

TAXONOMIC STRUCTURE OF POWERFUL TRACTION ASYNCHRONOUS MOTORS CLASS

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Introduction. At present, problems of creating efficient energy converters, optimizing parameters and operating modes of traction asynchronous motors are not completely solved. Further study and improvement of the methods of analysis of electromagnetic and thermal processes in such modes as start-up, acceleration, locking and braking will be required. Current problems are the creation of new methods and algorithms for optimal control of the traction engine and protection of electrical equipment against overload. The three-phase asynchronous regulated electric drive is now becoming a standard element on modern trunk, city and suburban electric transport. Almost all new motor-car electric trains in the leading countries of Europe and Asia are equipped with three-phase regulated asynchronous motors [1]. Structural and system studies of the specified classes of EM systems are directly related to the construction of their taxonomy, the formulation of which task in relation to the classes of electromechanical objects became possible on the basis of the fundamental provisions of the genetic theory of evolution of electromechanical systems developed at the Department of Electromechanics KPI them. Igor Sikorsky [2]. The correct formulation of the task of constructing the taxonomy of arbitrary functional classes of EM systems requires solving a number of problems fundamental to structural and system research: identification and analysis of genetic information of known representatives of the studied classes, determination of genetic programs at the level of species, genera and homologous series, identification of innovation potential and structure subordination of taxonomic units [2, 3].

The aim of the work. The purpose of this research is to develop and construct a taxonomic structure of the genetic systematics of powerful frequency-regulated traction asynchronous motors (TAM) class intended for use in modern vehicles, in particular in universal locomotives of a new generation taking into account basic species and twin species.

Materials of research. The purpose is achieved by involving the most advanced methods of development and research in the field of electromechanics, in particular, methodological developments in the field of structural and system research. Based on the results of the definition and decoding of the genetic program of the class of powerful traction asynchronous motors, carried out under the following restrictions: 1) the search is carried out within the first large period of the Genetic Classification; 2) the functional TAM class is represented by two subclasses that implement rotational and progressive spatial motions; 3) isotopes of group 0.0 are not considered due to the marginal complexity of spatial configurations of parent chromosomes; 4) sources-isotopes of groups 0.2, 2.0 and 2.2 are limited to spatial variants that are subject to technical

implementation; 5) does not take into account chromosomes with a two-sided active zone, which create inverse running or rotating fields; 6) the hybrid and combined structures of traction asynchronous motors are not considered, the initial information for the construction of the taxonomic structure of the investigated class is determined.

The type of spatial movement in the structure of the genome is determined by a combination of two genetic features: the spatial shape and orientation of the primary source of the field. The task of determining the subfields Q_{RM} and Q_{PM} reduces to the problem of determining the structure of the genome of the basic species and twin species of the class of traction asynchronous motors, whose chromosomal sets are endowed with a genetic property to implement rotational and translational spatial motions.

Taking into account the target search function and imposed restrictions, within the limits of five geometric classes (CL, KN, TP, SF, TC), the genome of the studied class with rotational motion is determined (in genetic codes) by the following chromosomal sets

$$F_{CL} = \mathbf{CL 0.0y}, \mathbf{CL 0.2y}, \mathbf{CL 0.2y_3}, \mathbf{CL 2.0x_2}, \mathbf{CL 2.2y}, \mathbf{CL 2.2y_2}, \quad (1)$$

$$F_{KN} = \mathbf{KN 0.0y}, \mathbf{KN 0.2y}, \mathbf{KN 0.2y_3}, \mathbf{KN 2.0x_2}, \mathbf{KN 2.2y}, \mathbf{KN 2.2y_2}, \quad (2)$$

$$F_{TP} = \mathbf{TP 0.0y}, \mathbf{TP 0.2y}, \mathbf{TP 0.2y_3}, \mathbf{TP 2.0x_2}, \mathbf{TP 2.2y}, \mathbf{TP 2.2y_2}, \quad (3)$$

$$F_{SF} = \mathbf{SF 0.0y}, \mathbf{SF 0.2y}, \mathbf{SF 0.2y_3}, \mathbf{SF 2.0x_2}, \quad (4)$$

$$\mathbf{SF 2.2y}, \mathbf{SF 2.2x}, \mathbf{SF 2.2y_2}, \mathbf{SF 2.2x_1},$$

$$F_{TC} = \mathbf{TC 0.0y}, \mathbf{TC 0.2y}, \mathbf{TC 0.2y_3}, \mathbf{TC 2.0x_2}, \mathbf{TC 2.2y}, \mathbf{TC 2.2y_2}. \quad (5)$$

Within the two geometric classes of cylindrical and plane spatial forms, we similarly define the structure of the genome of the traction asynchronous motors of progressive motion

$$G_{CL*} = \mathbf{CL 2.0x_1}, \mathbf{CL 2.2x}, \mathbf{CL 2.2x_1}, \quad (6)$$

$$G_{PL*} = \mathbf{PL 0.0y}, \mathbf{PL 2.0x}, \mathbf{PL 2.0x_1}, \mathbf{PL 2.2x}, \mathbf{PL 2.2y}, \mathbf{PL 2.2x_1}. \quad (7)$$

The expressions (1–7) in bold type indicate the genetic codes of the chromosomes of the basic level, and in italics (with the presence of lower digital indexes) – the codes of paired chromosomes-isotopes. Recent types of electromagnetic chromosomes are determined by the genome of twin species. Sources-isotopes, due to their non-traditional spatial forms, at this stage of evolution, largely determine the unclaimed structural potential of implicit classes of asynchronous traction engines, endowed with the inherent soleity of their individuality.

