated rac1 appears to translocate together with p47^{phox}/p67^{phox} and to influence the electron flow through the active oxidase [19, 24, 49]; rac2 is thought to translocate independently of the other cytosolic proteins [34]. Rap1A, on the other hand, is associated with the membrane-bound cytochrome *b*₅₅₈ [69] and may indirectly link the activity of the oxidase to intracellular cAMP levels [6].

Results obtained with a cell-free system indicate, finally, that the presence and polymerization of actin enhance the activation of the NADPH oxidase [58]. The impressive complexity of the activation of the enzyme and its intricate control mechanisms point to the importance of a tightly controlled, place- and time-restricted release of free oxygen radicals, since an uncontrolled release of these products would have devastating effects for the affected individual. This complexity, on the other hand, is the explanation for the fact that defects in different genes can lead to the same cellular dysfunction and disease.

Molecular defects

Defects in gp91^{phox}

Defects in gp91^{phox} comprise about two-thirds of the cases, and are as such the most frequent cause of CGD. All possible types of mutation, except gene conversions, have been found in CYBB, with single nucleotide substitutions accounting for 65% of the defects, and deletions and insertions for the remaining 35% [74]. Very large deletions, extending over other coding genes localized on the X-chromosome, can result in various clinical entities, such as Duchenne muscular dystrophy, retinitis pigmentosa or McLeod's syndrome, being associated with CGD.

In a recent multicenter review of the mutations found in 261 X-linked CGD kindreds, 65% of these mutations were found to be family specific, with the other 35% being clustered around a few hotspots, mainly around CpG sequences [72]. The large majority of X-linked mutations in CGD leads to a complete lack of gp91^{phox}, due to instability of the mRNA or of the translated protein. These are called X91⁰ variants, to differentiate them from the (few) cases with reduced or normal protein expression, called X91⁻ and X91⁺, respectively. In the cases of X91⁻, the reduced protein expression is accompanied by a roughly proportional decrease of superoxide production, whereas the X91⁺ variants express normal amounts of a non-functional protein.

While being clinically indistinguishable from the X91⁰ variants, the cases of X91⁺ CGD are of great interest for the understanding of the working mechanism of the oxi-

dase, because they allow analysis of how different defects block various steps of the activation process or in the electron transport. The ten X91⁺ mutations known so far have contributed in this way to our knowledge of gp91 phox, by identifying regions important for the binding of one of the heme groups, NADPH or the cytosolic oxidase components [48, 74, 79].

Two patients have been found with single nucleotide substitutions in the 5'promotor region of CYBB. Interestingly, both patients possessed small subsets (5%) of neutrophils with normal NADPH oxidase activity. The mutations abolished the binding of an undefined protein to the DNA of the promotor sequence, but enhanced the association of another, larger one. The investigators theorized that this might be an indication for different subsets of neutrophils controlling the gene for gp91^{phox} by means of different DNA-binding proteins [62, 95]. Only one (rare) polymorphism has been found in CYBB to date, further illustration of the extreme sensitivity of this protein for mutations.

Recently a regularly updated database (X-CGDbase) has been established, which is freely available for anonymous file transfer protocol (ftp) at ftp.csb.ki.se and ftp.helsinki.fi(in the directory pub/x-cgdbase). The WWW site is at <http://www.helsinki.fi/science/signal/databases/x-cgdbase> [72].

Defects in p22^{phox}

About 5% of the cases of CGD are caused by defects of p22^{phox}. In the nine families with A22-CGD investigated so far, ten different mutations were found in the 18 alleles involved [74]. The only A22⁺ mutation known, a substitution of glutamic acid for one of the prolines in its proline-rich region, apparently destroys the interaction with the SH3 domain of p47^{phox}, thereby interrupting the activation of the enzyme [22, 45, 47, 84]. In CYBA four polymorphisms are known.

Defects in p47^{phox}

Mutations in NCF1 account for about 30% of the cases of CGD. In strong contrast with the variation in the mutations found in the other subtypes of CGD, only four different mutations have been reported in A47 CGD to date. In 15 unrelated patients described, 11 were homozygotes and 4 compound heterozygotes for a dinucleotide deletion in the first four nucleotides of exon 2 (GTGT → GT) [74].

