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A HUNDRED YEARS OF NARCOLEPSY RESEARCH

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THE EMERGENCE OF A CLINICAL SYNDROME

The first convincing descriptions of narcolepsy-cataplexy were reported in German by Westphal (1877) (100) and Fisher (1878) (25). The unique association of episodes of muscle weakness triggered by excitement and sleepiness were described in these two reports. In both cases, hereditary factors were noted, with the mother of Westphal's patient and one sister of Fisher's patient presenting narcolepsy symptoms. The leading hypothesis to explain narcolepsy at the time was to refer to the well publicized case of von Zastrow. Von Zastrow was a recently arrested pathological rapist widely believed to experience pathological sleepiness as a result of repressed homosexuality and excessive masturbation.

Gélineau (1880) (28, 29) is widely recognized for giving narcolepsy its name and for recognizing the disorder as a specific clinical entity. His description of a wine cask maker with narcolepsy in la Gazette des hôpitaux de Paris was classical but Gélineau did not strictly differentiate muscle weakness episodes and sleep attacks triggered by emotions. Rather, Gelineau suggested a common physiology for these two symptoms. Loëwenfeld (1902), was the first to give a name to muscle weakness episodes triggered by emotions "cataplexy" (53).

The 1917-1927 epidemic of encephalitis lethargica led to a renewed interest in narcolepsy and sleep research but also added much confusion to the nosological definition of narcolepsy. Encephalitis lethargica often presented initially with somnolence and the term "narcolepsy" was often used to describe any form of daytime sleepiness. The association of somnolence and occulomotor paralysis also led to the pioneer work of Von Economo (1930) and the recognition of the posterior hypothalamus as a critical region for the promotion of wakefulness (98). In fact, Von Economo should be credited as being one of the first investigators to correctly propose that a region in the posterior hypothalamus was lesioned in human narcolepsy. In 1930, he wrote: "it is very probable, though not proved, that the narcolepsy of Gelineau, Westphal and Redlich has its primary cause in an yet unknown disease of that region" (98). As narcolepsy with cataplexy was also observed in some cases of encephalitis lethargica, clinicians long debated the existence of idiopathic narcolepsy and the importance of cataplexy for defining the clinical entity. Large case series of narcolepsy-cataplexy were reported by Addie (1926) (1), Wilson (1927) (101) and Daniels (1934) (17). The review by Daniels is considered by many as one of the most insightful clinical reviews published to this date. Further work at the Mayo Clinic, by Yoss and Daly (103) and in Prague by Bedrich Roth (91), then led to the classic description of the narcolepsy tetrad.

typed at the HLA-DR level were HLA-DR2 positive, when compared to 30% in controls (37, 38, 42). This discovery was quickly confirmed by British (49), German (75), French (11) and Canadian (86) investigators.

As most HLA associated disorder are autoimmune in nature, this discovery led to the hypothesis that human narcolepsy too was an autoimmune disorder (14, 68, 83). This possibility was addressed by Matsuki (58), Frederikson (27) and Rubin (92) but all results were negative, leading Matsuki to conclude "Narcolepsy is not an autoimmune disease" (58). The possibility that HLA-DR2 was only a linkage marker for another, non-immune related, narcolepsy gene located within the HLA complex was suggested ("the sleep gene hypothesis") (58). The existence of non-HLA-DR2 positive patients with narcolepsy was hotly debated, with Dr. Honda stressing the importance of carefully defining cataplexy to diagnose narcolepsy (30, 57). The finding that African-American narcoleptic patients were frequently DR2 negative added to the confusion (77).

Further studies in African-Americans showed that the HLA association was tighter with another HLA gene allele, HLA-DQB1*0602 (56, 61, 62, 63). HLA-DQB1 is another polymorphic HLA class II gene located very close to HLA-DRB1 on human chromosome 6 (6p21). This observation explained the lower association reported with HLA-DR2 in African- American patients by Neely et al. (77) but did not explain the rare reports of HLA-DR2 and DQB1*0602 negative cataplectic patients by other clinicians (6, 30, 31, 62, 64, 95).