Thus, the desired genetic program Q of the class of the traction asynchronous motors is determined by the structure of the genome (chromosome level), which corresponds to the two functional subclasses Q_{RM} and Q_{PM} (species level), differing in the species composition and the nature of the spatial motion of the moving part

$$Q = Q_{RM} + Q_{PM}, \quad (8)$$

$$Q_{RM} = (G_{CL}, G_{KN}, G_{TP}, G_{SF}, G_{TC}) \square S_0, \quad (9)$$

$$Q_{PM} = (G_{CL*}, G_{PL*}) \square S_0. \quad (10)$$

According to the results of genomic studies, it was found that the species diversity of the class is determined by the finite set of paired chromosomes. The chromosomal set of the studied class is determined by 19 chromosomes of the base level and 20

chromosomes of isotopic origin. This means that, at the species level, the type structure of the class of traction asynchronous motors will be determined by 19 basic species and 20 twin species (Fig. 1).

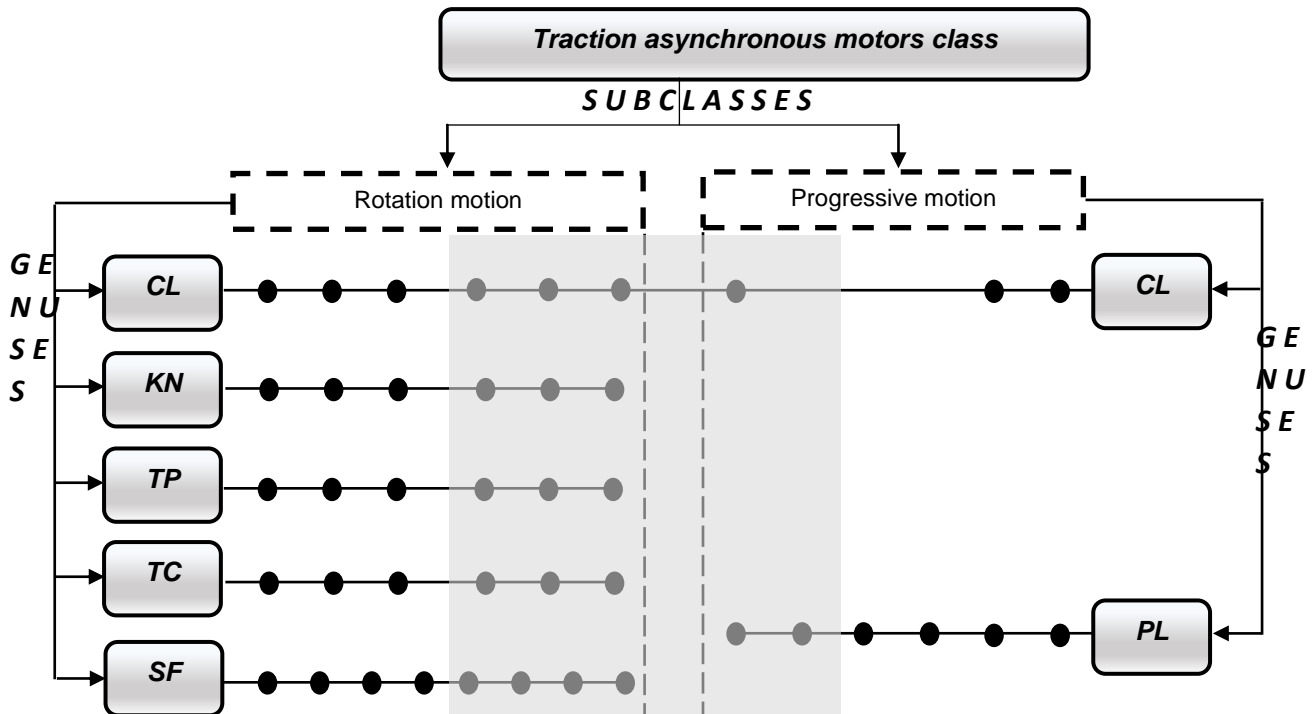


Figure 1 – Taxonomic structure of the traction asynchronous motors class (twin species are shown on a darkened background)

Conclusions. By the nature of the spatial movement of the moving part, the class is divided into two separate subclasses: with a rotary (31 species) and progressive motion (8 species). By the presence of species in the corresponding geometric classes, identified by the corresponding genetic codes, uniquely determined their distribution by 6 genres. The presence of such system information allows us to determine the rank structure of super-visible systematic units. The results of the genetics system constitute the systemic and informational basis for the development of the intraspecific taxonomy of the class, as well as for the development of further systemic research and the organization of knowledge about the studied class of traction asynchronous motors.

References

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