This situation has long remained unexplained, but the finding of the deletion-containing gene sequence (in addition to the wild-type sequence) also in healthy individuals has hinted at the existence of one or more pseudogenes in the human genome. It is now believed that recombination events between NCF1 and a pseudogene, which is a highly homologous but non-functional gene copy, cause the extremely high uniformity of mutations found in A47 CGD [33, 71].

Defects in p67^{phox}

With around 5% of the described cases, A67 CGD also represents a rare subtype of the disease. In the 11 A67 CGD patients characterized so far, 12 different mutations were

found among the 22 alleles [74]. While the level of mRNA is usually normal, no protein expression has been found in A67 CGD, with the exception of one A67⁺ patient, whose p67^{phox} protein is apparently non-functional due to the deletion of one amino acid. This deletion causes a strongly diminished binding of rac1, and thereby a disturbance in NADPH oxidase activation [49].

Defects in p40^{phox}

There are no known defects in this protein.

Correlations between genotype and phenotype

In general, the X91⁰, X91⁺, A22 and A67 subforms of CGD present with similar clinical severity. It might be expected, on the other hand, that the severity of the clinical symptoms in X91⁻ CGD correlates with the amount of residual superoxide production (3–30%) found in these patients' phagocytes. This is, while often true, not a dependable rule [73]. Possibly, variabilities in other host defense systems play an important role here.

A47 CGD, as borne out by a few clinical studies, seems to follow in general a more benign clinical course [53, 91]. Given the observations that p47^{phox} under certain in vitro conditions seems not to be essential for oxidase activity [30, 42, 43], it might be speculated that some residual superoxide generation is also possible in the in vivo situation [11].

Molecular diagnosis

CGD – once clinically suspected – can be diagnosed in the laboratory by the phagocytes' failure to produce reactive oxygen species. A number of methods are available for the assessment of superoxide production. The classical, and still widely used, test for this purpose is the so-called NBT slide test, where a yellow dye in solution (nitroblue tetrazolium) is reduced by superoxide to insoluble blue formazan. The fraction of stained and unstained cells and even the staining intensity in each cell are then evaluated under a microscope [55].

The activity of the NADPH oxidase can, furthermore, be measured by oxygen consumption (oxygen electrode), superoxide generation (reduction of ferricytochrome c, chemiluminescence) or hydrogen peroxide production (oxidation of homovanillic acid).

Today, flow cytometry is frequently used to assess the neutrophils' NADPH oxidase activity [70]. This method, which uses fluorescent dyes for the detection of hydrogen peroxide, is sensitive, measures at the single cell level (and can thus distinguish active and non-active cell fractions) and has the additional advantage that non-purified leukocyte suspensions can be used. Once the diagnosis of CGD is established, the missing subunit of the enzyme, and thereby the subgroup of the disease, can be determined by immunoblot analysis of neutrophil fractions. This simple-sounding principle is marred by the fact that the two components of cytochrome *b*₅₅₈ need each other for stable expression, so that the lack of one protein automatically

leads to absence of the other. In that case, the family history and a carrier pattern in the mother's neutrophils (see below) may indicate an X-linked type of disease. Still, since one-third of the X-linked defects are new mutations in the parental germline cells, X-linked CGD cannot be excluded in this way. If all four subunits of the NADPH oxidase are present on Western blot, an X⁺ or A⁺ variant, with a dysfunctional protein, is probable. In that situation, the cell-free assay, an *in vitro* system that reconstitutes the NADPH oxidase from its individual components, has to be employed, to localize the defective subunit in either the membrane (gp91^{phox}, p22^{phox}) or the cytoplasm (p47^{phox}, p67^{phox}) [12, 54]. The causative mutation is then determined by sequencing of polymerase chain reaction (PCR)-amplified cDNA or genomic DNA.

Carrier detection

Carriers of X-linked CGD have two subpopulations of neutrophils, one with the "healthy" X-chromosome in an active form and therefore rendering the cells capable of expressing a functional NADPH oxidase, and another one with the mutated X-chromosome active and therefore incapable of inducing superoxide generation. The ratio between these two populations is determined by the process of lyonization, the random inactivation of one of the two X-chromosomes in all female cells.