Investigators continued to search for potential narcolepsy genes in the Major Histocompatibility complex (MHC) region. Genomic sequencing studies in the HLA-DQ region indicated that no other expressed genes were present in the narcolepsy susceptibility region (23). Complex HLA-DQ genetic effects, with HLA-DQB1*0602 homozygotes (84) and DQB1*0602/DQB1*0301 (65) carrying the highest relative risks for narcolepsy susceptibility were reported. These data, paralleling those observed in other HLA associated diseases, suggested that HLA-DQ itself rather than an unknown gene in the MHC region was the susceptibility gene. Even using the improved DQB1*0602 genetic marker, however, a few cataplectic patients without the marker were reported (6, 30, 31, 62, 64, 95) suggesting possible heterogeneity in the etiology of narcolepsy. The high frequency of HLA-DQB1*0602 in the general population (12-38%, depending on the ethnic group) (61), also indicated that factors other than HLA-DQ had to be involved to produce narcolepsy in most cases.

POSITIONAL CLONING STUDIES IN NARCOLEPSY

In the early part of the century, human narcolepsy was frequently believed to be a familial disorder. More recent studies have shown that human narcolepsy is not a simple genetic disorder. Monozygotic twins are most frequently discordant for narcolepsy, indicating environmental factors in narcolepsy susceptibility (70). In fact, familial clustering of narcolepsy-cataplexy is the exception rather than the

rule. Only 1-2% of first degree relatives of patients with narcolepsy have narcolepsy-cataplexy (10, 31, 36, 70). This indicates a 20-40 fold increased relative risk when compared to the general population (70).

The complex picture in human narcolepsy led us to focus our genetic work in canines. In contrast to the human situation, narcolepsy is a simple autosomal recessive disorder in Dobermans and Labradors (26) thus making positional cloning theoretically possible in this species. Backcrosses were carried out and a genetic linkage study initiated in 1989. Our first focus was to exclude potential candidate genes. Canine narcolepsy was shown not to be associated (19, 74) or tightly linked with Dog Leukocyte Antigen (DLA) polymorphisms (69). This result suggested the canine narcolepsy gene was not an MHC gene. Other candidate genes and minisatellite probes were used in a second stage. Using a candidate gene approach, a band crossreacting with the human immunoglobulin μ-switch segment on a southern blot was shown to cosegregate with canine narcolepsy in 1991 (69). This result initially suggested an immunoglobulin/immune involvement in canine narcolepsy. Further studies however demonstrated that this linkage marker was only a crossreacting sequence of no functional significance for immune system regulation (60).

Considering the relatively small number of animals tested, the actual narcolepsy gene was likely to be located at a large genetic distance from our initial μ-switch like marker. Chromosome walking in the vicinity of the identified marker was difficult using available phage and cosmid genomic libraries. These libraries have small genomic inserts and chromosome walking is very slow, if not impossible. In 1997, a large insert Bacterial Artificial Library (BAC) genomic library was built in collaboration with Dr. De Jong (50). Fluorescence In Situ Hybridization (FISH) was also established in our laboratory and the canine narcolepsy marker was found to be located on dog chromosome 12 (51). We also found that the μ-switch like marker was on the same chromosome as the Dog Leukocyte Antigen (DLA) but that both loci were at a large genomic distance from each other (51).