The resultant mosaic pattern for superoxide production can best be analyzed by the NBT slide test or by flow cytometry. Because extreme lyonization can result in seemingly unaffected carriers, carrier analysis is nowadays most often performed by sequencing. In some circumstances, when the family-specific mutation is known, other techniques, such as allele-specific restriction enzyme analysis, single-strand conformational polymorphism (SSCP) or restriction fragment length polymorphism (RFLP), may also be employed. Autosomal carrier detection, which is best done by sequencing, is still difficult for A47 CGD.

Prenatal diagnosis

Prenatal diagnosis is best performed by sequencing of DNA from amniotic fluid cells or chorionic villi obtained during the 10th week of gestation. It should be performed when the known family-specific mutation is known. In principle, all subtypes of CGD can be diagnosed prenatally, but often the combined heterozygous mutations of autosomal diseases render such a diagnosis more difficult.

After verification of the fetal origin of the cells and determination of the fetus' sex, the sequencing is carried out on PCR-amplified fragments of the relevant genomic region. The results are compared to the simultaneously obtained sequences of the indicator patient in the family, the pregnant woman and a healthy control [16].

If the family-specific mutation is not known, allele-specific markers can be used, for which several have been described. If these markers are informative in the affected family, they offer a more than 50% reliable method for prenatal diagnosis.

Treatment

The prognosis of the syndrome originally called “fatal granulomatous disease of childhood” in its first description in 1957 [5, 44] has since dramatically improved, due, in part, to the emergence of several specialized centers that assembled larger groups of patients to improve the knowledge and treatment of this disease (e.g., the National Institutes of Health, Scripps Clinic/Stanford University, the Paediatric Clinics of the University of Amsterdam and of the University of Zürich).

While one retrospective study in 1989 found a survival rate of 50% at 10 years of age (with an improved prognosis thereafter) [59], nowadays most patients survive well into adulthood, especially those with A47 CGD.

Modern treatment of CGD rests on five pillars:

1. Prevention of infections through immunization of the patients and avoidance of probable sources of pathogens
2. Prophylaxis with trimethoprim-sulfamethoxazole or dicloxacillin
3. Prophylactic administration of recombinant human interferon-gamma (rIFN- γ)
4. Most important: early and aggressive use of parenteral antibiotics
5. Surgical drainage and/or resection of infectious foci

CGD patients should receive all routine immunizations (including the live-virus vaccines) on schedule, as well as a yearly influenza vaccination. Any skin damage should be promptly washed with soap and water and rinsed with antiseptic agents (e.g., 2% hydrogen peroxide, betadine solution). Since perirectal abscesses represent a common and often stubborn problem in CGD, careful rectal hygiene, including frequent soaking in warm soapy baths, and avoidance of constipation are recommended. The risk of pulmonary infections can be reduced by not smoking, not using bedside humidifiers and avoiding possible sources of *Aspergillus* (e.g. decaying plants, rotting wood, sawdust, hay or straw). Finally, attention should be paid to optimal dental cleaning, including flossing and antibacterial mouthwashes.

Prophylaxis with trimethoprim-sulfamethoxazole (5 mg trimethoprim/kg per day, given orally in one or two doses) can reduce the number of bacterial infections by more than half, as was borne out by three studies representing a total of 95 patients [53, 59, 90]. In case of allergy against sulfamethoxazole, dicloxacillin (25–50 mg/kg per day) may be given, but the prophylactic efficacy of this drug has been less well documented.

The merits of an antifungal therapy are not yet well established. While ketoconazole was shown in one study to convey no protection against *Aspergillus* [59], in another study itraconazole proved to be effective prophylactically [60]. However, the long-term safety of this latter drug in CGD-related prophylaxis remains to be investigated.

In 1991, a phase III multi-center, double-blind, randomized placebo-controlled study, encompassing 128 patients, demonstrated a by 70% reduced risk to develop a serious infection under prophylaxis with rIFN- γ , as compared with placebo [37]. This benefit is maintained over longer periods of time, as has since been shown in two phase IV studies [4, 92]. The side effects of this treatment – mild headaches, low-grade fevers a few hours after administration – are generally negligible. Recommended are 0.05 mg/m², given subcutaneously three times a week. (For infants with < 0.5 m² the recommended dose is 0.0015 mg/kg, given subcutaneously three times a week.)

This improved host defense, which is found independently of the subtype of the disease, is not paralleled by an improvement in superoxide production by purified

neutrophils or monocytes [37, 61]. Apparently rIFN- γ boosts other, oxygen-independent defense mechanisms.

One of the central guidelines in treating CGD is to initiate anti-infectious treatment promptly and to continue it until certain eradication of the pathogens. Later, in CGD, may be too late. Not every low-grade fever or minor infection needs maximal therapy, but patients should be observed closely, and action taken at the first signs of deterioration.

Before initiating treatment, reasonable (and rapid) efforts should be made to localize the infection and isolate the causative agent. However, since treatment in those situations should begin without delay, it often has to be an empirical one, to be modified later if shown to be necessary by the culture results.

Empirical treatment should provide strong coverage for *S. aureus* and gram-negative bacteria, including *B. cepacia* (e.g., a combination of nafcillin and ceftazidime). If there is no improvement within 24–48 h, more aggressive attempts at defining the responsible pathogen should be made. Additionally, empirical modifications of the treatment might be warranted, such as adding high-dose intravenous trimethoprim-sulfamethoxazole to cover ceftazidime-resistant *B. cepacia*.

While the basic strategy remains the same when a fungal infection is suspected, the necessity to expose the patient to a long and intensive treatment with amphotericin B should intensify the efforts to obtain a definite diagnosis. Fungal infections most often affect the lungs and/or bone, and are treated with amphotericin B for 5–6 months, even longer if warranted by the clinical data. For the first 2–3 months the drug is given on a daily basis, thereafter on an alternate-day schedule. After discontinuation of amphotericin B, oral itraconazole should be given over several years, to prevent a recurrence or reactivation of the infection.

Local foci of infection, such as abscesses, empyemas, necrotic infected tissue and bone infected by fungi, are often very resistant against anti-infection therapy, especially in an immunocompromised host, and warrant surgical resection or drainage. This is certainly true for pulmonary fungal infections, where cavity or necrotic lesions of the lung, continuous spread to the ribs or vertebral bodies or brain metastases all need the attention of the surgeon. But also cutaneous or hepatic/perihepatic abscesses require surgical or needle drainage, followed, especially in the latter case, by several months of parenteral antibiotics.

If all the medical and surgical measures outlined above fail, an attempt with granulocyte transfusions may be made. Additionally, the therapy with rIFN- γ can be intensified to a daily form of administration.

If the McLeod's syndrome is associated with the X-linked form of CGD (or has not been excluded by DNA analysis) special care has to be taken with the transfusion of erythrocytes, thrombocytes or granulocytes. Since certain Kell antigens are only weakly expressed in this mild form of hemolytic anemia, the patients are very rapidly sensitized against those antigens, which are ubiquitously present in the general population. As long as McLeod's syndrome has not been excluded, therefore, erythrocyte antigen phenotyping should be done prior to transfusing the patient for the first time, to administer, if necessary, only Kell-negative blood products.

Although the immunosuppressive corticosteroids should be avoided in CGD patients, they may sometimes be warranted by symptomatic granuloma formation or severe forms of CGD inflammatory bowel disease. Both complications respond well to these agents (e.g., 0.5–1 mg prednisone/kg per day) [8, 15]. After a few weeks treatment, the dose of corticosteroids should be tapered to prevent a rapid relapse.

CGD, as a defect of the hematopoietic stem cells, is, in principle, amenable to bone marrow transplantation. While this is a curative approach and has been successful in several cases [27, 35, 40], the overall results have been problematic, due to serious problems with failure of engraftment. Newer regimens, however, which make use of busulfan to achieve adequate myeloid suppression, may help to solve this problem, so that the place of bone marrow transplantation among the treatment options for CGD has to be reconsidered ([35] and Seger, personal communication).