Chromosome walking was initiated using the newly available BAC library. In this process, high density gridded library filters are hybridized with Polymerase Chain Reaction (PCR) products derived from end BAC sequences. The new clones are then isolated, PCR tested, their end sequenced and the filters rehybridized to extend the contig. Minilibraries are prepared and screened with microsatellite repeats to develop polymorphic markers. These markers are then tested in canine backcrosses to confirm genetic linkage and map possible recombinant animals (51). BAC end sequences are also analyzed using the BLAST algorithm to identify putative known genes. In 1998, one of the BAC end sequences was shown to contain Myosin VI (MYO6), a gene known to map on the long arm of human chromosome 6 (6q13). The finding that both DLA and MYO6 were on the same dog and human chromosomes led us to suspect a large region of conserved synteny between dog chromosome 12 and human chromosome 6. This result was a turning point as it gave us direct access to the human and mouse maps in the region. Human Expressed Sequenced Tags (ESTs) known to map between MHC and MYO6 on the

human map were then used as probes to screen the canine BAC library. The resulting canine BAC clones were then hybridized on canine metaphase spreads to verify localization onto dog chromosome 12 (51). Together with chromosome walking and microsatellite marker development and genetic testing in backcrosses, the process was refined until the canine narcolepsy gene was flanked in a small genetic segment known to contain only two potential genes. These two genes were tested for potential abnormalities and an abnormal hybridization pattern observed with one of the two ESTs, the hypocretin receptor 2 gene (Hcrtr2) (51). Further analysis then demonstrated that in both Labradors and Dobermans with autosomal recessive narcolepsy, the hypocretin receptor transcripts were disrupted by distinct exon splicing mutations (51). This report was the first to implicate hypocretins in the cause of canine narcolepsy.

HYPOCRETINS, OREXINS AND THEIR RECEPTORS

Hypocretins/orexins were identified almost simultaneously by DeLecea (18) and Sakurai (93) in 1998. DeLecea et al. identified the preprohypocretin transcript using a directional tag PCR substraction technique (18). Their aim was to identify novel hypothalamic specific transcripts. The identified hypocretin clone was shown to be only expressed in the lateral hypothalamus and to encode a precursor molecule for two related peptides having a possible homology with secretin (this weak homology is disputed by others). Based on the preferential expression of the gene in the lateral hypothalamus and their homology with the gut hormone secretin, the peptides were called hypocretin-1 and 2 by DeLecea (18), who also demonstrated neuroexcitatory properties for hypocretin-2 and suggested a possible role in feeding regulation based on the neuroanatomical localization in the lateral hypothalamus.

The existence of hypocretins was independently confirmed by Sakurai a few weeks later (93). These authors also identified and mapped two receptors for these peptides (Hcrtr1 and Hcrtr2). In this elegant work, a series of orphan G-Protein coupled receptors (e.g., receptor genes having no identified endogenous ligand identified) were expressed in cell lines (the "orphanage") and the resulting cell lines used to screen High Pressure Liquid Chromatography (HPLC) purified tissue fractions for biological activity (93). Cell lines containing the orphan receptor HFGAN72 (later shown to be the hypocretin receptor-1) were found to strongly react with purified brain fractions. These fractions were shown to evoke a calcium transient, suggesting activation of the G-Protein coupled receptor by an endogenous ligand. The resulting activity was purified and shown to be a 33 amino acid peptide that Sakurai et al. called orexin-A (93). Another weaker activity was also isolated and shown to be a 28 aminoacid sharing 13/28 aminoacid identity with orexin-A; this second peptide was called orexin-B (92). Both peptides were then shown to be processed from the same precursor, a transcript identical to DeLecea's previously reported preprohypocretin mRNA molecule (18). Hypocretin-1 and 2 and Orexin-A and B are thus identical with the caveat that DeLecea reported a 6 amino acid longer sequence for hypocretin-1versus orexin-A. The latter author

mentioned that the N-terminal of the hypocretin-1 peptide could not yet be established at the time (18). Sakurai et al. (93), also noted that hypocretin-2/orexin-B had a lower affinity for the hypocretin receptor-1 and found that another unknown EST had high nucleotide homology with HFGAN2. This receptor was expressed in CHO cell lines and was shown to bind and mobilize calcium in the presence of hypocretin-1 and 2. This second receptor was called the Orexin receptor 2 (officially called the hypocretin receptor-2).