Animal models

While there is no known natural animal model for CGD, recently two murine models have been presented. The group of M. Dinauer succeeded in constructing a model for X-CGD through gene targeting of murine embryonic stem cells [65], and the group of S. M. Holland created a p47^{phox} knockout mouse, using comparable techniques [38].

Those models will allow to study possible clinical differences between the genetic subgroups in detail, as well as to test the efficacy and safety of new therapeutic techniques, including gene therapy [23, 52].

Prospectives of new therapeutic advances

Treatment of CGD, for all the great progress seen since the first description of the disease, remains to this day largely symptomatic. With the advent of the new genetic technologies, however, a cure for (some) inherited diseases seems possible.

Gene therapy seeks to introduce a functional copy of the defective gene into the genome of the affected cells. For CGD, partial correction of the defect *in vitro* has been described, by treating CGD peripheral blood progenitor cells, B lymphocytes, monocytes or genetically modified myeloid cell lines with retroviral or adenoviral vectors that contain cDNA of one of the four genes involved in the pathogenesis of CGD [50, 82, 87, 93]. Only one attempt at clinical gene therapy has been published so far, involving five patients with the A47⁰ subtype of CGD. Modifying the patients' CD34⁺ hematopoietic progenitors, mobilized to the peripheral blood by granulocyte colony-stimulating factor, maximal levels of one corrected neutrophil in 1500 neutrophils analyzed were obtained after retransfusion of the transduced cells. These levels then declined below the detection limit during the following 3–6 months [51].

The optimism with regard to these trials is based on the observations that in some X91⁻ patients 3–5% of oxidase activity can result in a mild clinical phenotype, and that in some extremely lyonized X-CGD carriers as few as 5% fully functioning neutrophils are sufficient to confer substantial anti-infectious protection. A complete (100%) reconstitution of the oxidase activity seems, therefore, not necessary.

The major limitation of all gene therapy trials so far, CGD or otherwise, is the duration of expression of the transduced gene product. Nevertheless, in the case of CGD, the existing vector constructs might already be used to treat infections resistant to other forms of treatment. Another nascent therapeutic possibility is the *in utero* transplantation of hematopoietic stem cells, which has already been used in various circumstances and with mixed results [9], most successfully in a case of X-linked SCID [28]. This technique remains as yet limited to those instances where the donor cells have a

natural growth advantage over their fetal counterparts – which would not be the case in CGD – but future developments are likely to relativize this precondition.

Both methods are, of course, only at the beginning of their development, and much work remains to be done, but CGD, as a very well-characterized inherited affection of the hematopoietic stem cells, is likely to be among the first syndromes to profit from those advances.

Summary and conclusions

CGD is a rare inherited immunodeficiency syndrome, caused by the phagocytes' inability to produce (sufficient) reactive oxygen metabolites. This dysfunction is due to a defect in the NADPH oxidase, the enzyme responsible for the production of superoxide. It is composed of several subunits, two of which, gp91^{phox} and p22^{phox}, form the membrane-bound cytochrome *b*₅₅₈, while its three cytosolic components, p47^{phox}, p67^{phox} and p40^{phox}, have to translocate to the membrane upon activation. This is a tightly and intricately controlled process that involves, among others, several low-molecular weight GTP-binding proteins. Gp91^{phox} is encoded on the X-chromosome and p22^{phox}, p47^{phox} and p67^{phox} on different autosomal chromosomes, and a defect in one of these components leads to CGD. This explains the variable mode of inheritance seen in this syndrome.

Clinically CGD manifests itself typically already at a very young age with recurrent and serious infections, most often caused by catalase-positive pathogens.

Modern treatment options, including prophylaxis with trimethoprim-sulfamethoxazole and rIFN- γ as well as early and aggressive anti-infection therapy, have improved the prognosis of this disease dramatically.

CGD, as a very well-characterized inherited affection of the hematopoietic stem cells, is predestined to be among the first diseases to profit from the advances in cutting-edge therapeutics, such as gene therapy and in utero stem cell transplantation.

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