The discrete localization of these peptides in the lateral hypothalamus suggested a role for hypocretins in feeding behavior. In their initial publication, Sakurai (93) reported a stimulation of feeding after central administration of hypocretins/orexins and an increased preprohypocretin mRNA expression after fasting. The authors speculated that a main physiological function for these molecules could thus be the regulation of energy homeostasis (93). Further work indicated more minor and variable effects on feeding (22, 33, 40, 54, 96, 102). Neuroanatomical work indicating widespread projections for hypocretin neurons also suggested more complex physiological functions (76, 85). Of note, dense projections to monoaminergic cell groups such as the locus coeruleus suggested a possible involvement in sleep regulation (39). In 1999, a few weeks after canine narcolepsy was shown to be due to hypocretin receptor mutations, a knockout mouse for the preprohypocretin gene was generated and shown to have sleep abnormalities reminiscent of narcolepsy (16), thus independently suggesting a role for hypocretin in the sleep disorder.

HYPOCRETINS IN HUMAN NARCOLEPSY

The potential role of hypocretins in the human disorder is still under investigation. Hypocretin-1 levels were measured in the cerebrospinal fluid of 9 narcoleptic subjects and 8 controls by Nishino et al. (81). Seven narcoleptic subjects were found to have undetectable hypocretin-1 levels. Two narcoleptic patient had normal and very elevated levels of hypocretin-1 respectively. Hypocretin-1 levels were detectable in all controls. This result suggests that human narcolepsy is caused by a deficiency in hypocretin production (81). A simple explanation might be that hypocretin producing cells are destroyed by an autoimmune process in HLA-associated narcolepsy. Only a few thousand cells in the hypothalamus produce hypocretins and a discrete lesion in this area might not have been detected in previous neuropathological studies.

PERSPECTIVES

The observation that human narcolepsy is associated with low/absent hypocretin levels opens novel therapeutic and diagnostic perspectives. Measuring hypocretin levels in the CSF might become a standard diagnostic procedure. Hypocretin levels are undetectable in plasma using current technology but the existence of hypocretin

Table 1. - *A few milestones in narcolepsy research and therapy.*

1877	First description in the medical literature (100)
1880	Gelineau called the disorder "narcolepsy" (28)
1902	Loewenfeld coined the term "cataplexy" (53)
1935	First use of amphetamines in the treatment of narcolepsy (87)
1960	Description of Sleep Onset REM periods in a narcoleptic subject (99)
1970	Description of the Multiple Latency Test (15, 90)
1973	First report of a narcoleptic dog (47, 72)
1983	Association of narcolepsy with HLA-DR2 (37)
1985	Monoaminergic and cholinergic imbalance in narcolepsy (7, 80)
1992	Association of narcolepsy with HLA-DQB1*0602 (56, 63)
1998	Identification of hypocretins/orexins and their receptors (18, 93)
1999	Hypocretin mutations cause narcolepsy in mice and dogs (16, 51)
2000	Human narcolepsy is also associated with an hypocretin deficiency (81)

and receptors in the gut (45) and on the adrenal medulla (52) suggests that very low levels might be circulating in the periphery. These could one day be measured. Novel therapies are also likely to be developed. Hypocretin-1 has recently been shown to promote wakefulness *in vivo* (32). Hypocretin receptors are probably functional in most cases of human narcolepsy. It might thus be possible to administer analogues or receptor agonists to supplement a deficient hypocretin neurotransmission. Hypocretin antagonists might also have desirable hypnotic properties.

The finding that hypocretins are centrally involved in narcolepsy also opens new research avenues in basic sleep research. The excitatory neurotransmitter system is uniquely positioned at the neuroanatomical level to modulate aminergic and cholinergic transmission. Some of these projections are likely to be more important than others and a challenge of the next decade will be to establish functional relevance. The respective role of Hcrtr1 and Hcrtr2 (97) and the relationship with reported neuronal degeneration in the basal forebrain and the amygdala of narcoleptic dogs (94) also needs further clarification. Narcolepsy being primarily characterized by disrupted sleep state organization, hypocretin cells might be critical coordinators of the sleep cycle via their monoaminergic projections.

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